

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:06:00 ; Search time 188.365 Seconds
(without alignments)
4355.452 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

Sequence: 1 MLPRVPRCVTPPLRGSR.....KDTLSLGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 23Sep04:*

1: geneseq1980s:*

2: geneseq1990s:*

3: geneseq2000s:*

4: geneseq2001s:*

5: geneseq2002s:*

6: geneseq2003as:*

7: geneseq2003bs:*

8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	12028	100.0	2287	4	AAB66475	Aab66475 Rat alpha
2	11657	96.9	2254	2	AAU14590	Aay14590 Rat T-typ
3	11626	96.7	2272	2	AAU14592	Aay14592 Rat T-typ
4	11610.5	96.5	2265	2	AAU14591	Aay14591 Rat T-typ
5	11606.5	96.5	2247	2	AAU14593	Aay14593 Rat T-typ
6	11542.5	96.0	2428	3	AAU70720	Aay70720 Rat pancr
7	10857	90.3	2250	2	AAU14586	Aay14586 Human T-t
8	10833	90.1	2268	2	AAU14588	Aay14588 Human T-t
9	10820.5	90.0	2273	4	AAE01019	Aae01019 Human T-t
10	10810.5	89.9	2261	2	AAU14589	Aay14589 Human T-t
11	10806.5	89.8	2243	2	AAU14587	Aay14587 Human T-t
12	10806.5	89.8	2243	7	ADJ68819	Adj68819 Human hea
13	10533	87.6	2266	4	AAB66481	Aab66481 Human alp
14	6226.5	51.8	2359	4	AAB66476	Aab66476 Rat alpha
15	6222	51.7	2353	2	AAY06299	Aay06299 Human act
16	6222	51.7	2353	6	ABP72254	Abp72254 Human T-t
17	6222	51.7	2353	7	ADJ69322	Adj69322 Human hea
18	6221	51.7	2353	2	AAU06298	Aay06298 Human hea
19	6195.5	51.5	2353	5	ABG30840	Abg30840 Human vol
20	5872	48.8	1207	4	AAU00474	Aau00474 Human T-t
21	5835	48.5	2044	2	AAU14594	Aay14594 Human T-t
22	5827	48.4	2038	2	AAU14595	Aay14595 Human T-t
23	5718.5	47.5	2034	2	AAU06300	Aay06300 Human act
24	5409	45.0	2175	5	AU10535	Au10535 Human T-t
25	5409	45.0	2175	6	ABU08511	Abu08511 Human T-t

ALIGNMENTS

RESULT 1

AAB66475

ID AAB66475 standard; protein; 2287 AA.

XX AC AAB66475;

XX XX

DT 09-APR-2001 (first entry)

XX XX

DE Rat alpha-IG calcium channel protein.

XX XX

Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;

hypotensive; cardiac; nootropic; T-type calcium channel subunit;

cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;

epilepsy; alpha-IG calcium channel.

XX OS Rattus sp.

XX XX

PN WO200102561-A2.

XX PD 11-JAN-2001.

XX PF 04-JUL-2000; 2000WO-CA000794.

XX XX

PR 02-JUL-1999; 99US-00346794.

XX XX

PA (NEUR-) NEUROMED TECHNOLOGIES INC.

XX XX

PI Snutch TP, Baillie DL;

XX XX

DR WPI; 2001-123111/13.

XX XX

DR N-PSDB; AAF31677.

XX XX

PT Novel T-type calcium channel alpha-1 subunit gene useful for treating

cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and

epilepsy.

XX XX

PS Disclosure; Page 63-72; 103pp; English.

XX XX

CC The present sequence is given in a specification providing sequences and

partial sequences for three types of mammalian (human and rat) T-type

calcium channel subunits. An expression cassette has been generated which

comprises a nucleotide sequence encoding a T-type calcium channel alpha_1

subunit operably linked to control sequences to effect its expression.

CC The novel calcium channel nucleic acids and proteins are useful for

treating conditions characterised by undesirable levels of T-type calcium

channel activity such as cardiac hypertrophy, cardiac arrhythmia,

hypertension, sleep disorder and epilepsy

XX XX

Adh69265 Human TCC
Asu10536 Human T-t
Abu08512 Human T-t
Adh69267 Human TCC
Aay14597 Rat T-typ
Adh69268 Rat T-typ
Aay14596 Human T-t
Aab66477 Rat brain
Aam23743 Human EST
Aaw79161 Human cal
Aab66472 Protein e
Abb60448 Drosophil
Aab66478 Human alp
Abg10954 Novel hum
Aam93437 Human pol
Ad131041 Human pro
Aab66479 Human alp
Aar33549 Sequence
Adm31026 Human cal
Aay31809 N-type Ca

QY 2101 IRLPAPCGLEPSWAKPPETRSSLELDTELWISGDLPLSSQEBELFPRDLKCKYSVET 2160
 Db 2101 IRLPAPCGLEPSWAKPPETRSSLELDTELWISGDLPLSSQEBELFPRDLKCKYSVET 2160
 QY 2161 QSCRRPFGWLDQRRHSIAVCLSGSGQPRLCPSPSLGGQPLGGPGSRPKKLSPPSI 2220
 Db 2161 QSCRRPFGWLDQRRHSIAVCLSGSGQPRLCPSPSLGGQPLGGPGSRPKKLSPPSI 2220
 QY 2221 SIDPPESQSRPPCPGVCRLRRAPASQKPSVSLDSTAASPKKDTLSLGLSSD 2280
 Db 2221 SIDPPESQSRPPCPGVCRLRRAPASQKPSVSLDSTAASPKKDTLSLGLSSD 2280
 QY 2281 PTMDPZ 2287
 Db 2281 PTMDPZ 2287

RESULT 2

AA14590
 ID AA14590 standard; protein; 2254 AA.

XX
 AC AA14590;

XX 07-DEC-1999 (first entry)

XX Rat T-type voltage-gated Ca channel alpha-1-G (rCavTla).

DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
 KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
 XX

OS Rattus sp.

XX WO929847-A1.

XX 17-JUN-1999.

PD 30-OCT-1998; 98WO-US023161.

PF 05-DEC-1997; 97US-00985809.

XX (LOYO) UNIV LOYOLA CHICAGO.

XX Perez-Reyes E, Cribbs LL;

XX WPI; 1999-394972/33.

XX N-PSDB; AAX83485.

XX New T-type voltage-gated calcium channels.
 XX Disclosure; Page 67-76; 138pp; English.

XX This sequence represents a rat T-type voltage-gated calcium (Ca) channel
 CC alpha-1-G designated rCavTla. Voltage gated channels are membrane bound
 CC glycosylated proteins formed of several subunits. The large alpha
 CC subunits form a pore in the membrane that is selective for a given ionic
 CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
 CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
 CC -type Ca channels are activated at a lower voltage than L- or N-type
 CC channels. Characteristics of T-type channels include short current time,
 CC slow activation kinetics near threshold, fast inactivation kinetics and
 CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
 CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
 CC channels contains a putative IVS4 region comprising the amino acid
 CC sequence AA14598. Cells expressing the T-type voltage-gated calcium
 CC channel proteins can be used to screen for drugs which affect calcium
 CC channels. Methods are also disclosed for treating a disease or disorder
 CC associated with a deficiency in a native T-type calcium channel nucleic
 CC acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX Sequence 2254 AA;

Query Match 96.9%; Score 11657; DB 2; Length 2254;

Best Local Similarity 99.7%; Pred. No. 0;

	Matches	2219;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
QY	62	GAAGAGSTEKDGSDADSAEGLPYPALAPVVFYIYQDSRPSRSCWCLRTVCNFWFERVSM	121							
Db	30	GRQSGFSTEKDGSDADSAEGLPYPALAPVVFYIYQDSRPSRSCWCLRTVCNFWFERVSM	89							
QY	122	VILNLCVLTGMPFPCEDACQORCIIQAQDDFIAPFAVEMVVMKVALGFGKKCYLG	181							
Db	90	VILNLCVLTGMPFPCEDACQORCIIQAQDDFIAPFAVEMVVMKVALGFGKKCYLG	149							
QY	182	DTWNRDLFFVIAGMLYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTLP	241							
Db	150	DTWNRDLFFVIAGMLYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTLP	209							
QY	242	MLGNVLLLCFFVFFIFGIVGVOLWAGLLNRNCFLENFSLPLSVLEPYQYTENDESPFF	301							
Db	210	MLGNVLLLCFFVFFIFGIVGVOLWAGLLNRNCFLENFSLPLSVLEPYQYTENDESPFF	269							
QY	302	ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLDYETVNSSTNTTCVNWQYVTCNSAGEHN	361							
Db	270	ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLDYETVNSSTNTTCVNWQYVTCNSAGEHN	329							
QY	362	PFKGAINFDNIGYAWIAIFQVITLLEGWVDIMYFVMDAHSFYNIYFILLIIVGSPFMINL	421							
Db	330	PFKGAINFDNIGYAWIAIFQVITLLEGWVDIMYFVMDAHSFYNIYFILLIIVGSPFMINL	389							
QY	422	CLVVIATQFSETKQRESQIMREQVRPLSNASTLASFSEPGSCYBELLYLVLIRKAAR	481							
Db	390	CLVVIATQFSETKQRESQIMREQVRPLSNASTLASFSEPGSCYBELLYLVLIRKAAR	449							
QY	482	RLAQVSRAGVRAIGLLSPVARSQEPQSGCTSHRRLSVHHLVHHHHHHHHHHLGN	541							
Db	450	RLAQVSRAGVRAIGLLSPVARSQEPQSGCTSHRRLSVHHLVHHHHHHHHHHLGN	509							
QY	542	GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPPSGGPRGAESVHSFYHADCHLEPVRQ	601							
Db	510	GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPPSGGPRGAESVHSFYHADCHLEPVRQ	569							
QY	602	APPRCPSEASGRVTGSGKVPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNTPGPF	661							
Db	570	APPRCPSEASGRVTGSGKVPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNTPGPF	629							
QY	662	SSMHKLETSQTGACHSSCKISSPCSKADSGACGDCPCYARTGAGPESADHWMPDSD	721							
Db	630	SSMHKLETSQTGACHSSCKISSPCSKADSGACGDCPCYARTGAGPESADHWMPDSD	689							
QY	722	SEAVVEFTQDAQHSDLRDPHRRRQSRSLGPDAPESVLAFLWRLICDTRFKIVDSKYFGRG	781							
Db	690	SEAVVEFTQDAQHSDLRDPHRRRQSRSLGPDAPESVLAFLWRLICDTRFKIVDSKYFGRG	749							
QY	782	IMAILVNTLSMGIEYHQPELTNALBISNIVFTSLFALEMLKLLVYGPFGYTKNPYN	841							
Db	750	IMAILVNTLSMGIEYHQPELTNALBISNIVFTSLFALEMLKLLVYGPFGYTKNPYN	809							
QY	842	IFDGVIVVISWEIVGQGGGLSVLRTFLMRVLKLVFLPALQRLVLMKTDNDNVATF	901							
Db	810	IFDGVIVVISWEIVGQGGGLSVLRTFLMRVLKLVFLPALQRLVLMKTDNDNVATF	869							
QY	902	CMLMLFFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILITQEDWNKV	961							
Db	870	CMLMLFFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILITQEDWNKV	929							
QY	962	LYNGMASTSSWAALFYFALMTFGNYVLPNLLVALVVGQFQAGDATKSESPDFPSVD	1021							
Db	930	LYNGMASTSSWAALFYFALMTFGNYVLPNLLVALVVGQFQAGDATKSESPDFPSVD	989							
QY	1022	GDGRKKRLALVAIHAELKSLPLLIHTAATPMHSHPKSSSTGYCEALGSSSRRTSS	1081							
Db	990	GDGRKKRLALVAIHAELKSLPLLIHTAATPMHSHPKSSSTGYCEALGSSSRRTSS	1049							
QY	1082	SGSAEPGAAHHEMKCPPSARSSPHSPWSAASWTSSRRSSRLGRAPSLKRSPSGERRS	1141							
Db	1050	SGSAEPGAAHHEMKCPPSARSSPHSPWSAASWTSSRRSSRLGRAPSLKRSPSGERRS	1109							

QY 1142 LLSGEGQESQDEBESSEEDRASAGSDHHRGSLEREAKSSFDLPDTLQVPGGLHRTASGR 1201
DB 1110 LLSGEGQESQDEBESSEEDRASAGSDHHRGSLEREAKSSFDLPDTLQVPGGLHRTASGR 1169
QY 1202 SSASEHQDCNGKASGRARTLTDDPQDGDNDDEGNLSKGERIQAWVRSLPACCCE 1261
DB 1170 SSASEHQDCNGKASGRARTLTDDPQDGDNDDEGNLSKGERIQAWVRSLPACCCE 1229
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVLIPLNCITITAMBRPKTIDPHSABRIFL 1321
DB 1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVLIPLNCITITAMBRPKTIDPHSABRIFL 1289
QY 1322 TLSNYIFTAVFLAEMTKVVALGWCFCGEQAYLRSSWNVDGLLVLISVIDILVSMVSDSG 1381
DB 1290 TLSNYIFTAVFLAEMTKVVALGWCFCGEQAYLRSSWNVDGLLVLISVIDILVSMVSDSG 1349
QY 1382 TKILGMLRVLRILRTLRPLRVISRAOGLKLVWETLMSLSLKPIGNIVVICCAFFIIFGILG 1441
DB 1350 TKILGMLRVLRILRTLRPLRVISRAOGLKLVWETLMSLSLKPIGNIVVICCAFFIIFGILG 1409
QY 1442 VOLFKGKFFVCQGEDFRNIINKSDCAEASRYRVRHKYFNFNLGQALMSLFLVASKGQWVD 1501
DB 1410 VOLFKGKFFVCQGEDFRNIINKSDCAEASRYRVRHKYFNFNLGQALMSLFLVASKGQWVD 1469
QY 1502 IMYDGLDAGVDQOOPIMNHNPMMLLYFISPLLIVAFVFLNMFGVVVENFHKCRQOEER 1561
DB 1470 IMYDGLDAGVDQOOPIMNHNPMMLLYFISPLLIVAFVFLNMFGVVVENFHKCRQOEER 1529
QY 1562 EARRREKRLRLLEKKERSKEKMAEQAQCKPYSDYSRFRLLVHLLCTSHYLDLFIGVI 1621
DB 1530 EARRREKRLRLLEKKERSKEKMAEQAQCKPYSDYSRFRLLVHLLCTSHYLDLFIGVI 1589
QY 1622 GLNVVTMAMHYQOQILDBALKICNYIFTVIFVFSVFKLVAFAPFRFPQDRWNQDLDA 1681
DB 1590 GLNVVTMAMHYQOQILDBALKICNYIFTVIFVFSVFKLVAFAPFRFPQDRWNQDLDA 1649
QY 1682 IVLLSINGITLERIEVNLSPINPTIIRIMRVLRIRARVLKLVAGMRALLHTVMQALP 1741
DB 1650 IVLLSINGITLERIEVNLSPINPTIIRIMRVLRIRARVLKLVAGMRALLHTVMQALP 1709
QY 1742 QVGNLGLLFMLFFIFAALGVELFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTG 1801
DB 1710 QVGNLGLLFMLFFIFAALGVELFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTG 1769
QY 1802 DNNWNGIMKPSRDCDQSTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1861
DB 1770 DNNWNGIMKPSRDCDQSTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1829
QY 1862 KEAELEAELEEMKTLSPHSPPLSGPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
DB 1830 KEAELEAELEEMKTLSPHSPPLSGPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1889
QY 1922 SLEHPTMVPHEEVPVPLGPDLLTVRKSGVSRTHSLFNDSYMCNMGSTAEISLGHQWGL 1981
DB 1890 SLEHPTMVPHEEVPVPLGPDLLTVRKSGVSRTHSLFNDSYMCNMGSTAEISLGHQWGL 1949
QY 1982 PKAQSGLSVHSOPADTSCILQPKDVHLLQPHGAPTWCAIPKLPKPPGSPLAQPLR 2041
DB 1950 PKAQSGLSVHSOPADTSCILQPKDVHLLQPHGAPTWCAIPKLPKPPGSPLAQPLR 2009
QY 2042 RQAARTDSLDOVLGSRREDLLSVSPGSCPLTRSSSFWGSSITQVQORSGIQSKVSKHI 2101
DB 2010 RQAARTDSLDOVLGSRREDLLSVSPGSCPLTRSSSFWGSSITQVQORSGIQSKVSKHI 2069
QY 2102 RLPAPCGLEFSWAKDPETRSLSLELDTLSWISGDLPLPSQEBEPLPRDLKKCYVETQ 2161
DB 2070 RLPAPCGLEFSWAKDPETRSLSLELDTLSWISGDLPLPSQEBEPLPRDLKKCYVETQ 2129
QY 2162 SCRPRPGFWLDEQRHSTAVSLGSGOPRLCPSPSISGGOPLGSGSRPKKLSPPSIS 2221
DB 2130 SCRPRPGFWLDEQRHSTAVSLGSGOPRLCPSPSISGGOPLGSGSRPKKLSPPSIS 2189

QY 2222 IDPPESQGRPPCSPGVCLRRRAPASDSKDPVSPLDSTAASPSPKKDTLSLSGLSSDP 2281
DB 2190 IDPPESQGRPPCSPGVCLRRRAPASDSKDPVSPLDSTAASPSPKKDTLSLSGLSSDP 2249
QY 2282 TMDP 2286
DB 2250 TMDP 2254
RESULT 3
AAV14592
ID AAY14592 standard; protein; 2272 AA.
XX
AC AAY14592;
XX 07-DEC-1999 (first entry)
XX Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1c).
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX Rattus sp.
OS
XX WO9929847-A1.
PN
XX
XX 17-JUN-1999.
XX
XX 30-OCT-1998; 98WO-US023161.
PF
XX
XX 05-DEC-1997; 97US-00985809.
PR
XX
XX (LOYO) UNIV LOYOLA CHICAGO.
PA
XX
XX Perez-Reyes E, Cribbs LL;
PI
XX
XX WPI; 1999-394972/33.
DR
XX
XX N-PSDB; AAX83487.
PT New T-type voltage-gated calcium channels.
XX
XX Disclosure; Page 85-94; 138pp; English.
XX
XX This sequence represents a rat T-type voltage-gated calcium (Ca) channel
XX alpha-1-G designated rCavT1c. Voltage gated channels are membrane bound
XX glycosylated proteins formed of several subunits. The large alpha
XX subunits form a pore in the membrane that is selective for a given ionic
XX species. Each alpha subunit contains 4 domains (I, II, III and IV) and
XX each domain contains 6 putative transmembrane helical segments (S1-S6). T
XX -type Ca channels are activated at a lower voltage than L- or N-type
XX channels. Characteristics of T-type channels include short current time,
XX slow activation kinetics near threshold, fast inactivation kinetics and
XX voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
XX channels contains a putative IVS4 region comprising the amino acid
XX sequence AAY14598. Cells expressing the T-type voltage-gated calcium
XX channel proteins can be used to screen for drugs which affect calcium
XX channels. Methods are also disclosed for treating a disease or disorder
XX associated with a deficiency in a native T-type calcium channel nucleic
XX acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 2272 AA;
Query Match 96.7%; Score 11626; DB 2; Length 2272;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 221; Conservative 0; Mismatches 8; Indels 18; Gaps 1;
QY 62 GAAGAGSTKDPGSADSEAGLPYALAPVVFYLSQDSRPSRCLRTVCNPFERSVML 121
DB 30 GRQFGSTKDPGSADSEAGLPYALAPVVFYLSQDSRPSRCLRTVCNPFERSVML 89
QY 122 VILLNCVTILGMFRCEIACDSQCRILOAFDDFIFFAVEMVVMVALGFGKCYLG 181

Db 90 VILLNCVTLGMFRPCEDCIADCSQRCKILQAFDDFIFAFFAVEMVVMKVALGIFGKKCYLG 149
QY 182 DTWRNLDFEIIWAGMLEYSLDLQNVFSFSAVTVRLRLRAINRVPSMRILVTLTLLDTP 241
Db 150 DTWRNLDFEIIWAGMLEYSLDLQNVFSFSAVTVRLRLRAINRVPSMRILVTLTLLDTP 209
QY 242 MLGNVLLCCFFVFFIFGIVGQWAGLLRNRCFLPENFSPLSLVDLEPYQYQTEDESPFF 301
Db 210 MLGNVLLCCFFVFFIFGIVGQWAGLLRNRCFLPENFSPLSLVDLEPYQYQTEDESPFF 269
QY 302 ICSPRENGMSCRSVPTLRREGGGGPPCCSDIYETYNSSNTTCVNNQYVNTCSAGBN 361
Db 270 ICSPRENGMSCRSVPTLRREGGGGPPCCSDIYETYNSSNTTCVNNQYVNTCSAGBN 329
QY 362 PFKGAINFDNIYAWIAIFOVITILEGWDIMYFVMDAHSFYNFYIFILLIIVGSEFFMNL 421
Db 330 PFKGAINFDNIYAWIAIFOVITILEGWDIMYFVMDAHSFYNFYIFILLIIVGSEFFMNL 389
QY 422 CLVVIATQFSETKQESQIMREQVRFLSNASTLASFSEPGSCYBELLKYVILRKAAR 481
Db 390 CLVVIATQFSETKQESQIMREQVRFLSNASTLASFSEPGSCYBELLKYVILRKAAR 449
QY 482 RLAQVSRAIGVRAGLLSPVARSQBPPOPSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 541
Db 450 RLAQVSRAIGVRAGLLSPVARSQBPPOPSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 509
QY 542 GTLRVPASPEIQDRDANGSRRLMLPPSTTPSGPPRGAEVSHSFVHADCHLEPVRCQ 601
Db 510 GTLRVPASPEIQDRDANGSRRLMLPPSTTPSGPPRGAEVSHSFVHADCHLEPVRCQ 569
QY 602 APPPRCPSEASGRVTGSGKVPTVHTSPPEILKDKALVEVAPSPGPTLTSFNIPGPF 661
Db 570 APPPRCPSEASGRVTGSGKVPTVHTSPPEILKDKALVEVAPSPGPTLTSFNIPGPF 629
QY 662 SSMKLLTQGTGACHSCCKTSSPCSKADSGACGDPSCPYCARTGAGBPESADHVPDSD 721
Db 630 SSMKLLTQGTGACHSCCKTSSPCSKADSGACGDPSCPYCARTGAGBPESADHVPDSD 689
QY 722 SEAVVEFTQDACHDLRPHRRRQRSIGPDAEPSSVLAFWRLICDTPRKIVDSKYFGRG 781
Db 690 SEAVVEFTQDACHDLRPHRRRQRSIGPDAEPSSVLAFWRLICDTPRKIVDSKYFGRG 749
QY 782 IMIAILVNTLSMGIEYHEQPEELNALEISNIVFTSLFALEMLKLLVYGFPGVGIKNPYN 841
Db 750 IMIAILVNTLSMGIEYHEQPEELNALEISNIVFTSLFALEMLKLLVYGFPGVGIKNPYN 809
QY 842 IFDGVIVIVISWEIVGQGGGLSVLRTPRLMRVLKVRFLPALORQLVLMKTMNDVATF 901
Db 810 IFDGVIVIVISWEIVGQGGGLSVLRTPRLMRVLKVRFLPALORQLVLMKTMNDVATF 869
QY 902 CMLMLFIFIPSILGMHLFGCKFASERDGTLPDRKNFDSLILWALTIVTFQILTOEDMNKV 961
Db 870 CMLMLFIFIPSILGMHLFGCKFASERDGTLPDRKNFDSLILWALTIVTFQILTOEDMNKV 929
QY 962 LYNMGMASTSSWAALFYFIALMTFGNYVLNLLVAILVEGFQAEQDATKSESEPDFFSVD 1021
Db 930 LYNMGMASTSSWAALFYFIALMTFGNYVLNLLVAILVEGFQAEQDATKSESEPDFFSVD 989
QY 1022 GDGRKRLALVALGEHAELRKSLLPPLIIHTAATPMHSHPKSSSTGVEGALGSGSRRTSS 1081
Db 990 GDGRKRLALVALGEHAELRKSLLPPLIIHTAATPMHSHPKSSSTGVEGALGSGSRRTSS 1049
QY 1082 SGSAPGAAHHMKCPPSARSPPHSPWASASWTSRRSRNSLGRAPSLKRSPPGERS 1141
Db 1050 SGSAPGAAHHMKCPPSARSPPHSPWASASWTSRRSRNSLGRAPSLKRSPPGERS 1109
QY 1142 LLSGEGQESQDEESSEEDRASPAGEHRRHRSGLEREAKSSFDLPDITQVPLHRTASGR 1201
Db 1110 LLSGEGQESQDEESSEEDRASPAGEHRRHRSGLEREAKSSFDLPDITQVPLHRTASGR 1169
QY 1202 SSASEHQDCNGKASGRILARTLTDTPOLGDDNDDEGNLSKGERRIQAWVRSRLPACCRE 1261
Db 1170 SSASEHQDCNGKASGRILARTLTDTPOLGDDNDDEGNLSKGERRIQAWVRSRLPACCRE 1229

QY 1262 RDSWSAYIFPPQSRPRLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
Db 1230 RDSWSAYIFPPQSRPRLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289
QY 1322 TLSNYIFTAVELABMTVKVVALGWCFCGEQAVLRSSWNVDGLLVLSVIDILVSMVDSG 1381
Db 1290 TLSNYIFTAVELABMTVKVVALGWCFCGEQAVLRSSWNVDGLLVLSVIDILVSMVDSG 1349
QY 1382 TKILGMLRVLLRLTLRLPLRVISRAQGLKLVVETLMSLKPIGNIVITCCAFFIIFGILG 1441
Db 1350 TKILGMLRVLLRLTLRLPLRVISRAQGLKLVVETLMSLKPIGNIVITCCAFFIIFGILG 1409
QY 1442 VOLPKGPFVFCOGSDTRNITNKSDCAEASYRWRHRYNFDNLQALMSLFLVLASXGWD 1501
Db 1410 VOLPKGPFVFCOGSDTRNITNKSDCAEASYRWRHRYNFDNLQALMSLFLVLASXGWD 1469
QY 1502 IMYDGLDAVGVDQOPIMNHNPMMLLYFISFLIIVAFVFINNFVGVVNFHFKCRHQBE 1561
Db 1470 IMYDGLDAVGVDQOPIMNHNPMMLLYFISFLIIVAFVFINNFVGVVNFHFKCRHQBE 1529
QY 1562 BARREBKRLRLBKRSKEKQMA-----BAQCKPYYSYDSYRPFLL 1603
Db 1530 BARREBKRLRLBKRSKEKQMA-----BAQCKPYYSYDSYRPFLL 1589
QY 1604 VHLLCTSHYLDFTITGVIGLNVVTMAMEHYQOPOILDEALKICNYIFTVIFVFSVFKLV 1663
Db 1590 VHLLCTSHYLDFTITGVIGLNVVTMAMEHYQOPOILDEALKICNYIFTVIFVFSVFKLV 1649
QY 1664 AFAFRFPQDRWNQDLAIALLSIMGITLIEIYNLSIPNPTIIRIMRVLIARVLKLL 1723
Db 1650 AFAFRFPQDRWNQDLAIALLSIMGITLIEIYNLSIPNPTIIRIMRVLIARVLKLL 1709
QY 1724 KMAVGMALLHTVMQALPOVGNLGLLPMFLPFIIPALGVELFGLEDCDETHPCBGLRHA 1783
Db 1710 KMAVGMALLHTVMQALPOVGNLGLLPMFLPFIIPALGVELFGLEDCDETHPCBGLRHA 1769
QY 1784 TFRNFGMAFLTPRVSTGDNWNGIMKDPDRDCDOESTCYNTVISPFIYFVSFVLAQFVLV 1843
Db 1770 TFRNFGMAFLTPRVSTGDNWNGIMKDPDRDCDOESTCYNTVISPFIYFVSFVLAQFVLV 1829
QY 1844 NVIATVLMKHLEENKEAKEAELEAELEMKTLSPQHSPLGSPFLWPGVEGVNSTDS 1903
Db 1830 NVIATVLMKHLEENKEAKEAELEAELEMKTLSPQHSPLGSPFLWPGVEGVNSTDS 1889
QY 1904 PKGAPHTTAHIGAASGFSLEHPTVMHPBEVPVPLGPDLLTVRKSGVSRTHSLPNDSYM 1963
Db 1890 PKGAPHTTAHIGAASGFSLEHPTVMHPBEVPVPLGPDLLTVRKSGVSRTHSLPNDSYM 1949
QY 1964 CRNGSTAERSLGHKGWGLPKAQSGSILSVHSQPADTSCILQPKDVHLLQPHGAPTGA 2023
Db 1950 CRNGSTAERSLGHKGWGLPKAQSGSILSVHSQPADTSCILQPKDVHLLQPHGAPTGA 2009
QY 2024 IPLPPPCRSPLAQRPLRRQAARTDSDVQGLGSRREDLLSEVSGPCPLTRSSSFWGGS 2083
Db 2010 IPLPPPCRSPLAQRPLRRQAARTDSDVQGLGSRREDLLSEVSGPCPLTRSSSFWGGS 2069
QY 2084 SIQVQSGSGSQSKVSKHIRLPAPCPGLEPWSAKDPPETRSLDLDTLSWISGOLLPSQ 2143
Db 2070 SIQVQSGSGSQSKVSKHIRLPAPCPGLEPWSAKDPPETRSLDLDTLSWISGOLLPSQ 2129
QY 2144 EEPFLPDLKKCVSETQSCRRRPGFWLDEQRHSHIAVSCLDGSGORLCPSPSILGQOP 2203
Db 2130 EEPFLPDLKKCVSETQSCRRRPGFWLDEQRHSHIAVSCLDGSGORLCPSPSILGQOP 2189
QY 2204 LGPGSRPKKLLSPSISIDPPESQSGSRPPCSGVCVCLRRRAPASDSKDPVSSPLDSTA 2263
Db 2190 LGPGSRPKKLLSPSISIDPPESQSGSRPPCSGVCVCLRRRAPASDSKDPVSSPLDSTA 2249
QY 2264 SPSPKXDTLSLSGLSSDPTMDP 2286
Db 2250 SPSPKXDTLSLSGLSSDPTMDP 2272

RESULT 4
 AAY14591
 ID AAY14591 standard; protein; 2265 AA.
 XX AC
 XX AAY14591;
 XX AC
 XX 07-DEC-1999 (first entry)
 XX DE
 XX Rat T-type voltage-gated Ca channel alpha-1-G (rCav1b).
 XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
 KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
 XX OS
 XX Rattus sp.
 XX XX
 XX W09929847-A1.
 XX PN
 XX 17-JUN-1999.
 XX PD
 XX 30-OCT-1998; 98WO-US023161.
 XX PF
 XX 05-DEC-1997; 97US-00985809.
 XX PR
 XX (LOYO) UNIV LOYOLA CHICAGO.
 XX PA
 XX Perez-Reyes E, Cribbs LL;
 XX PI
 XX WPI; 1999-394972/33.
 XX DR
 XX N-PSDS; AAX83486.
 XX PT
 XX New T-type voltage-gated calcium channels.
 XX XX
 XX Disclosure; Page 76-85; 138pp; English.
 XX PS
 XX This sequence represents a rat T-type voltage-gated calcium (Ca) channel
 CC alpha-1-G designated rCav1b. Voltage gated channels are membrane bound
 CC glycosylated proteins formed of several subunits. The large alpha
 CC subunits form a pore in the membrane that is selective for a given ionic
 CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
 CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
 CC -type Ca channels are activated at a lower voltage than L- or N-type
 CC channels. Characteristics of T-type channels include short current time,
 CC slow activation kinetics near threshold, fast inactivation kinetics and
 CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
 CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
 CC -channels contains a putative IVS4 region comprising the amino acid
 CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
 CC channel proteins can be used to screen for drugs which affect calcium
 CC channels. Methods are also disclosed for treating a disease or disorder
 CC associated with a deficiency in a native T-type calcium channel nucleic
 CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
 XX SQ
 XX Sequence 2265 AA;
 Query Match 96.5%; Score 11610.5; DB 2; Length 2265;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 2213; Conservative 1; Mismatches 11; Indels 11; Gaps 1;
 QY 62 GAAGAGSTKDPGSADEAGSLPYPALAPVVFYLSQDSRPRWCURTCNPFERSVSM 121
 DB 30 GQQPGSTKDPGSADEAGSLPYPALAPVVFYLSQDSRPRWCURTCNPFERSVSM 89
 QY 122 VILLNCVTGLWGFPCEDICDSQRCILQAFDDPIFAFAVEMVKVWALGIFGKKCYLG 181
 DB 90 VILLNCVTGLWGFPCEDICDSQRCILQAFDDPIFAFAVEMVKVWALGIFGKKCYLG 149
 QY 182 DTWNRDLFFTVIAGMLEYSLDLQNVSFSAVTRVRLRPLRINRVPMSRILVTLTDLTP 241
 DB 150 DTWNRDLFFTVIAGMLEYSLDLQNVSFSAVTRVRLRPLRINRVPMSRILVTLTDLTP 209
 QY 242 MLGNVLLCFFVFFIFGIQVQVQLWAGLLRNRCFLPENFSLPSVDLEPPYQTEDESPF 301

DB 210 MLGNVLLCFFVFFIFGIQVQVQLWAGLLRNRCFLPENFSLPSVDLEPPYQTEDESPF 269
 QY 302 ICSQPRENCRSCRSVPTLRGGGGPPCGLDYETVNSSTNTTCVNWNQYYTNCSSAGEHN 361
 DB 270 ICSQPRENCRSCRSVPTLRGGGGPPCGLDYETVNSSTNTTCVNWNQYYTNCSSAGEHN 329
 QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 421
 DB 330 PFKGAINFDNIGYAWIAIFQVITLEGWDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 399
 QY 422 CLVVIATQFSETKQRESQMLRQVRVPLNSASTLASFPGSGCYEELLKYLVLKKAAR 481
 DB 390 CLVVIATQFSETKQRESQMLRQVRVPLNSASTLASFPGSGCYEELLKYLVLKKAAR 449
 QY 482 RLQAQVSRALGVRAGLLSSPVARSQGPQSPGSCSTRSHRRLSVHHLVHHHHHHHHVHLGN 541
 DB 450 RLQAQVSRALGVRAGLLSSPVARSQGPQSPGSCSTRSHRRLSVHHLVHHHHHHHHVHLGN 509
 QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHGFYHADCHLEPVRQ 601
 DB 510 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHGFYHADCHLEPVRQ 569
 QY 602 APPPRCPSEASGRTVGSGKVIYTVHTSPPEILKDKALVEVADSPGPPTLTSNIPGPF 661
 DB 570 APPPRCPSEASGRTVGSGKVIYTVHTSPPEILKDKALVEVADSPGPPTLTSNIPGPF 629
 QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGAGCPDSCPYCARTGAGEPESADHVMPSD 721
 DB 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGAGCPDSCPYCARTGAGEPESADHVMPSD 689
 QY 722 SEAVYFTQDAQHSDLRDPHSRRRQSLGFDAPSSVLAPFWRLICDTFRKIVDSKYFGRG 781
 DB 690 SEAVYFTQDAQHSDLRDPHSRRRQSLGFDAPSSVLAPFWRLICDTFRKIVDSKYFGRG 749
 QY 782 IMTALVNTLSMGIYHEQPEELTNALEISNIVFTSLFALEMLLKLLVGPFGYIKNPYN 841
 DB 750 IMTALVNTLSMGIYHEQPEELTNALEISNIVFTSLFALEMLLKLLVGPFGYIKNPYN 809
 QY 842 IPFGVIVLISVWEIVGQQGGSLVRLTFRMLRVLKLVRFLPALQROLVLMKTMNDNVATF 901
 DB 810 IPFGVIVLISVWEIVGQQGGSLVRLTFRMLRVLKLVRFLPALQROLVLMKTMNDNVATF 869
 QY 902 CMLLMLEIFIFSLGMHLEFGCKFASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNKV 961
 DB 870 CMLLMLEIFIFSLGMHLEFGCKFASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNKV 929
 QY 962 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFSPSVD 1021
 DB 930 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFSPSVD 989
 QY 1022 GDGDRKKRLALVALGEHAELRKSLPLLIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
 DB 990 GDGDRKKRLALVALGEHAELRKSLPLLIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1049
 QY 1082 SGSAEPGAAHENKCPSPASRSPHSPWSAASSWTSSRSNSNIGRAPSLKRRSPSGHRS 1141
 DB 1050 SGSAEPGAAHENKCPSPASRSPHSPWSAASSWTSSRSNSNIGRAPSLKRRSPSGHRS 1109
 QY 1142 LLSGEGQESODEESESDEDRASPAQSDHRRHRSGLEREAKSSFDLPDTLQVPGHLRTASGR 1201
 DB 1110 LLSGEGQESODEESESDEDRASPAQSDHRRHRSGLEREAKSSFDLPDTLQVPGHLRTASGR 1169
 QY 1202 SSASEHQDCNGKSGSLARTLTDDPQLDGDNDNDEGNLSKGERIQAWVRSLPACCRE 1261
 DB 1170 SSASEHQDCNGKSGSLARTLTDDPQLDGDNDNDEGNLSKGERIQAWVRSLPACCRE 1229
 QY 1262 RDSWSAYIPPOQRFRLLCHRIITHKMFHVHVLIIFLNCITITAMERPKIDPHSAERIFL 1321
 DB 1230 RDSWSAYIPPOQRFRLLCHRIITHKMFHVHVLIIFLNCITITAMERPKIDPHSAERIFL 1289
 QY 1322 TLSNYIFTAVFLAEMTVKVVVALGWCFOAYLRSSWNVLGLLVLSVIDILVSMVSDSG 1381
 DB 1290 TLSNYIFTAVFLAEMTVKVVVALGWCFOAYLRSSWNVLGLLVLSVIDILVSMVSDSG 1349

330 PFKALNEDNIGYATIAFQVITTEGWDIMVFMDAHGYNFYFIILLIIVGSPFMINL 389
422 CLVVIATQSETHKQRESQLMREORVFLSNASTLASFSPPGSCYBELLKVLVYLKKAAR 481
390 CLVVIATQSETHKQRESQLMREORVFLSNASTLASFSPPGSCYBELLKVLVYLKKAAR 449
482 RLAAQVSRALIGVRAGLLSSPVARGSQPQPSGSTRSHRRLSVHHLVHHHHHHHHHVLGN 541
450 RLAAQVSRALIGVRAGLLSSPVARGSQPQPSGSTRSHRRLSVHHLVHHHHHHHHHVLGN 509
542 GTLRVPRAPEIQDRDANGSRRLMLPPPTPTSPGGPPRGAGSVHGFYHADCHLEVPVRCQ 601
510 GTLRVPRAPEIQDRDANGSRRLMLPPPTPTSPGGPPRGAGSVHGFYHADCHLEVPVRCQ 569
602 APPPRCPSEASGTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSTNIPGPF 661
570 APPPRCPSEASGTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSTNIPGPF 629
662 SSMHKLLETQSTGACHSSCKISSPCKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
630 SSMHKLLETQSTGACHSSCKISSPCKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689
722 SEAVYFTQDAQSHDLRDPHSRRRQSLGPDABPSSVLAFWRLICDTFRKIVDSKYFGRG 781
690 SEAVYFTQDAQSHDLRDPHSRRRQSLGPDABPSSVLAFWRLICDTFRKIVDSKYFGRG 749
782 IMTALLVNTLSMGIEVHEQPEELTNALEISNIYFTSLFALEMLLKLLVYGPFGYIKNPYN 841
750 IMTALLVNTLSMGIEVHEQPEELTNALEISNIYFTSLFALEMLLKLLVYGPFGYIKNPYN 809
842 IFDGVIVISWEIVGQGGGLSVLRTRFLMRVLKLVRFPLALQRIQVLMKTMNDVATF 901
810 IFDGVIVISWEIVGQGGGLSVLRTRFLMRVLKLVRFPLALQRIQVLMKTMNDVATF 869
902 CMLLMFLIFITPSILGMHLFGCKPASERDGTLPORKNFDSLWAIIVTVFOILQEDNKNV 961
870 CMLLMFLIFITPSILGMHLFGCKPASERDGTLPORKNFDSLWAIIVTVFOILQEDNKNV 929
962 LYNMGASTSSWAALYFTALMTFGNVVLFNLLVALLVVGFOAGDATKSESEPPFFSPSVD 1021
930 LYNMGASTSSWAALYFTALMTFGNVVLFNLLVALLVVGFOAGDATKSESEPPFFSPSVD 989
1022 GDGDRKRLALVALGEHAELKSLPLLIHTAATPMSPKSSSTGVGEALGSGSRRTSS 1081
990 GDGDRKRLALVALGEHAELKSLPLLIHTAATPMSPKSSSTGVGEALGSGSRRTSS 1049
1082 SGSNEPGAHHKCPSPARSPPSPWSAASSWTSRSSRNSLGRAPSLKRRSPSGRRS 1141
1050 SGSNEPGAHHKCPSPARSPPSPWSAASSWTSRSSRNSLGRAPSLKRRSPSGRRS 1109
1142 LLSGEGQESQDEESESSEDSPASGDRHRHGSLEAKSSFDLPDTLOVPLHRTASGR 1201
1110 LLSGEGQESQDEESESSEDSPASGDRHRHGSLEAKSSFDLPDTLOVPLHRTASGR 1169
1202 SSASEHQDCNGKSASGLARTLRTDDPOLGDGDDNDNEGNSLKGRIQAWVRSRLPACC 1261
1170 SSASEHQDCNGKSASGLARTLRTDDPOLGDGDDNDNEGNSLKGRIQAWVRSRLPACC 1229
1262 RDSWSAYIFPQSRPRLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
1230 RDSWSAYIFPQSRPRLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289
1322 TLSNVIPTAVFLAEMTKVAVLWCFGEQAVLRSSWNVLDGLLVLSVIDILVMSVSDSG 1381
1290 TLSNVIPTAVFLAEMTKVAVLWCFGEQAVLRSSWNVLDGLLVLSVIDILVMSVSDSG 1349
1382 TKILGMLRVLRLLRTRLPRLVSRAGLKLUVVETLMSLKGRIQAWVRSRLPACC 1441
1350 TKILGMLRVLRLLRTRLPRLVSRAGLKLUVVETLMSLKGRIQAWVRSRLPACC 1409
1442 VOLPKGKFFVCGEDTRNITNKSDCAEASYRWRHKNYFNDLQALMSLFLVLSKDGWVD 1501
1410 VOLPKGKFFVCGEDTRNITNKSDCAEASYRWRHKNYFNDLQALMSLFLVLSKDGWVD 1469

1502 IMYDGLDAVGVDQOQPIIMNHNPMWLLYFISLLIIVAFVFLNMFGVVVVENPHKCRQHEEE 1561
1470 IMYDGLDAVGVDQOQPIIMNHNPMWLLYFISLLIIVAFVFLNMFGVVVVENPHKCRQHEEE 1529
1562 EARRREKRLRLLEKKRSEKQMAEAOCKPYSDYSRRLLVHHLCTSHYLDLFTTGV 1621
1530 EARRREKRLRLLEKKR-----KAOCKPYSDYSRRLLVHHLCTSHYLDLFTTGV 1582
1622 GLNVVTMAHEVQOQPOILDEALKICNYIFTVIFVPSVFKLVAFAPRRFFQDRWNOLDLA 1681
1583 GLNVVTMAHEVQOQPOILDEALKICNYIFTVIFVPSVFKLVAFAPRRFFQDRWNOLDLA 1642
1682 IIVLSIMGITLLEBIEVNLISLPINPTIIRIMRVLRIARVILKLLQAVGMRALHUTVMQALP 1741
1643 IIVLSIMGITLLEBIEVNLISLPINPTIIRIMRVLRIARVILKLLQAVGMRALHUTVMQALP 1702
1742 QVGNLGLLFWLFFIFAAALGVELFGDLBCDETHPCGELGRHATFRFGMAFLTLFRVSTG 1801
1703 QVGNLGLLFWLFFIFAAALGVELFGDLBCDETHPCGELGRHATFRFGMAFLTLFRVSTG 1762
1802 DNWNGIMKDPSPDCDOESTCYNTVISPFIYFVSFVLTAQFVLVNVVIAVLMKHLSEENKEA 1861
1763 DNWNGIMKDTLRDCDOESTCYNTVISPFIYFVSFVLTAQFVLVNVVIAVLMKHLSEENKEA 1822
1862 KEAEAELEAELEEMKTLSPQHPSPGLSPFLWPQVEGVNSTDSKPGAPHTTAHIGAASGF 1921
1823 KEAEAELEAELEEMKTLSPQHPSPGLSPFLWPQVEGVNSTDSKPGAPHTTAHIGAASGF 1882
1922 SLBHTMVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAESLGHRCWGL 1981
1883 SLBHTMVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAESLGHRCWGL 1942
1982 PKAQSGIILSVHQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPLPPGSRPLAQRLR 2041
1943 PKAQSGIILSVHQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPLPPGSRPLAQRLR 2002
2042 RQAAIRTSLDVQGLSGREDLLSEVSPSCPLTRSSSFWGSSIQVOQSRGSIQSKVSKHI 2101
2003 RQAAIRTSLDVQGLSGREDLLSEVSPSCPLTRSSSFWGSSIQVOQSRGSIQSKVSKHI 2062
2102 RLPAFCPLPSWAKOPPETRSSILELDTLSLWISGDLTPSSQREPLFPRLDKKCYVETO 2161
2063 RLPAFCPLPSWAKOPPETRSSILELDTLSLWISGDLTPSSQREPLFPRLDKKCYVETO 2122
2162 SCRRRPFWLDEQRHRSIAVSCLDGSPQLCPSPSSLGQPLGGPSRPPKXLSPPSIS 2221
2123 SCRRRPFWLDEQRHRSIAVSCLDGSPQLCPSPSSLGQPLGGPSRPPKXLSPPSIS 2182
2222 IDPPESQGRPPCPSPGVCLRRRAPASDKSPSVSSPLDSTAAASPCKDTLSLGLSDP 2281
2183 IDPPESQGRPPCPSPGVCLRRRAPASDKSPSVSSPLDSTAAASPCKDTLSLGLSDP 2242
2282 TDMDP 2286
2243 TDMDP 2247

RESULT 6
AAY70720 standard; protein; 2428 AA.
XX AAY70720;
XX AC
XX DT 18-JUL-2000 (first entry)
XX DE Rat pancreatic T-type calcium channel.
XX KW Rat; pancreatic T-type calcium channel alpha1 subunit; insulin;
XX KW pancreatic beta cell; alpha1g; low voltage activated Ca2+ channel family;
XX KW antidiabetic; calcium influx; L type calcium channel; NIDDM;
XX KW type II diabetes; non-insulin dependent diabetes mellitus.

QY 1051 THTAATPMNSHPKSSSTGVCEALGSGSRRTSSSGSAEPGAAHHEMKCPGSGARSSPHSPWSA 1110
DB 1094 IHTAATPMNSHPKSSSTGVCEALGSGSRRTSSSGSAEPGAAHHEMKCPGSGARSSPHSPWSA 1153
QY 1111 ASSWTSRRSRNSLGRAPSLKRRSPGERRSLLSGEGQSDDEESSEEDRASPAQSDHR 1170
DB 1154 ASSWTSRRSRNSLGRAPSLKRRSPGERRSLLSGEGQSDDEESSEEDRASPAQSDHR 1213
QY 1171 HGRSLERAKSPDLPDTLQVPLGHTASGRSSASDHQCNKSGASGRARTLRTDDPOL 1230
DB 1214 HGRSLERAKSPDLPDTLQVPLGHTASGRSSASDHQCNKSGASGRARTLRTDDPOL 1273
QY 1231 DGGDDNDENGLSKGERIQAWRSRLPACCRERDSWYIFPPQSRFLLCHRIITHKMPD 1290
DB 1274 DGGDDNDENGLSKGERIQAWRSRLPACCRERDSWYIFPPQSRFLLCHRIITHKMPD 1333
QY 1291 HVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGQ 1350
DB 1334 HVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGQ 1393
QY 1351 AYLRSSNNVLGGLLVLSVIDIILVMSVSDSGTKILGMLRVLRLLRTRPLRVISRAQGLK 1410
DB 1394 AYLRSSNNVLGGLLVLSVIDIILVMSVSDSGTKILGMLRVLRLLRTRPLRVISRAQGLK 1453
QY 1411 LVVETILMSILKPTGNIVVICAFIIFGILGVOLFVKGFVCOGEDTRNITNKSDCAEAS 1470
DB 1454 LVVETILMSILKPTGNIVVICAFIIFGILGVOLFVKGFVCOGEDTRNITNKSDCAEAS 1513
QY 1471 YRWVRHKYNFDNLGOALMSLFLVASKGWDVIMYDGLDVGVDQOQPMNHNPMWLLYFIS 1530
DB 1514 YRWVRHKYNFDNLGOALMSLFLVASKGWDVIMYDGLDVGVDQOQPMNHNPMWLLYFIS 1573
QY 1531 FLIIIVAFVLMVGVVVENFHKRQHQEBEAREEKEKRLRLEKRR----- 1579
DB 1574 FLIIIVAFVLMVGVVVENFHKRQHQEBEAREEKEKRLRLEKRRNMLDDVTASG 1633
QY 1580 SKEQWAEAOCKPYSDYSYFRLLVHLCTSHYLDLFTITGVLNVVTAMAHYQOPQIL 1639
DB 1634 SSASAASEAOCKPYSDYSYFRLLVHLCTSHYLDLFTITGVLNVVTAMAHYQOPQIL 1693
QY 1640 DEALKICNYIFTVIFVESYFKLVAFAPRRFQDRWNQDLAIVLISIMGITLEEIEVNL 1699
DB 1694 DEALKICNYIFTVIFVESYFKLVAFAPRRFQDRWNQDLAIVLISIMGITLEEIEVNA 1753
QY 1700 SLPINPITIIIRMVLRITARVILKLLKMAVGMRLHTVMQALPQVGNLGLLFFLFFIAA 1759
DB 1754 SLPINPITIIIRMVLRITARVILKLLKMAVGMRLHTVMQALPQVGNLGLLFFLFFIAA 1813
QY 1760 LGVELFGDLECDTHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPDRCDQES 1819
DB 1814 LGVELFGDLECDTHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDLTRCDQES 1873
QY 1820 TCYNTVTISPIYFVSFLVTAQVPLVNVVIAVIMKHLSESNKEAEAELEAELEMTLS 1879
DB 1874 TCYNTVTISPIYFVSFLVTAQVPLVNVVIAVIMKHLSESNKEAEAELEAELEMTLS 1933
QY 1880 PQHSPGLSGPLWGVGVNSTDPKCAEHTTAHIGAAGSFLSEHTMPHPPEVVPVL 1939
DB 1934 PQHSPGLSGPLWGVGVNSTDPKCAEHTTAHIGAAGSFLSEHTMPHPPEVVPVL 1993
QY 1940 GPDLITVRKSGVSTHSLPNDSYMCRNGSTAERSLGRHGMGLPKAQSGSILSVHSQPADT 1999
DB 1994 GPDLITVRKSGVSTHSLPNDSYMCRNGSTAERSLGRHGMGLPKAQSGSILSVHSQPADT 2053
QY 2000 SCILQLPKDVHLLQPHGAPTWGAIPKLPPLPGRSPLAQRPLRQAARTDLSLVQGLGSR 2059
DB 2054 SCILQLPKDVHLLQPHGAPTWGAIPKLPPLPGRSPLAQRPLRQAARTDLSLVQGLGSR 2113
QY 2060 EDLLSEVSGPCPLTRSSFWGSGSIQVQQRSGIQSKVSKHRLPAPCGLEPSPWAKDPP 2119
DB 2114 EDLLSEVSGPCPLTRSSFWGSGSIQVQQRSGIQSKVSKHRLPAPCGLEPSPWAKDPP 2173
QY 2120 ETRSSLEIDTELSWISGDLFPSSQBEPLFRDLKCKYCVSVETQSCRRRPGFWLDEQRHSI 2179

DB 2174 ETRSSLEIDTELSWISGDLFPSSQBEPLFRDLKCKYCVSVETQSCRRRPGFWLDEQRHSI 2233
QY 2180 AYSCLDSSQOPRLCPSPSLGGQPLGGGSRPKKLSPPSIDPPESQSGRPPPCSPGVC 2239
DB 2234 AYSCLDSSQOPRLCPSPSLGGQPLGGGSRPKKLSPPSIDPPESQSGRPPPCSPGVC 2293
QY 2240 LRRRAPASDKPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP 2286
DB 2294 LRRRAPASDKPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP 2340
RESULT 7
ID AAY14586 standard; protein; 2250 AA.
XX AAY14586;
AC AAY14586;
DT 07-DEC-1999 (first entry)
XX Human T-type voltage-gated Ca channel alpha-1-G (hCav1.1a).
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX Homo sapiens.
OS WO9929847-A1.
PN 17-JUN-1999.
PD 30-OCT-1998; 98WO-US023161.
PF 05-DEC-1997; 97US-00985809.
PR (LOYO) UNIV LOYOLA CHICAGO.
XX Perez-Reyes E, Cribbs LL;
PI WPI; 1999-394972/33.
DR N-PSDB; AAX83481.
XX New T-type voltage-gated calcium channels.
XX Disclosure; Page 31-40; 138pp; English.
XX This sequence represents a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCav1.1a. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and voltage-gated Ca channel genes from humans and rats. Each of the novel Ca channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX Sequence 2250 AA;

Query Match 90.3%; Score 10857; DB 2; Length 2250;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 2084; Conservative 32; Mismatches 104; Indels 6; Gaps 4;
QY 62 GAACAGSTEDKPGSADSEAEGLPYPALAPVVFYLSQDSRPSRCLRTVCNPFERSML 121
DB 30 GRPFGSAEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPSRCLRTVCNPFERSML 89

122 VILLNCVTLMGMRPCEDIAQDSORCILQAFDDFIAPFAVAVMVKVVALGFGKCKYL 181
Db
90 VILLNCVTLMGMRPCEDIAQDSORCILQAFDDFIAPFAVAVMVKVVALGFGKCKYL 149
182 DTWNRDLFFIAGMLEYSLDQNSVFSFSAVRTVRVLRPLRAINRPSMRILVTLDDTLP 241
Db
150 DTWNRDLFFIAGMLEYSLDQNSVFSFSAVRTVRVLRPLRAINRPSMRILVTLDDTLP 209
242 MUGNVLLLCFFVFFFIAGVQVQWAGLLRNRCFLPENFSLPLSDVLEPYQFENEDESP 301
Db
210 MUGNVLLLCFFVFFFIAGVQVQWAGLLRNRCFLPENFSLPLSDVLEPYQFENEDESP 269
302 ICSPRENGMRCRSVPTLRGSGGPPCSDLYETVNSNNTTCVNNQYVTCNCSAGHN 361
Db
270 ICSPRENGMRCRSVPTLRGSGGPPCGLDYEAYNSSNNTTCVNNQYVTCNCSAGHN 329
362 PFKGAINFDNICYAWIAIQVITLEGWVDIMYFVMDAHSFYNIYFILLIIVGSFFMINL 421
Db
330 PFKGAINFDNICYAWIAIQVITLEGWVDIMYFVMDAHSFYNIYFILLIIVGSFFMINL 389
422 CLAVIATQFSETKQRESQIMRQVRFLSNASTLASFSEPGSCYBELLKYLVIILRKAAR 481
Db
390 CLAVIATQFSETKQRESQIMRQVRFLSNASTLASFSEPGSCYBELLKYLVIILRKAAR 449
482 RLAQVSRAGVRAGLLSSPVARSQBPQSGCTRSRRLSVHLLVHHHHHHHHVHLGN 541
Db
450 RLAQVSRAGVRAGLLSSPAPJGGQETQPSSCSRSHRRLSVHLLVHHHHHHHHVHLGN 509
542 GTLRVPASPEIQDRDANGSRRLMLPPSTPTPSGPPRGAEVSHSFYHADCHLEPVRQC 601
Db
510 GTLRVPASPEIQDRDANGSRRLMLPPSTPALSGAPPGAEVSHSFYHADCHLEPVRQC 569
602 APPPCPEASRTVSGKVPYVHTSPPPEILKDKALVEVAPSGPPTLSNFPPGPF 661
Db
570 APPPCPEASRTVSGKVPYVHTSPPPEILKEKALVEVAASSGPPTLSNTPPGPY 629
662 SSMHKLLETQSGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGPEGAHVPDSD 721
Db
630 SSMHKLLETQSGACHSSCKISSPCSKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689
722 SEAVYEFTQDACHSLDRPHSRRRQSLGDAEPSSVLAFWRLICDTRKIVDSKYFGRG 781
Db
690 SEAVYEFTQDACHSLDRPHS-RRQSLGDAEPSSVLAFWRLICDTRKIVDSKYFGRG 748
782 IMIALVNTLSMGIEYHQPPELTNVALEISNIVFTSLFALEMLKLYVGPFGYIKPNYN 841
Db
749 IMIALVNTLSMGIEYHQPPELTNVALEISNIVFTSLFALEMLKLYVGPFGYIKPNYN 808
842 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLRFLPALQRLVVLKMTMDNVATF 901
Db
809 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLRFLPALQRLVVLKMTMDNVATF 868
902 CMLMLFIFISILGMHLFGCKFASERDGLTPDRKNFDSLWLAIVTVFQILTQEDMNKV 961
Db
869 CMLMLFIFISILGMHLFGCKFASERDGLTPDRKNFDSLWLAIVTVFQILTQEDMNKV 928
962 LYNWMASTSSWAALYFIALMTFGNYVLENLVAILEVEGQFEGDATKSESEPPFSPSD 1021
Db
929 LYNWMASTSSWAALYFIALMTFGNYVLENLVAILEVEGQFEGDATKSESEPPFSPSD 988
1022 GDGDRKRLALVALGEHAELRKSLLPPLIHTAATPMHSPKSSSTGVGEALGSGSRRTSS 1081
Db
989 GDGDRKRLALVALGEHAELRKSLLPPLIHTAATPMHSPKSSSTGVGEALGSGSRRTSS 1048
1082 SGSAPGAHHEMKPPSARSSPHSPWSAASWTSRRSRSLGRAPSLKRRSPSGERS 1141
Db
1049 SGSAPGAH-HEMKPPSARSSPHSPWSAASWTSRRSRSLGRAPSLKRRSPSGERS 1107
1142 LLSGEGQSEDEBESSEEDRASPGSDHRRHGRSLEREAKSFDLPDTLQVPLHRTASGR 1201
Db
1108 LLSGEGQSEDEBESSEEDRASPGSDHRRHGRSLEREAKSFDLPDTLQVPLHRTASGR 1167

1202 SSASBHODCNGKSASGRRLARTLRTDDPOLDGGDDDDNDEGNLSKGRIOAWVRGLPACCBE 1261
Db
1168 GSASHODCNGKSASGRRLARALRPDDPLDGGDDADDNDEGNLSKGRVRAIRARLPACCLE 1227
1262 RDSWASAYIPPPQSRPRLCHRIITHKMPDHVVLVIFLNCITTIAMERPKIDPHSABRIEL 1321
Db
1228 RDSWASAYIPPPQSRPRLCHRIITHKMPDHVVLVIFLNCITTIAMERPKIDPHSABRIEL 1287
1322 TILSNYIFTAVFLAEMTVKVALGWCFGQAYLRSSWNVLDDGLLVLSIVISVMVSDSG 1381
Db
1288 TILSNYIFTAVFLAEMTVKVALGWCFGQAYLRSSWNVLDDGLLVLSIVISVMVSDSG 1347
1382 TKILGMLRVLRLLRTRPLRVLSRAQGLKLVVETLMSSLKPIGNIWVICCAFIFIGILG 1441
Db
1348 TKILGMLRVLRLLRTRPLRVLSRAQGLKLVVETLMSSLKPIGNIWVICCAFIFIGILG 1407
1442 VOLFKGKFVCOGEDTRNITNKSDCAEASYSRVRHKNFNDNLGOALMSLFVLASKDGWD 1501
Db
1408 VOLFKGKFVCOGEDTRNITNKSDCAEASYSRVRHKNFNDNLGOALMSLFVLASKDGWD 1467
1502 IMYDGLDVGVDQOQPIMNHNPMMLLYFISFLIIVAFFVLNMPVGVVVENFHKCRQOBE 1561
Db
1468 IMYDGLDVGVDQOQPIMNHNPMMLLYFISFLIIVAFFVLNMPVGVVVENFHKCRQOBE 1527
1562 EARREERKLRLREKKRSKQMAEACKVYSYSRFRLLVHLLCTSHYLDLITGVI 1621
Db
1528 EARREERKLRLREKKRSKQMAEACKVYSYSRFRLLVHLLCTSHYLDLITGVI 1587
1622 GINVVYMAHEVYQOQIILDEALKICNYIFTVIFVPESVFKLVAFAFRFFQDRWNQOLDIA 1681
Db
1588 GINVVYMAHEVYQOQIILDEALKICNYIFTVIFVLESVFKLVAFAFRFFQDRWNQOLDIA 1647
1682 IVLISIMGITLLEEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGRALLHTYMQALP 1741
Db
1648 IVLISIMGITLLEEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGRALLHTYMQALP 1707
1742 QVGNLGLLFMLFFIIFAAALGVLEFGLDECDETHRCCEGLGRHATFRNFGMAFLTLFRVSTG 1801
Db
1708 QVGNLGLLFMLFFIIFAAALGVLEFGLDECDETHRCCEGLGRHATFRNFGMAFLTLFRVSTG 1767
1802 DNWNGIMKDPSRDCDQESTCVNTVISPFIYFVSFVLTAQFVLNVVIVAVLMKHLESNEKA 1861
Db
1768 DNWNGIMKDPSRDCDQESTCVNTVISPFIYFVSFVLTAQFVLNVVIVAVLMKHLESNEKA 1827
1862 KEAELEAELEMLKTLSPQPHSPLGSPFLWPVEGVNSTDSPKGPAPHTTAHGAASGF 1921
Db
1828 KEAELEAELEMLKTLSPQPHSPLGSPFLWPVEGVNSTDSPKGPALHPAARASASHF 1887
1922 SLEHPTWVPHPEVPVPLGPDLLTVRKSGVSRTHSLNDSYMCNGSTAESRSLHGRWGL 1981
Db
1888 SLEHPTWVPHPEVPVPLGPDLLTVRKSGVSRTHSLNDSYMCNGSTAESRSLHGRWGL 1944
1982 PKAQSGSILSVHSPADTSCILQPKDVHVLLOPHGAPTGWAIKPLPPGSRPLAQRPLR 2041
Db
1945 PKAQSGSILSVHSPADTSCILQPKDVHVLLOPHGAPTGWAIKPLPPGSRPLAQRPLR 2004
2042 RQAIRTDSDVQGLGREDLLSEVSPCPLTRKSSFWGSSSQVQORSGIQSKVSKHI 2101
Db
2005 RQAIRTDSDVQGLGREDLLSEVSPCPLTRKSSFWGSSSQVQORSGIQSKVSKHI 2064
2102 RLPACPLEPSMAKDPETESSLELDELTELWSIGDILL-PSQOBEPLFPRLKCYSVET 2160
Db
2065 RLPACPLEPSMAKDPETESSLELDELTELWSIGDILL-PSQOBEPLFPRLKCYSVET 2124
2161 QSCRRRPFGLDEORRHRSIAVSCILDSQSPRLCPSPSLGGQPLGGPSRPPKXLSPPSI 2220
Db
2125 QSCRRRPFGLDEORRHRSIAVSCILDSQSPRLCPSPSLGGQPLGGPSRPPKXLSPPSI 2184
2221 SIDPPESQGRPPCPGVCLRRRAPASDKDPSVSSPLDSTAASFPKXDTLSLGLSSD 2280
Db
2185 SIDPPESQGRPPCPGVCLRRRAPASDKDPSVSSPLDSTAASFPKXDTLSLGLSSD 2244
2281 PTMDP 2286

	db	2245 PADLDP 2250	: :
		RESULT 8	
	ID	AAV14588 standard; protein; 2268 AA.	
	XX	AAV14588;	
	XX	AC	
	XX	07-DEC-1999 (first entry)	
	XX	Human T-type voltage-gated Ca channel alpha-1-G (hCavT1c).	
	DE	Human; T-type voltage-gated calcium channel; membrane; pore; ion;	
	XX	activation; current; rat; screen; drug; cardiomyopathy; epilepsy.	
	XX	Homo sapiens.	
	OS	WO929847-A1.	
	XX	PN	
	XX	17-JUN-1999.	
	PD	30-OCT-1998; 98WO-US23161.	
	XX	05-DEC-1997; 97US-00985809.	
	PR	(LOYO) UNIV LOYOLA CHICAGO.	
	XX	PA	
	XX	Perez-Reyes E, Cribbs LL;	
	PI	WPI; 1999-394972/33.	
	XX	N-PSDB; AAX83483.	
	DR	New T-type voltage-gated calcium channels.	
	XX	Disclosure; Page 49-58; 139pp; English.	
	PT	This sequence represents a human T-type voltage-gated calcium (Ca)	
	XX	channel alpha-1-G designated hCavT1c. Voltage gated channels are membrane	
	CC	bound glycosylated proteins formed of several subunits. The large alpha	
	CC	subunits form a pore in the membrane that is selective for a given ionic	
	CC	species. Each alpha subunit contains 4 domains (I, II, III and IV) and	
	CC	each domain contains 6 putative transmembrane helical segments (SI-S6). T	
	CC	-type Ca channels are activated at a lower voltage than L- or N-type	
	CC	channels. Characteristics of T-type channels include short current time,	
	CC	slow activation kinetics near threshold, fast inactivation kinetics and	
	CC	slow tail current. The sequences AAX83481-X83492 represent novel T-type	
	CC	voltage-gated Ca channel genes from humans and rats. Each of the novel Ca	
	CC	-channels contains a putative IVS4 region comprising the amino acid	
	CC	sequence AAY14598. Cells expressing the T-type voltage-gated calcium	
	CC	channel proteins can be used to screen for drugs which affect calcium	
	CC	channels. Methods are also disclosed for treating a disease or disorder	
	CC	associated with a deficiency in a native T-type calcium channel nucleic	
	CC	acid, e.g. to treat cardiomyopathy, epilepsy, etc	
	XX	Sequence 2268 AA;	
	SQ	Query Match 90.1%; Score 10833; DB 2; Length 2268;	
		Best Local Similarity 92.8%; Pred. No. 0;	
		Matches 2083; Conservative 32; Mismatches 105; Indels 24; Gaps 5;	
	QY	62 GAAGAGSTKDPGSDAASAEGLPYPALAPVVFYLISODSRPSCRLATVCNPFERYSMIL 121	
	Dd	30 GRPGSAEKDPSGADSAEGLPYPALAPVVFYLISODSRPSCRLATVCNPFERYSMIL 89	
	QY	122 VILLNCVTIGMPFCEDIAQSQRCEIIQAEDDFIFAFVMMVMVALGIFGKKCYLG 181	
	Dd	90 VILLNCVTIGMPFCEDIAQSQRCEIIQAEDDFIFAFVMMVMVALGIFGKKCYLG 149	
	QY	182 DTWNRLDFFIVTAGMLEYSLDQNVSFSAVRTRVLRIAINRVPMSRLLVTLITLTP 241	
	Dd	150 DTWNRLDFFIVTAGMLEYSLDQNVSFSAVRTRVLRIAINRVPMSRLLVTLITLTP 209	

1322 TLSNYIFTAVFLAEMTVKVVAGWCFGEQAYLRSSWNVLGDLALLISVIDIILVSVSDSG 1381
1288 TLSNYIFTAVFLAEMTVKVVAGWCFGEQAYLRSSWNVLGDLALLISVIDIILVSVSDSG 1347
1382 TKILGMLRVLRLLRTRPLRVLSRAQGLKLVVETLMSLSKPIGNVVICCAFFIIFGILG 1441
1348 TKILGMLRVLRLLRTRPLRVLSRAQGLKLVVETLMSLSKPIGNVVICCAFFIIFGILG 1407
1442 VOLFKGKPVCOGEDTRNITKNSDCASRYVRVHKYNFDNI.GQALMSLFLVLSKDGWD 1501
1408 VOLFKGKPVCOGEDTRNITKNSDCASRYVRVHKYNFDNI.GQALMSLFLVLSKDGWD 1467
1502 IMYDGLDVGVDQOQPMNHNPMLLYFISFLILVAFVFLNMFVGVVFNHFKRQHOEE 1561
1468 IMYDGLDVGVDQOQPMNHNPMLLYFISFLILVAFVFLNMFVGVVFNHFKRQHOEE 1527
1562 EARRREKRRLRLEKKRSKEKOMA-----EAQCKPYYSDYSRFRLL 1603
1528 EARRREKRRLRLEKKRSKEKQADLMDLDDVIASSGASASAASEAQCKPYYSDYSRFRLL 1587
1604 VHLCTSHVLDLFTIGVIGLVNVTWAMSHYQOQIILDEALKICNYIFTVIFVFSVFKLV 1663
1588 VHLCTSHVLDLFTIGVIGLVNVTWAMSHYQOQIILDEALKICNYIFTVIFVFSVFKLV 1647
1664 AFARFRFPQDRWNQDLALVLLSIMGITLLEIEVNLSLPINPTIIRIMRVLRIRAVLKIL 1723
1648 AFGFRFPQDRWNQDLALVLLSIMGITLLEIEVNLSLPINPTIIRIMRVLRIRAVLKIL 1707
1724 KMAYGMRALLHTVMQALPQVGNLGLLPMLLFFIPAALGVELFGDLECDETHPCEGLGRHA 1783
1708 KMAYGMRALLHTVMQALPQVGNLGLLPMLLFFIPAALGVELFGDLECDETHPCEGLGRHA 1767
1784 TFRNFGMAFLTLFRVSTGDNNGIMKPSRCDQESTCYNTVISPIYFVSFLTAQFVLV 1843
1768 TFRNFGMAFLTLFRVSTGDNNGIMKOTLRCDQESTCYNTVISPIYFVSFLTAQFVLV 1827
1844 NVVIAVLMKHLEENKEAEAELEEMKTLSPQHPGLSGPFLPWGVEGVNSTDS 1903
1828 NVVIAVLMKHLEENKEAEAELEEMKTLSPQHPGLSGPFLPWGVEGVNSTDS 1887
1904 PKGAPHTTAHGAAGSFLSBHPTMPHPEVVPVLPGLDITVRKSGVSRTHSLPNDSYM 1963
1888 PKGALHPAAHARGASHSLEBHTMQPHTTLP---GPDLLTVRKSGVSRTHSLPNDSYM 1944
1964 CRNGSTAEISLHGKGLPKAQSGSILSVHSQADTSCILQIPKDVHVLLOPHGAPTWA 2023
1945 CRHGSTAEGPLHGKGLPKAQSGSILSVHSQADTSCILQIPKDVHVLLOPHGAPTWA 2004
2024 IPKLPPFGSRPLAQRPLRRQAARTDSDVQGLSREDLLSEVSGPCLTRSSSFWGGS 2083
2005 IPKLPPFGSRPLAQRPLRRQAARTDSDVQGLSREDLLSEVSGPCLTRSSSFWGGS 2064
2084 SIQVQSGTQSKVSKHILRPAPCPGLEPWSWAKDPPETRSLSLELDTLSWISGDL--PSS 2142
2065 STQAQCSRSKSHSKISKEMTPPAPCPGEPBNMGKPPETRSLSLELDTLSWISGDL--PSS 2124
2143 QEEPLFRDLKCKYSVETQSCRRPGLWLDQRHSTAVSCLDGSGQRLCPSPSSLGQ 2202
2125 QEEPLFRDLKCKYSVETQSCRRPGLWLDQRHSTAVSCLDGSGQRLCPSPSSLGQ 2184
2203 PLGGFGRPKKLSPPSISIDPPESQSGSRPPCPGVLRRRAPASDSDKPSVSSPLDSTA 2262
2185 PLGGFGRPKKLSPPSISIDPPESQSGSRPPCPGVLRRRAPASDSDKPSVSSPLDSTA 2244
2263 ASPSPKDTLSLGLSSDPTMDP 2286
2245 ASPSPKDTLSLGLSSDPTMDP 2268

RESULT 9

AAE01019

ID AAE01019 standard; protein; 2273 AA.

XX

AC AAE01019;
XX 17-JUL-2001 (first entry)
DT Human T-type low voltage activated calcium channel alphaG-c protein.
XX Human T-type low voltage activated calcium channel alphaG-c; stress;
DE epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease;
KW endocrine disorder; respiratory disorder; peripheral muscle disorder;
KW muscle excitability; fertilisation; contraception; hypertension;
KW neuronal firing regulation; cardiovascular disorder; gene therapy;
KW forensic analysis; epidemiological study; neuroleptic.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 1138 /note= "Encoded by GAG"
FT Misc-difference 1142 /note= "Encoded by GAA"
FT Misc-difference 1680 /note= "Encoded by ACG"
FT Misc-difference 1683 /note= "Encoded by GRA"
XX WO200130844-A1.
XX 03-MAY-2001.
XX 06-OCT-2000; 2000WO-US027761.
XX 26-OCT-1999; 99US-00426998.
XX (ORTH) ORTHO-MCNEIL PHARM INC.
XX Dublin AE, Galindo JE, Pyati J, Zhu JY, Erlander MG;
XX WPI; 2001-300486/31.
XX N-PSDB; AAD04756.
XX New nucleic acid encoding human calcium channel protein, useful for
identifying specific modulators and potential pharmaceuticals for
treating e.g. epilepsy.
XX Claim 11; Page 81-99; 115pp; English.
XX The invention relates to isoform of human T-type low voltage activated
calcium channel (alphaG-c) cDNA and protein. Cells transformed with
calcium channel DNA to express calcium alphaG-c channel protein are used
to identify specific modulators (antagonists or agonists). These
modulators are useful as therapeutic agents and are used for treating
a wide range of calcium alphaG-c channel-mediated disorders, e.g. stress
epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease,
endocrine disorders, respiratory disorder, peripheral muscle disorder,
muscle excitability, fertilisation, contraception, disorders involving
hyperextension, neuronal firing regulation, potentiation of synaptic
signals and cardiovascular disorders (e.g. atherosclerosis, cardiac
hypertrophy, angina pectoris). Calcium alphaG-c channel DNA is useful
for isolating and identifying related molecule mutations. It is also
optionally used as antisense sequences, in gene therapy. Calcium channel
alphaG-c DNA, protein and antibodies are useful for forensic analysis,
diagnosis and epidemiological studies, by standard hybridisation or
immunological assays. The present sequence is T-type low voltage
activated calcium channel alphaG-c protein
XX Sequence 2273 AA;

Query Match

Best Local Similarity 90.0%; Score 10820.5; DB 4; Length 2273;

Matches 2080; Conservative 35; Mismatches 105; Indels 29; Gaps 5;

QY

62 GAAGAGSTEXDKGSADSEAGLPPALAPVVFYQLSDSPRSWCLRTVCNPFERSVML 121

Db 30 GRPGSAEKDPGSADSEAGLPPALAPVVPFYLSQDSRPSRWCLRTVCNPFERI SML 89
QY 122 VILLNCVTILGMRPCBDIACDSORCRILQAFDDFIAPFAVEMVVRWALGIFGKKCYLG 181
Db 90 VILLNCVTILGMRPCBDIACDSORCRILQAFDDFIAPFAVEMVVRWALGIFGKKCYLG 149
QY 182 DTWNRLDFFIVITAGMLEYSLDQNVSPSAVRTVRVLRPLRAINRVFSMRLVTLTLLDTLP 241
Db 150 DTWNRLDFFIVITAGMLEYSLDQNVSPSAVRTVRVLRPLRAINRVFSMRLVTLTLLDTLP 209
QY 242 MLGNVLLLCFFVFIFIGIVGVQLWAGLLNRCPENFSLPLSDVLEPYQOTENEDESPP 301
Db 210 MLGNVLLLCFFVFIFIGIVGVQLWAGLLNRCPENFSLPLSDVLEPYQOTENEDESPP 269
QY 302 ICSQPRENGWRSRCSVPTLURGEGBGPPCGLDYETNNSSTNTCVWNQYQYTNCSAGEHN 361
Db 270 ICSQPRENGWRSRCSVPTLURGEGBGPPCGLDYETNNSSTNTCVWNQYQYTNCSAGEHN 329
QY 362 PFKGAINFDNIGYAWTAIFOVITILEGWVDIMYFVMDAHSFYNFYIFILLIIVGSPFMINL 421
Db 330 PFKGAINFDNIGYAWTAIFOVITILEGWVDIMYFVMDAHSFYNFYIFILLIIVGSPFMINL 389
QY 422 CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEELLKYLVLKRAAR 481
Db 390 CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEELLKYLVLKRAAR 449
QY 482 RLAQVRAIGVRAGLISSPVARGOEPQPSGCTSRHRRLSVHHLVHHHHHHHHVHLGN 541
Db 450 RLAQVRAIGVRAGLISSPVARGOEPQPSGCTSRHRRLSVHHLVHHHHHHHHVHLGN 509
QY 542 GTLRVRPASPEIQRDRANGSRRLMLPPSTPTSGGPPRGAESVHSFYHADCHLEPVRCQ 601
Db 510 GTLRVRPASPEIQRDRANGSRRLMLPPSTPTSGGPPRGAESVHSFYHADCHLEPVRCQ 569
QY 602 APPPRCSEASGRTVGSKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSPNIPGPFF 661
Db 570 APPPRCSEASGRTVGSKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSPNIPGPFF 629
QY 662 SSMHKLLETOSTGACHSCSKISSPCSKADGACGPDSPCYCARTGAGEPESADHWMPDSD 721
Db 630 SSMHKLLETOSTGACHSCSKISSPCSKADGACGPDSPCYCARTGAGEPESADHWMPDSD 689
QY 722 SEAVYETQDAQCHSDLRDRSRQRSLGPDAPSSVLAFWRLICDTRKIVDSKYFGRG 781
Db 690 SEAVYETQDAQCHSDLRDRPHS - RQRSLGPDAPSESSVLAFWRLICDTRKIVDSKYFGRG 748
QY 782 IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGVIKNPYN 841
Db 749 IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGVIKNPYN 808
QY 842 IFDGVIVIVISWEIVGQGGGLSVLRTRFLMRVLKLVRFPLALQRLVLMKTMNDVATF 901
Db 809 IFDGVIVIVISWEIVGQGGGLSVLRTRFLMRVLKLVRFPLALQRLVLMKTMNDVATF 868
QY 902 CMLMLFIFIPISILGMHLFGCKFASERDGLTLPDRKNFDSLLMAIVTVFQILTQEDWNKV 961
Db 869 CMLMLFIFIPISILGMHLFGCKFASERDGLTLPDRKNFDSLLMAIVTVFQILTQEDWNKV 928
QY 962 LYNMGMASTSSWAALYFIATMFTGNVYLVNLLVAILVEGFQAE----- 1003
Db 929 LYNMGMASTSSWAALYFIATMFTGNVYLVNLLVAILVEGFQAEISKREDASGQSCIQLP 988
QY 1004 -----GATKSESPDRFSPVDGGDRKKRLVALVALGEHAELRKSLLPLLIHTAATPM 1058
Db 989 VDSQGGDANKSESPDRFSPVDGGDRKKRLVALVALGEHAELRKSLLPLLIHTAATPM 1048
QY 1059 SHPKSSSTGVGEALGSGSRRTSSSGSAPPGAHHHEMKCPPGAARSPSPHSPWAAASWTSSRR 1118
Db 1049 SLPKSTSTGLGEALGPAKRRTSSSGSAPPGA - HEMKPPSARSPSPHSPWAAASWTSSRR 1107
QY 1119 SSRNSLGRAPSLKRSPGERRSLLSGQBSQDEEESSEEDRASPGASHRRHRSGLERE 1178
Db 1108 SSRNSLGRAPSLKRSPGERRSLLSGQBSQDEEESSEEDRASPGASHRRHRSGLERE 1167

QY 1179 AKSFDLPDTLOVPGHLRTASGRSSASSEHQDCNGKSASGRLARTLRTDDPOLDGGDDNDE 1238
Db 1168 AKSFDLPDTLOVPGHLRTASGRSSASSEHQDCNGKSASGRLARLRPDDPPLDGGDDADDE 1227
QY 1239 GNLSKGERIQAWVRSRRLPACCRERDSWSAYIIFPPQSRFLLCHRIITHKMFQHVVLVIF 1298
Db 1228 GNLSKGERVRAWIRARLPACCLERDSWSAYIIFPPQSRFLLCHRIITHKMFQHVVLVIF 1287
QY 1299 LNCITIAMERPKIDPHSAERIIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEOAYLRSSWN 1358
Db 1288 LNCITIAMERPKIDPHSAERIIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEOAYLRSSWN 1347
QY 1359 VLDGLVLVLSVIDILVSMVSDSGTKILGMLRVLRLTLRLPLRVLRSVRAOGLKLVWETLMS 1418
Db 1348 VLDGLVLVLSVIDILVSMVSDSGTKILGMLRVLRLTLRLPLRVLRSVRAOGLKLVWETLMS 1407
QY 1419 SLKPIGNIIVICCAFFIIFGILGVQLFKGFFVCCQGEDRNTITNKSDCAEASVWRVHKY 1478
Db 1408 SLKPIGNIIVICCAFFIIFGILGVQLFKGFFVCCQGEDRNTITNKSDCAEASVWRVHKY 1467
QY 1479 NFDNLGQALMSLFLVASKDGWVDIMYDGLDVGVDQOQPIMNHNPMWMLLYFISPELLIVAFF 1538
Db 1468 NFDNLGQALMSLFLVASKDGWVDIMYDGLDVGVDQOQPIMNHNPMWMLLYFISPELLIVAFF 1527
QY 1539 VLMNFVGVVVENFHKCRQHQBEEARREKRRLRLEKKRRSKEKQMAEAQCKPYYSYDS 1598
Db 1528 VLMNFVGVVVENFHKCRQHQBEEARREKRRLRLEKKRRSKEKQMAEAQCKPYYSYDS 1587
QY 1599 RPELLVHLLCTSHYLDLFTIGVIGLVNVTWAMEHYQOQPTLDEALKICNVIFVIFVFE 1658
Db 1588 RPELLVHLLCTSHYLDLFTIGVIGLVNVTWAMEHYQOQPTLDEALKICNVIFVIFVFE 1647
QY 1659 VFKLVAFAFRFPQDRWNQDLALVLLSIMGITLEEIVNLSLPINPTIIRIMRVLIAR 1718
Db 1648 VFKLVAFAFRFPQDRWNQDLALVLLSIMGITLEEIVNLSLPINPTIIRIMRVLIAR 1707
QY 1719 VLKLLXVAVGMRALLHTVMQALPQVGNLGLFLMLLFFIFAALGVVELFGDECETHPC 1778
Db 1708 VLKLLXVAVGMRALLHTVMQALPQVGNLGLFLMLLFFIFAALGVVELFGDECETHPC 1767
QY 1779 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDSRDCDOESTCVNTVISPIYFVSFVLTA 1838
Db 1768 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDSRDCDOESTCVNTVISPIYFVSFVLTA 1827
QY 1839 QFVLNVVIAVLMKHLSESNKEAEAELEMLEMKTLSPOPHSPLGSPFLWPVGVEG 1898
Db 1828 QFVLNVVIAVLMKHLSESNKEAEAELEMLEMKTLSPOPHSPLGSPFLWPVGVEG 1887
QY 1899 NSTDSPKPGAPHTTAHIGAAAGSFLHPTWVPHPEVVPVLPGLDILLTVRKSQVSRTHSLP 1958
Db 1888 DSPDSPKPGALHPAAHARSASHFSLEHPTMQPHTELP---GPDLLTVRKSQVSRTHSLP 1944
QY 1959 NDSYMCNGSTAESRSLGHRGWLPKAQSGLSVHSOPADTSCITQLPKDQVHLYLQPHGA 2018
Db 1945 NDSYMCNGSTAESRSLGHRGWLPKAQSGLSVHSOPADTSCITQLPKDQVHLYLQPHGA 2004
QY 2019 PTWCAIKLPPGSRPLAQRLRQAAIRTDLSLVQGLSGREDLLSEVSGSCPLTRSS 2078
Db 2005 PTWCAIKLPPGSRPLAQRLRQAAIRTDLSLVQGLSGREDLLSEVSGSCPLTRSS 2064
QY 2079 FWGSSSTQVQORSGIQSKVSKHTRLPAPCGLEPSPWAKDPPETRSSLELDTLSWISGDL 2138
Db 2065 FWGSSSTQVQORSGIQSKVSKHTRLPAPCGLEPSPWAKDPPETRSSLELDTLSWISGDL 2124
QY 2139 L-PSSQSEELPRLDKCYSVETOSCTOSCTRRRPGFWLDEORRHSIAVSCLDGSOPLRCPSPS 2197
Db 2125 LPPGGQBEPSRDLKKCYSVQASQCORRPTISWLDQORRHSIAVSCLDGSOPLRCPSPS 2184
QY 2198 SLGQPLGGPGRPKKLSPPSISIDPPESQGRPPCPGVCILRRRAPASDKDPSVSSP 2257
Db 2185 NLGGQPLGGPGRPKKLSPPSITIDPPESQGRPTTSPGICLRRRAPSSDKDPSVSSP 2244

QY 1322 TTSNYIFTAVFLAETVKVVALGWCPCGEQAYIRSSWNVLDDLGLLVLSIVDILVSMVSDSG 1381
 Db 1288 TTSNYIFTAVFLAETVKVVALGWCPCGEQAYIRSSWNVLDDLGLLVLSIVDILVSMVSDSG 1347
 QY 1382 TKILGMLRVLRILRTLRPLRVTSRAQGLKLVVETLMSSLKPIGNIVVICAPFIIRGILG 1441
 Db 1348 TKILGMLRVLRILRTLRPLRVTSRAQGLKLVVETLMSSLKPIGNIVVICAPFIIRGILG 1407
 QY 1442 VOLFKGKFFVCOGEDTNTKSDCAEASVYRHHKYNFNDLQALMSLFLVASKDGWD 1501
 Db 1408 VOLFKGKFFVCOGEDTNTKSDCAEASVYRHHKYNFNDLQALMSLFLVASKDGWD 1467
 QY 1502 IMYDGLDVGVDQOQIMNHNPMMLLYFISPLLIIVAFVFLNMFGVVVENFHKRQHEE 1561
 Db 1468 IMYDGLDVGVDQOQIMNHNPMMLLYFISPLLIIVAFVFLNMFGVVVENFHKRQHEE 1527
 QY 1562 EARRREKRLRLLEKRR-----SKEQMAEAOCKPYSDYSRPRLLVHHLCTS 1610
 Db 1528 EARRREKRLRLLEKRRNMLDDVIASGSASAASEAQCKPYSDYSRPRLLVHHLCTS 1587
 QY 1611 HYDLFTITVIGLVNVTMAEHYQOQILDEALKICNYIFTVIFVSVFKLVAFAPRRP 1670
 Db 1588 HYDLFTITVIGLVNVTMAEHYQOQILDEALKICNYIFTVIFVSVFKLVAFAPRRP 1647
 QY 1671 FQDRWNQDLAIIVLLSIMGITLSEIEVNLSLPNTIIRIMVLRIRARVLKILKMAVGM 1730
 Db 1648 FQDRWNQDLAIIVLLSIMGITLSEIEVNLSLPNTIIRIMVLRIRARVLKILKMAVGM 1707
 QY 1731 ALHTVMOALPOVGNLGLLPMFLFFIPAAALGVLEFGDECHPCBGLGRHATFRNFGM 1790
 Db 1708 ALHTVMOALPOVGNLGLLPMFLFFIPAAALGVLEFGDECHPCBGLGRHATFRNFGM 1767
 QY 1791 AFLTLFRVSTGDNWNGIMKPSRDCQESTCYNTVISPFIYFVSVFLTAQFVLNVVIAVL 1850
 Db 1768 AFLTLFRVSTGDNWNGIMKPSRDCQESTCYNTVISPFIYFVSVFLTAQFVLNVVIAVL 1827
 QY 1851 MKHLEENKAKAEAELEAELEBMKTLSPQPHSLGSPFTWQEGVGNSTDSKPCAPH 1910
 Db 1828 MKHLEENKAKAEAELEAELEBMKTLSPQPHSLGSPFTWQEGVGNSTDSKPCAPH 1887
 QY 1911 TTAHGAAGSFLSHPTWHPPEVPVPLGPDMLTVKSGVSRTHSLPNDSYMCRNGSTA 1970
 Db 1888 PAHARSASHFSLSHPTWHPPEVPVPLGPDMLTVKSGVSRTHSLPNDSYMCRNGSTA 1944
 QY 1971 ERSILGHRGWGLPKAQSGSILSVHSQPADTSCILQPKDVMHVLQPHGAPTWGAIPKLP 2030
 Db 1945 EGPLGHRGWGLPKAQSGSILSVHSQPADTSCILQPKDVMHVLQPHGAPTWGAIPKLP 2004
 QY 2031 GRSPLAQPLRQAAIRTDSDVOGLGSRREDLLSEVSGPCPLTRSSFWGSGSIQVQOR 2090
 Db 2005 GRSPLAQPLRQAAIRTDSDVOGLGSRREDLLSEVSGPCPLTRSSFWGSGSIQVQOR 2064
 QY 2091 SGIOSKYSKHURLPAPCPGLEPSPWAKOPPETRSSLELDTLSWISGDL-PSQEEPLFP 2149
 Db 2065 SRSHKISKHTPPAPCPGLEPSPWAKOPPETRSSLELDTLSWISGDL-PSQEEPLFP 2124
 QY 2150 RDLKKCYSVETQSCRRRPFGLWDEORRHSIAVSCLDGSGQRLCPSPSSLGQPLGGPGS 2209
 Db 2125 RDLKKCYSVETQSCRRRPFGLWDEORRHSIAVSCLDGSGQRLCPSPSSLGQPLGGPGS 2184
 QY 2210 RPKKLSPPSISIDPPESQGRPPCGVCLRRAPASDSKDPSSVPLDSTAASPSPKK 2269
 Db 2185 RPKKLSPPSISIDPPESQGRPPCGVCLRRAPASDSKDPSSVPLDSTAASPSPKK 2244
 QY 2270 DTLISGLSSDPTMDP 2286
 Db 2245 DVLISGLSSDPTMDP 2261

RESULT 11
 AAY14589
 ID AAY14589 standard; protein; 2243 AA.

XX AAY14589;
 AC 07-DEC-1999 (first entry)
 DT Human T-type voltage-gated Ca channel alpha-1-G (hCavT1d).
 DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
 KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
 KW Homo sapiens.
 OS WO929847-A1.
 PN 17-JUN-1999.
 PD 30-OCT-1998; 98WO-US023161.
 PF 05-DEC-1997; 97US-00985809.
 PR (LOYO) UNIV LOYOLA CHICAGO.
 PA Perez-Reyes E, Cribbs LL;
 PI WPI; 1999-394972/33.
 XX N-PSDB; AAX83484.
 DR New T-type voltage-gated calcium channels.
 PT Disclosure; Page 58-67; 138pp; English.
 FS This sequence represents a human T-type voltage-gated calcium (Ca)
 CC channel alpha-1-G designated hCavT1d. Voltage gated channels are membrane
 CC bound glycosylated proteins formed of several subunits. The large alpha
 CC subunits form a pore in the membrane that is selective for a given ionic
 CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
 CC each domain contains 6 putative transmembrane helical segments (SI-S6). T
 CC -type Ca channels are activated at a lower voltage than L- or N-type
 CC channels. Characteristics of T-type channels include short current time,
 CC slow activation kinetics near threshold, fast inactivation kinetics and
 CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
 CC channels contains a putative IVS4 region comprising the amino acid
 CC sequence AAY14589. Cells expressing the T-type voltage-gated calcium
 CC channel proteins can be used to screen for drugs which affect calcium
 CC channels. Methods are also disclosed for treating a disease or disorder
 CC associated with a deficiency in a native T-type calcium channel nucleic
 CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
 XX SQ Sequence 2243 AA;
 Query Match 89.8%; Score 10806.5; DB 2; Length 2243;
 Best Local Similarity 93.3%; Pred. No. 0;
 Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;
 QY 62 GAAGAGSTEXDPSADSEAEGLPYPALAPVFFYLSQDSRPSWCLRTVCNPFERSM 121
 Db 30 GRPGGSAEKDPSADSEAEGLPYPALAPVFFYLSQDSRPSWCLRTVCNPFERSM 89
 QY 122 VILLNCVTLMFRCEDIACDSQCRILQAFDDFIFAFFAVEMVVKVVALGIFGKCYLG 181
 Db 90 VILLNCVTLMFRCEDIACDSQCRILQAFDDFIFAFFAVEMVVKVVALGIFGKCYLG 149
 QY 182 DTWNRLOFFVIAGMLEYSLDQNVFSFSAVTVRLRPLRAINEVPSMRILVTLTLP 241
 Db 150 DTWNRLOFFVIAGMLEYSLDQNVFSFSAVTVRLRPLRAINEVPSMRILVTLTLP 209
 QY 242 MLGNVLLCFVFFIFGIVGVQLWAGLLRNRCFLPENFSLVDLEPYQTENEDESPF 301
 Db 210 MLGNVLLCFVFFIFGIVGVQLWAGLLRNRCFLPENFSLVDLEPYQTENEDESPF 269
 QY 302 ICSQPRENGMESCSVPTLRGEGGGPPCSLDIETYNSSNTTCVNMVQYVTCNCSAGBN 361

270 ICSPRENGMRCRSVPTLRGDGGGPPCGLDYEAYNSSNTTCVWNQYITNCSAGEHN 329
362 PFKGAINFDNIYAMIAI FQVITLGGWDIMYFVMDAHSFYNFYIFILLIIVGSEFMNL 421
330 PFKGAINFDNIYAMIAI FQVITLGGWDIMYFVMDAHSFYNFYIFILLIIVGSEFMNL 389
422 CLVVIATOFSETKORESOLMREQRVFLSNASTLASFSEPGSCYBELLYVILRKAAR 481
390 CLVVIATOFSETKORESOLMREQRVFLSNASTLASFSEPGSCYBELLYVILRKAAR 449
482 RLQVSRALGRAGLLSEPVARSQEPQPSGCTSHRRLSVHHVLUHHHHHHHHYHLGN 541
450 RLQVSRAGVREVGLLSPALPGQETQPSSSCSRSRRRLSVHHVLUHHHHHHHHYHLGN 509
542 GTLRVPASPEIQDRDANGSRRLMLPPSTPTPPSGPPRGAEVSHSFYHADCHLEPVRQ 601
510 GTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVSHSFYHADCHLEPVRQ 569
602 APPRCPSEASGRVYGVKVTYVHTSPPEILKDKALVEVAPSPGPTLTLSFNIPPGPF 661
570 APPRPSSEASGRVYGVKVTYVHTSPPEILKEKALVEVAASSGPTLTLSNIPPGPY 629
662 SSMHKLLETQSTGACHSCCK:SSPCSADGACGPDSCPYCARTGAGPESADHWMPDS 721
630 SSMHKLLETQSTGACQSCCK:SSPCLKADGACGPDSCPYCARAGAGEVELADREMPDS 689
722 SEAVVEFTQDAQHSDLRPHSRRORSIGLPAERSSVLAFWELICDTERKIVDSKYVGRG 781
690 SEAVVEFTQDAQHSDLRPHS-RRORSIGLPAERSSVLAFWELICDTERKIVDSKYVGRG 748
782 IMIAILVNTLSNGIEYHQEPELTNALBISNIVFTSLFALEMLKLLVYGPFGYIKPNYN 841
749 IMIAILVNTLSNGIEYHQEPELTNALBISNIVFTSLFALEMLKLLVYGPFGYIKPNYN 808
842 IFDGVIVIVISWEIVGQGGGLSVLRTFLMRVLKLVFLPALQOLVLMKTMNDNVATP 901
809 IFDGVIVIVISWEIVGQGGGLSVLRTFLMRVLKLVFLPALQOLVLMKTMNDNVATP 868
902 CMLMLFIFISILGMHLFGCKEASERDGTLPORKNFDLSLLWAIVTVFQILTQEDMNKV 961
869 CMLMLFIFISILGMHLFGCKEASERDGTLPORKNFDLSLLWAIVTVFQILTQEDMNKV 928
962 LYNMGMASTSSWAALFYIALMTFGVNYFLNLLVALIVEGFAEGDATKSESEPPDFPSVD 1021
929 LYNMGMASTSSWAALFYIALMTFGVNYFLNLLVALIVEGFAEGDATKSESEPPDFPSVD 988
1022 GDGRKRLALVAL:GEHAELPKSLPLI IHTAATPMHPSKSTGVGEALGSSGSRRTSS 1081
989 GDGRKKCLALVSLGEHPELRSKSLPLI IHTAATPMHPSKSTGTGLGEALGPSARRTSS 1048
1082 SGSAPGAHHKCPSPARSPPHSPWASASWTSRRSSNSLGRAPSLKERSPSGERS 1141
1049 SGSAPGAA-HEMKSPPARSPPHSPWASASWTSRRSSNSLGRAPSLKERSPSGERS 1107
1142 LLSGEGQESQDEBESSBEDRASPAGSDHRRHRSGLEREAKSFDLPDITLQVPEGLHRTASGR 1201
1108 LLSGEGQESQDEBESSBEDRASPAGSDHRRHRSGLEREAKSFDLPDITLQVPEGLHRTASGR 1167
1202 SSASEHQDCNGKSGSLARTLRTDDLPQDGDNDDEGNLSKGERIOAWVRSRLPACCRE 1261
1168 GSASEHQDCNGKSGSLARALRPDDPLDGDGDADDEGNLSKGERVRAWIRARLPACCLE 1227
1262 RDSMSAVIFPPQSPRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERFL 1321
1228 RDSMSAVIFPPQSPRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERFL 1287
1322 TLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSWSDSG 1381
1288 TLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSWSDSG 1347
1382 TKILGMLRVLLRLTLRPLRVISRAQGLKLVWETLMSLKPIGNIVVICAFFIIFGILG 1441
1348 TKILGMLRVLLRLTLRPLRVISRAQGLKLVWETLMSLKPIGNIVVICAFFIIFGILG 1407

QY 1442 VOLFKGKFFVCGEDTRNITNKSDCABASRYRVRHXYNFDNLGOALMSLFLVLASDQGWVD 1501
Db 1408 VOLFKGKFFVCGEDTRNITNKSDCABASRYRVRHXYNFDNLGOALMSLFLVLASDQGWVD 1467
QY 1502 IMYDGLDAVGDVQDQPIMNHNPMMLLYFISLLIIVAFFVLNMFVGVVVENFHKCRQHEE 1561
Db 1468 IMYDGLDAVGDVQDQPIMNHNPMMLLYFISLLIIVAFFVLNMFVGVVVENFHKCRQHEE 1527
QY 1562 BARRREXRLRLEKRRSKEKQMAEAQCKPYSDYSRFLLVHHLCTSHYLDLFTITGYI 1621
Db 1528 BARRREXRLRLEKRR- - - - -KAQCKPYSDYSRFLLVHHLCTSHYLDLFTITGYI 1580
QY 1622 GNVVVTWAMEHYQOQIILDEALKICNYIFTVI FVFESEVFKLVAFAPRFPQDRWNQDLA 1681
Db 1581 GNVVVTWAMEHYQOQIILDEALKICNYIFTVI FVLESVEFKLVAFGFRFPQDRWNQDLA 1640
QY 1682 IVLLSIMGITLBEIEVNLSPINPTIIRIMRVLRIRARVLLKLMKAVGMRALLHTVMQALP 1741
Db 1641 IVLLSIMGITLBEIEVNLSPINPTIIRIMRVLRIRARVLLKLMKAVGMRALLHTVMQALP 1700
QY 1742 QVGNLGLLFFMLFFIFPAALGVLEFDECEDETHPCCEGLRHATFRNFCMAFLTLFRVSTG 1801
Db 1701 QVGNLGLLFFMLFFIFPAALGVLEFDECEDETHPCCEGLRHATFRNFCMAFLTLFRVSTG 1760
QY 1802 DNWNGIMKDPSCDCDQSTCYNTVISPIYFVSFVLTQAQFVLNVTVAIIVMKHLESKEA 1861
Db 1761 DNWNGIMKDTURDCDQSTCYNTVISPIYFVSFVLTQAQFVLNVTVAIIVMKHLESKEA 1820
QY 1862 KEEAELEAELEMKTLSPQHSPLGSPFLWPVGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
Db 1821 KEEAELEAELEMKTLSPQHSPLGSPFLWPVGVEGVNSTDSPKPGALHPAAHAKASHP 1880
QY 1922 SLEHPTWVHPDEEVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRCWGL 1981
Db 1881 SLEHPTWQHPTELP- - -GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRCWGL 1937
QY 1982 PKAQSGLSVHSQPADTSCILQPKDVHYLLQHPGAPTWCAI PKLPPGSRPLAQRPLR 2041
Db 1938 PKAQSGLSVHSQPADTSCILQPKDAPHLQHPASPTWTGTI PKLPPGSRPLAQRPLR 1997
QY 2042 RQAARITDSLTVQGLSGREDLLSEVSGPSCPLTRSSSFWSGSSIQVOORSGIQSKVSKHI 2101
Db 1998 RQAARITDSLTVQGLSGREDLLAEVSGPSPPLARAYSFWGQSSSTQAQHSRSHSKISKHM 2057
QY 2102 RLPAFCPLGEPWSKADPPETRSSLELDELTELISWISGDL- - -PSSOEPFLPRDLKCYSVET 2160
Db 2058 TTPAPCPGPEPNWKGPPETRSSLELDELTELISWISGDL- - -PPGQEQEPSPRDLKCYSVET 2117
QY 2161 QSCRRRPGFMDDEORRHSHAVSCLDSSGQPLCPSPSLGQPLGGGSRPKKLSPPSI 2220
Db 2118 QSCRRRPTMLDEORRHSHAVSCLDSSGQPLGDPNGLGQPLGGGSRPKKLSPPSI 2177
QY 2221 SIDPPESQGRPPGSPGVCLRRRAPADSDDPSVSSPLDSTAASPSPKDTLSLGLSSD 2280
Db 2178 TIDPPESQGRTPPSPOICLRRRAPSDSKDPLASGPPDSMAASPSPKDVLSLGLSSD 2237
QY 2281 PTMDP 2286
Db 2238 PADLDP 2243

RESULT 12

ADJ68819

ID ADJ68819 standard; protein; 2243 AA.

XX AC ADJ68819;

XX DT 06-MAY-2004 (first entry)

XX DE Human heat mitochondrial protein as a therapeutic target SeqID625.

XX KW mitochondrial; human; screening assay; diabetes mellitus;


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Db 450 RLAQVSRAGVTVGLSSPAPLGGQETQPSSSCSRSHRELNVNHLVHHNEMHNHVLGN 509
QY 542 GTLRVPRASPETQDRDANGSRIMLPDPPTPTPGGPRGAESVHSFYHADCHLEVRQC 601
Db 510 GTLRAPRASPEIQDRDANGSRIMLPDPPTPTPGGPRGAESVHSFYHADCMLEVRQC 569
QY 602 APPRCPSEASGRVGVVHTSPPEILKDKALVEVAPSPPEPTLTSENIIPGPF 661
Db 570 APPRSPSASGRVGVVHTSPPEILKDKALVEVAPSPPEPTLTSENIIPGPF 529
QY 662 SSMHKLLETQSTGACHSSCKISPCSKADSGAGCPDSCPCYARTGAGEPESADHWMPDSD 721
Db 630 SSMHKLLETQSTGACHSSCKISPCSKADSGAGCPDSCPCYARTGAGEPESADHWMPDSD 689
QY 722 SEAVYEFTQDAQHSIDLPHSRRRRQSLGPDAPSSVLAFWRLLCDTFRKIIVDSKYFGRG 781
Db 690 SEAVYEFTQDAQHSIDLPHSRRRRQSLGPDAPSSVLAFWRLLCDTFRKIIVDSKYFGRG 748
QY 782 IMAILAVNTLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLLKLIVVGPFGYIKNPYN 841
Db 749 IMAILAVNTLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLLKLIVVGPFGYIKNPYN 808
QY 842 IFDGVTVIWSVMBIVGQGGGLSVLRTRFLMRVLKLVRLPALQROLVLMKTMNDVATF 901
Db 809 IFDGVTVIWSVMBIVGQGGGLSVLRTRFLMRVLKLVRLPALQROLVLMKTMNDVATF 868
QY 902 CMLLMLEFIIFSLGMLHFCCKFASERDGTLPDRKNFDSLWAIIVTVQILTOEDWNV 961
Db 869 CMLLMLEFIIFSLGMLHFCCKFASERDGTLPDRKNFDSLWAIIVTVQILTOEDWNV 928
QY 962 LYNGMASTSWAALYFIATMFGNYVFNLLVAILVEGFOAE----- 1003
Db 929 LYNGMASTSWAALYFIATMFGNYVFNLLVAILVEGFOAEISKEEDASGQLSCIQLP 988
QY 1004 -----GDATKSESEPPFFSPVDGDRKKRLALVALGEHAEIRKSLPLLIHTAATPM 1058
Db 989 VDSQGGDANKSESEPPFFSPVDGDRKKRLALVALGEHAEIRKSLPLLIHTAATPM 1048
QY 1059 SHPKSSTGVGEALGSGSRSTSSGSAEPGAAHEMKCPSABSSHPMSAASSWTSSR 1118
Db 1049 SLPKSTSTGVGEALGSGSRSTSSGSAEPGAAHEMKCPSABSSHPMSAASSWTSSR 1107
QY 1119 SSNSLCRAPSLKRRSPSGRRSLLSGEGQESQDEEESSEEDRASPAQSRRHRGSLERE 1178
Db 1108 SSNSLCRAPSLKRRSPSGRRSLLSGEGQESQDEEESSEEDRASPAQSRRHRGSLERE 1167
QY 1179 AKSSFDLPDLTVQVGLHRTASGRSSASEHQDNGKSASGLARTLTPTDDPOLGDDNDDE 1238
Db 1168 AKSSFDLPDLTVQVGLHRTASGRSSASEHQDNGKSASGLARTLTPTDDPOLGDDNDDE 1227
QY 1239 GNLKGBRIQAWRSRLPACCRBDSWSAVIFPQSRFLLICHRITTHKMFHDHVLNIIIF 1298
Db 1228 GNLKGBRIQAWRSRLPACCRBDSWSAVIFPQSRFLLICHRITTHKMFHDHVLNIIIF 1287
QY 1299 LNCITIAMERPKIDPHGAERIFITLSNYIFTAFLAEMTVKVALGWCFCGEQAYLRSSN 1358
Db 1288 LNCITIAMERPKIDPHGAERIFITLSNYIFTAFLAEMTVKVALGWCFCGEQAYLRSSN 1347
QY 1359 VLDGLLVLSIVDILVMSVDSGFKILGMLRVLRLLRTPLRVISAQGLKLVETLMS 1418
Db 1348 VLDGLLVLSIVDILVMSVDSGFKILGMLRVLRLLRTPLRVISAQGLKLVETLMS 1407
QY 1419 SLKPIGNIVTCACAFFIIFGLVQLFKGPFVCCGSDTRNITNKSACAASVYEWVHKY 1478
Db 1408 SLKPIGNIVTCACAFFIIFGLVQLFKGPFVCCGSDTRNITNKSACAASVYEWVHKY 1467
QY 1479 NFDNLGQALMSLFLVASKDGVWDIMYDGLDVGVDQOPIMNHPNMLLYIFISFLIVAFP 1538
Db 1468 NFDNLGQALMSLFLVASKDGVWDIMYDGLDVGVDQOPIMNHPNMLLYIFISFLIVAFP 1527
QY 1539 VLNMFVGVVNFHFKRQHQEBEERARRERREIRLEKKRSKQKWAEOCKPYSDYS 1598
Db 1528 VLNMFVGVVNFHFKRQHQEBEERARRERREIRLEKKRSKQKWAEOCKPYSDYS 1580
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QY 1599 RPELLVHLLCTSHYLDLFTITVIGLVNVTMAMEHYQQOILDEALKICNYIFTVIFVFS 1658
Db 1581 RPELLVHLLCTSHYLDLFTITVIGLVNVTMAMEHYQQOILDEALKICNYIFTVIFVFS 1640
QY 1659 VFELVAFAPRRFQDRWNQDLAIIVLLSIMGITLBEIEVNLSPINPTIIRMRVLRIAR 1718
Db 1641 VFELVAFAPRRFQDRWNQDLAIIVLLSIMGITLBEIEVNLSPINPTIIRMRVLRIAR 1700
QY 1719 VLKLLKMAVGMALLHTVMQALPOCNLGLLFWLLFFIFAALGVELFGLDEDETHPCG 1778
Db 1701 VLKLLKMAVGMALLHTVMQALPOCNLGLLFWLLFFIFAALGVELFGLDEDETHPCG 1760
QY 1779 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOPSRDCDOESTCYNTFVISPFIYFVSFLTA 1838
Db 1761 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOPSRDCDOESTCYNTFVISPFIYFVSFLTA 1820
QY 1839 QFVLNVVIAVIMKHLAESNKEAELEAELEEMKTLSPQSPHSPGLSPFLNPGVEGP 1898
Db 1821 QFVLNVVIAVIMKHLAESNKEAELEAELEEMKTLSPQSPHSPGLSPFLNPGVEGP 1880
QY 1899 NSTDSPKCPGAPHTTAHIGAASGFSLEHPTMVPHPEVPVPLGPDLLTVRKSGVSRTHSLP 1958
Db 1881 DSPDSPKCPGALPAAHARSASHFSLEHPTMQHPTELP--GPDLLTVRKSGVSRTHSLP 1937
QY 1959 NDSYMCRCNGSTAESRSLGHRGWLGPKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGA 2018
Db 1938 NDSYMCRCNGSTAESRSLGHRGWLGPKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGA 1997
QY 2019 PTWGAIPKLPDPPGRSPLAQRPRLRQAARTSDLDVQGLSREDLLSEVSGSPCLTRSSS 2078
Db 1998 PTWGTIPKLPDPPGRSPLAQRPRLRQAARTSDLDVQGLSREDLLSEVSGSPCLTRSSS 2057
QY 2079 FMGSSIOVQORSIGIOSKVSXHLRPAFCPLGPPSWAKPPETRRSSLELDTLSWISGDL 2138
Db 2058 FMGSSIOVQORSIGIOSKVSXHLRPAFCPLGPPSWAKPPETRRSSLELDTLSWISGDL 2117
QY 2139 L-PSSQEEELFPFRDLKKCYSVETQSCRRRPFGLMDEQRHSHIAVSCLDGSGQRLCPSPS 2197
Db 2118 LPFGGQEEELFPFRDLKKCYSVETQSCRRRPFGLMDEQRHSHIAVSCLDGSGQRLCPSPS 2177
QY 2198 SLGGQPLGGGSPKPKLLSPPSISIDPPSPQSGSPSPCVCLRRAPASDSKDPSSVP 2257
Db 2178 NLGGQPLGGGSPKPKLLSPPSISIDPPSPQSGSPSPCVCLRRAPASDSKDPSSVP 2237
QY 2258 LDSTAASPEPKDLSLGLSSDPTDMDP 2286
Db 2238 PDMAASPEPKDLSLGLSSDPTDMDP 2266
RESULT 14
AAB66476
ID AAB66476 standard; protein; 2359 AA.
XX
AC AAB66476;
XX
DT 09-APR-2001 (first entry)
XX
DE Rat alpha-IH calcium channel protein.
XX
KW Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;
KW hypotensive; cardiact; nootropic; T-type calcium channel subunit;
KW cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;
KW epilepsy; alpha-IH calcium channel.
XX
OS Rattus sp.
XX
FN WO200102561-A2.
XX
PD 11-JAN-2001.
XX
PF 04-JUL-2000; 2000WO-CA000794.
XX
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PR 02-JUL-1999; 99US-00346794.
PA (NEUR-) NEUROMED TECHNOLOGIES INC.
XX Snutch TP, Baillie DL;
XX WPI; 2001-123111/13.
DR N-PSDB; AAF31678.
XX Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT epilepsy.
XX Disclosure; Page 75-85; 103pp; English.
XX The present sequence is given in a specification providing sequences and
CC partial sequences for three types of mammalian (human and rat) T-type
CC calcium channel subunits. An expression cassette has been generated which
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC subunit operably linked to control sequences to effect its expression.
CC The novel calcium channel nucleic acids and proteins are useful for
CC treating conditions characterised by undesirable levels of T-type calcium
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC hypertension, sleep disorder and epilepsy
XX Sequence 2359 AA;
Query Match 51.8%; Score 6226.5; DB 4; Length 2359;
Best Local Similarity 56.1%; Pred. No. 0;
Matches 1357; Conservative 246; Mismatches 506; Indels 311; Gaps 59;
QY 30 LARGWTRRRMERAPSRDPSV-ASRSSTTCPO---PGAAGAG-STKXDPGS---AD---S 78
DB 6 LAADVVRVPLGASPPAPAPVRASPASGAGREEGGGSGCVLAPESPFGTECGADLAD 65
QY 79 EAGLPLYPALAPVFFYLQSQRPSWCLRTVCPNPFVSMVLVILLNCVILGMPFPCD 138
DB 66 EEPVFPYALAAATVFCFLGQTRPRSWCLRLVCPNPFVSMVLVILLNCVILGMPFPCD 125
QY 139 IACDSORCILQAPDDTFAFAFVEMVVMVALGIFGKKCYLGDWNLDFIVTAGMLE 198
DB 126 VECSEKCSILEAFDDTFAFAFVEMVVMVALGIFGKKCYLGDWNLDFIVTAGMLE 185
QY 199 YSLDLQNVFSAVRTVRVLRPLRINRVPSRIILVTLDDTLPLMGNVLLLCFFVFIFG 258
DB 186 YSLDGHKVSLSAIRTVRLRPLRINRVPSRIILVTLDDTLPLMGNVLLLCFFVFIFG 245
QY 259 IVGVQLWAGLLRNRCFLDENFSLPLSD-LBPYYQTEDESPFCSQPRENGMRSCRSV 317
DB 246 IVGVQLWAGLLRNRCFLDSAFVRNNNLTLFLRPYYQTEDEENPFCSRRDNGMKCSHI 305
QY 318 PT---LRGEGGGPPCSLDYETV-----NSSNTTCVMNQYNTCSAGEHNPFGAI 367
DB 306 PSRELRVQ-----CILGWFAVQQAEDGGAGRNACINQYNNVCRSGEFNPHNGAI 359
QY 368 NFDNIGYAWIAFQVITLEGWVDIMYFMDAHSFNFYIFILLIIVGSGFFMINCLVVIA 427
DB 360 NFDNIGYAWIAFQVITLEGWVDIMYFMDAHSFNFYIFILLIIVGSGFFMINCLVVIA 419
QY 428 TQFSETQKRSQLMREORVPLSNASTLASPEGSCYEELLYLVYLKAAARLQVVS 487
DB 420 TQFSETQKRENQLMREORVPLSNASTLASPEGSCYEELLYLVYLKAAARLQVVS 479
QY 488 RAIGVRAGLLSSPVAR-----SGEPQPSGCTSHRLSLVHVLV-HHHHHHHHHYHFN 541
DB 480 ARWQSRWRKVKVDPSTVHGQPGRRPRAG-----RETASVHLLVYHHHHHHHHYHFN 534
QY 542 GTLRVPASPEIQORDANGSRRLM-LPPSPSTPSPGPRGASVHSFVHADCHLFPVR 599
DB 535 GGPR--RPSE-----PGAGNRLVRACAPSPSPGHPGP--DSVSHSIYHADCHVEGPQ 587
QY 600 CQAPPPPCSEASGRTVSGS---KVYPTV-----HTSPPEILDKALVEVAPSP 646

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DB 642 GAAVHSPLSGSPRVEKIQDVVGQGLGRASHLSGLSVPCFELPSQAGTLTCELKSCP 701
QY 701 YCARTGAGEP--ESADHVMPDSDSAVYFTQDAQHSJLDRP-----HSRROR 747
DB 702 YCA-SALEDEPEFESGSDSAHVYFTQDVVRHGDRCRDPVQVQPHVEGTGPHSNERRR 760
QY 748 S-LGPDAPSSVLAFWRLICDTRFKIVDSKYFGRGIMTALVNTLSMGTGYEHOPELTN 806
DB 761 TPLRKASQPGGICHLWASFSGKLRRIVDSKYFNRGIMAILVNTLSMGTGYEHOPELTN 820
QY 807 ALEISNIVFTSLFALEMLLKLAVYGGFYKPNYINIFDGVIVVISWEIVGQGGSLSVL 866
DB 821 ALEISNIVFTSMFALEMLLKLACGLGYIRPNYINIFDGVIVVISWEIVGQGGSLSVL 880
QY 867 RTFRLMRVLKLVRFPLALORQVLVLMKTDVNVATFCMLLMLEFIFISILGMHLFGCKPAS 926
DB 881 RTFRLMRVLKLVRFPLALORQVLVLMKTDVNVATFCMLLMLEFIFISILGMHLFGCKPAS 940
QY 927 BRD-GDTLPDRKNFDSLLWAIIVTFQILTOEDWNVLYNGMASTSSWAALYFVALMTGN 985
DB 941 KTDGDTVPDRKNFDSLLWAIIVTFQILTOEDWNVLYNGMASTSSWAALYFVALMTGN 1000
QY 986 YVLFNLLVAILVEGQAEGDATKSEDPFFSPVDGDDGRKKRL-----ALVALG 1036
DB 1001 YVLFNLLVAILVEGQAEGDATKSEDPFFSPVDGDDGRKKRL-----ALVALG 1060
QY 1037 EHAELKSLPLLIHTAATPMSPKSS-STGVGEALSGSRRTSSSGSABPAAAHENK 1095
DB 1061 GLEGRGSLPLLIHTAATPMSPKSS-STGVGEALSGSRRTSSSGSABPAAAHENK 1116
QY 1096 CPPARSPPHSPWMAASWTSSRNSLGRAPSLKPSPSGERSLSSGSGSODREE 1155
DB 1117 SLASRSPCTPWGPNSSAGSRSSWNLGRAPSLKPSPSGERSLSSGSGSODREE 1175
QY 1156 SSEDRA-----PAGSDHHRGSLEREAKSFDL-----PDTLVQVGLHRTAS 1199
DB 1176 -AEDSRSTGTHPGASPGPRATPLRRAESLDH--RSTLDLCPRPAPPVAVQV----- 1224
QY 1200 GRSASHEQDNGKASGRRLARTLRTDDPQDGDGDDDEGNLSKGERIQAWRSLRSLPACC 1259
DB 1225 -----HDCGNQVALPSEFFLRIDSHKEDAAEFDDIEDSCCFRLHKVLEYPAPWC 1276
QY 1260 RERDSWAIYPPQSPRFLCHRIITHKMFDPVVLVIIIFLNCITIAMERPKIDPHSAERI 1319
DB 1277 RSRESWAIYFPQNRRLRVSCQVIAHKMFDPVVLVIIIFLNCITIAMERPKIDPHSAERI 1336
QY 1320 FLTLNVIYFAVFAEMTVKVALGWCFOAYLRSSNVLVLDGLLVLISVIDILVSVMSVD 1379
DB 1337 FLVSNIYFAVFAEMTVKVALGWCFOAYLRSSNVLVLDGLLVLISVIDILVSVMSVD 1396
QY 1380 SGTKILGMLVRLRLRLRLRPLRISRAQGLVWVETLMSLKPIGNIVVICAPFIIFI 1439
DB 1397 GGAKILGMLVRLRLRLRLRPLRISRAQGLVWVETLMSLKPIGNIVVICAPFIIFI 1456
QY 1440 LGVOLFKGKFFVQCGEDTRNITNKSDCABASYRWVRHKYNFNDLGOALMSIFVLASKDGW 1499
DB 1457 LGVOLFKGKFFVQCGEDTRNITNKSDCABASYRWVRHKYNFNDLGOALMSIFVLASKDGW 1516
QY 1500 VDIWYDGLDAVGVDQPPIMNHPMLLYFISFLLIIVAFVFLNMFVGVVFNHFKCRHQE 1559
DB 1517 VNIWYDGLDAVGVDQPPIMNHPMLLYFISFLLIIVAFVFLNMFVGVVFNHFKCRHQE 1576
QY 1560 EEARREERKRLRLEKRSKQMAEACKPYSDYSRFLRVHHLCTSHYLDLFTG 1619
DB 1577 AEARREERKRLRLEKRSKQMAEACKPYSDYSRFLRVHHLCTSHYLDLFTG 1629
QY 1620 VIGLVVTVMAEYHQQPILDEALKTCNYLFTVIFVESVFKLVAFAFRFFQDRWNOLD 1679
DB 1630 IICLVNITSMEHYNQPKSLDEALKTCNYLFTVIFVESVFKLVAFAFRFFQDRWNOLD 1689

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QY 495 GLLSFPVARSQEPQPSGSCSTRSHRR-----LSVHHLV-HHHHHHHHHYHLGNGTLRV 546
Db 487 RKKVDPESAQQGP-----GHRORRAGRHTASVHHLVYHHHHHHHHYHFSHGSPPR 538
QY 547 PRASFEIQDRDANGSRRLML--PPSTPTSPGPPRGAESVHSFYHADCHLE--PVRQOA 602
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QY 647 --GPPLTSFNIPGPFSSMHKLELTQSTGAC--HSS-----CKISSPCKADSGACGPD 697
Db 645 GHGPLSLNS-----PDPEYKIPHVVGEGHGLQAPGHLGSLVPCPLSP--PAGTILCELK 698
QY 698 SCPIYART-GAGEPESADHWPDSSEAVYETQDAQSHSDURDP----- 740
Db 699 SCPIYTRALEPDEGELSGESDSDGRGVYETQDVRHGDWRDTPRPRATDTPGPGPS 758
QY 741 HSRRRQSLGDAEPSSVLAFWRLICDTPRKIVDSKYFGRGTMIALVNTLSMGLEYHEQ 800
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QY 801 PEELTNALEISNIVFTSLFALEMLKLIVYGPFGYIKNPYINIFDGVIVVISVWEIVGQG 860
Db 818 PEELTNALEISNIVFTSMFALEMLKLLACGPLGYIRNPYINIFOGIIVVISVWEIVGQAD 877
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Db 878 GGLSVLRFRMLRVLKVRFIPALORQVLVLMKTMNDVNATFCTLLMFIPIFSLGMHLF 937
QY 921 GCKPASERD-GDTLPDRKNFDSLLWAIIVTQILTOEDNKNVLYNGMASTSSWALYETA 979
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QY 980 LMTFGNYVFNLLVAILVEGFAEGDQATKSESEDPFSPSDGDRKKRLALVAL----- 1035
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QY 1036 -----GEHAELRKSLLPLIITHAATPMHPSKSS-TGVGALGSGSRRTSSSGSAEPA 1089
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Db 1266 --CDSRAWALYLFSPQNRFRVSCQVITHKMDHVLVLIIFLNCVITIALERPIDPGST 1323
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QY 1377 VDSGKILGMLRVLRLLRTRPLRVISRAOGLKLVVETLMSLKPIGNIVVICAPFII 1436
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QY 1437 FGIIGVOLFKGKFFVCGGEDTRNTKSDCAEASRYRWRHKNYFEDNLGOALMSLFLVASK 1496
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Db 1623 ITFIICVNVITMSMEHYNQPSLDEALKYCNVYFTIVFEEAALKLVAFGFRFRFDRWN 1682
QY 1677 OLDLAIVLLSMGITLEEIEVNLSPINPTIIRMRVRIARVLKLLKXWCMRALLHTV 1736
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QY 1854 LEENKEAKEAELEAELEEMKTLSPQHPSPGLSPFLWPGVEGVNSTDSPKPGAPHTTA 1913
Db 1863 LEENKEAREDAELDAELELEMA-----QPGGARVVDADRP----- 1899
QY 1914 HIGASGFSLEHTVMVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA--- 1970
Db 1900 -----PLPQSSPGARDAPNLVARKVSVSRMLSLPNDSYMFRPVVPASAP 1943
QY 1971 -----ERSLGHRCWGLPKAOSGILSVHSOPADTSCILQPKDVH-----YLLQP 2015
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QY 2016 HGAPTGAIPKLPPLPPGRSPLAQRPLRQAARTDSDLVQGLGSRREDLLSEV---SGPSC 2071
Db 2001 RGT-----ARSPSLRLLCQEAHVHTDLSLEG-IDSPRDLTPAEPGEKTEVR 2047
QY 2072 PLTRSSSFWGSSIQVQORSGIQSKV--SKH-----IRLPAPCPGLESPSWAKPPETRS 2123
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QY 2174 QRRHSIAVCLDSGSPRLCPSPSSLGQPLGGP--GSRPKKLSPPSISIDPP-ESQGS 2230
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QY 2275 SGLSSDPTDM-----DP 2286
Db 2264 PSFAPELDLGVSPGDP 2280

Search completed: November 18, 2004, 13:23:47

Job time : 201.365 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:41 ; Search time 40.6868 seconds
(without alignments)
3727.727 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVPCVRTPPLRGSAR.....KKDTLSLGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10820.5	90.0	2273	3	US-09-426-998-5
2	6221	51.7	2353	3	US-08-984-709A-50
3	5872	48.8	1207	4	US-09-398-522-52
4	5409	45.0	2175	3	US-09-404-650-2
5	5409	45.0	2175	4	US-09-935-541-2
6	5405.5	44.9	2188	3	US-09-404-650-4
7	5405.5	44.9	2188	4	US-09-935-541-4
8	5345	44.4	1835	3	US-09-404-650-5
9	5345	44.4	1835	4	US-09-935-541-5
10	1678	14.0	2343	3	US-09-268-163-4
11	1677	13.9	2337	3	US-08-713-118-2
12	1677	13.9	2337	3	US-09-452-007-2
13	1676	13.9	2339	1	US-08-455-543A-47
14	1676	13.9	2339	2	US-08-223-305C-47
15	1674	13.9	2339	3	US-09-268-163-6
16	1642.5	13.7	2237	1	US-08-455-543A-48
17	1642.5	13.7	2237	2	US-08-223-305C-48
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19	1642	13.7	1985	4	US-09-495-714C-6
20	1640.5	13.6	2237	3	US-09-268-163-8
21	1634.5	13.6	1984	3	US-08-836-325-10
22	1634.5	13.6	1984	4	US-09-457-571-10
23	1628.5	13.5	1977	4	US-09-495-714C-4
24	1628	13.5	1873	1	US-08-435-675B-4
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27	1625	13.5	2161	1	US-08-455-543A-51

28 1625 13.5 2161 2 US-08-223-305C-51 Sequence 51, Appl
29 1622 13.5 2161 1 US-07-745-206A-2 Sequence 2, Appl
30 1622 13.5 2161 1 US-08-455-543A-49 Sequence 49, Appl
31 1622 13.5 2161 2 US-08-223-305C-49 Sequence 49, Appl
32 1622 13.5 2161 2 US-08-311-363-2 Sequence 2, Appl
33 1617.5 13.4 1969 3 US-08-836-325-16 Sequence 16, Appl
34 1617.5 13.4 1969 4 US-09-457-571-16 Sequence 16, Appl
35 1616 13.4 1873 1 US-08-336-257A-7 Sequence 7, Appl
36 1614.5 13.4 1977 4 US-09-976-594-757 Sequence 757, App
37 1614.5 13.4 1977 4 US-09-919-039-367 Patent No. 5386025
38 1614 13.4 1872 6 5386025-6 Sequence 2, Appl
39 1595.5 13.3 1912 4 US-09-495-714C-2 Sequence 2, Appl
40 1589.5 13.2 2516 3 US-08-374-077C-2 Sequence 2, Appl
41 1589.5 13.2 2516 3 US-08-895-590-2 Sequence 2, Appl
42 1589.5 13.2 2516 4 US-09-539-879A-2 Sequence 2, Appl
43 1588.5 13.2 2016 4 US-09-514-907A-2 Sequence 2, Appl
44 1588.5 13.2 2016 4 US-09-896-994-2 Sequence 2, Appl
45 1585.5 13.2 2016 3 US-09-634-920-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-426-998-5
; Sequence 5, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAVASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
; FILE REFERENCE: CHANNEL (ALPHAIG-C)
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 5
; LENGTH: 2273
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-426-998-5

Query Match 90.0%; Score 10820.5; DB 3; Length 2273;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2080; Conservative 35; Mismatches 105; Indels 29; Gaps 5;
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Db 30 GRPGSAEKDPGSADSEAGLPYPALAPVVFFYLSQDSRPSRCLRTVCNWPFRYSML 89
Qy 122 VILLNCVTLMGRPCEDIACDSORCRLQAFDFPIFAFFAVEMVVMVALIGFKKCYLG 181
Db 90 VILLNCVTLMGRPCEDIACDSORCRLQAFDFPIFAFFAVEMVVMVALIGFKKCYLG 149
Qy 182 DTNRLDFFVIAGMLEYSLDLQNVFSFSAVRTVRVLRPLRINRVPMSRLVTLTLLDTP 241
Db 150 DTNRLDFFVIAGMLEYSLDLQNVFSFSAVRTVRVLRPLRINRVPMSRLVTLTLLDTP 209
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Db 210 MLGNVLLCFVFFIFGIVGVQLWAGLLNRCLPENFSLPSVDLEPPYYQTENEDESPF 269
Qy 302 ICSPQRENGMRCRSVPTLREGGGGPPCSDLYETYNSSNTTCVMNQYITNCSEH 361
Db 270 ICSPQRENGMRCRSVPTLREGGGGPPCSDLYETYNSSNTTCVMNQYITNCSEH 329
Qy 362 PFKGAINFNDIGYAWIAIIFOVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFMINL 421
Db 330 PFKGAINFNDIGYAWIAIIFOVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFMINL 389

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482 RLAAQVSRATGVRAGLLSPVARSQBPQSGCTSRHRLSVHLLVHHHHHHHHYHLGN 541
Db RLAAQVSRATGVRAGLLSPVARSQBPQSGCTSRHRLSVHLLVHHHHHHHHYHLGN 509
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Db GTLRVPRASPEIQDRDANGSRRLMLPPSTPTSGGPPRGABSVHSFYHADCHLEPVRCQ 569
602 APPRCPSASGRTVSGKVPTVHTSPPEILKDXALVEVAPSPGPTLTSPNPPGP 661
Db APPRCPSASGRTVSGKVPTVHTSPPEILKDXALVEVAPSPGPTLTSPNPPGP 629
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Db SSMHKLLETQSTGACHSSCKISSPCKADSGAGCPDSCPCYARTGAGEPESADHVMPSD 689
722 SEAVYEFTQDAQHSJLDRPHRRRQSLGDPBSPSVLAFWRLLCDTFRKIVDSKYFGRG 781
Db SEAVYEFTQDAQHSJLDRPHRRRQSLGDPBSPSVLAFWRLLCDTFRKIVDSKYFGRG 748
782 IMTALIVNLSMGIEYHEQPEELTNALETISNIVFTSLFALEMLLKLVYCPGYIKNPYN 841
Db IMTALIVNLSMGIEYHEQPEELTNALETISNIVFTSLFALEMLLKLVYCPGYIKNPYN 808
842 IFDGVITWISVMBIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDVATF 901
Db IFDGVITWISVMBIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDVATF 868
902 CMLLMFLIFIFSLGMHLCFCKFASERDGTLPDRKNFDSLWAI VTVFOILTOEDWNV 961
Db CMLLMFLIFIFSLGMHLCFCKFASERDGTLPDRKNFDSLWAI VTVFOILTOEDWNV 928
962 LYNGMASTSWAALYFTALMTFGNYVLFNLVAILVEGFOAE----- 1003
Db LYNGMASTSWAALYFTALMTFGNYVLFNLVAILVEGFOAEISKREDASGQSLCIQLP 988
1004 ----GDATKSESEPPDFSFSDGDRKKRLALVALGEHAELKSLPLLIHTAATPM 1058
Db VDSQGGDANKSESEPPDFSFSDGDRKKRLALVALGEHAELKSLPLLIHTAATPM 1048
1059 SHPKSSSTGVGEALGSGSRRTSSGSAEPGAANHMKCPSARSSPHSPWSAASSWTSRR 1118
Db SHPKSSSTGVGEALGSGSRRTSSGSAEPGAANHMKCPSARSSPHSPWSAASSWTSRR 1107
1119 SSRNSIGRAPSLKRRSPSGRRSLSGEGQESODEESSBEDRASPGSDHRRHGSLERE 1178
Db SSRNSIGRAPSLKRRSPSGRRSLSGEGQESODEESSBEDRASPGSDHRRHGSLERE 1167
1179 AKSFDLPDITLQVPLHRTASGRSSASEHQCNGKSASGRILARTLRTDDPQLDGDNDDE 1238
Db AKSFDLPDITLQVPLHRTASGRSSASEHQCNGKSASGRILARTLRTDDPQLDGDNDDE 1227
1239 GNLSKGRIQAWKRSRIPACCRERDSWSAIFPPQSRFRLLCHRIITHKMPDHVVLVIF 1298
Db GNLSKGRIQAWKRSRIPACCRERDSWSAIFPPQSRFRLLCHRIITHKMPDHVVLVIF 1287
1299 LNCITIAMERPKIDPHSAERIFLTLNVIYFAVLAEMTVKVALGCMCFQEAVALRSSWN 1358
Db LNCITIAMERPKIDPHSAERIFLTLNVIYFAVLAEMTVKVALGCMCFQEAVALRSSWN 1347
1359 VLDGLLVLSVIDILVMSVSDSGTKILGMLRVLLRLTLRLRVLISRAQGLKLVVETLMS 1418
Db VLDGLLVLSVIDILVMSVSDSGTKILGMLRVLLRLTLRLRVLISRAQGLKLVVETLMS 1407
1419 SLKPIGNIVWICCAFFIIFGILGVQLFKGKFFVCGEDTRNITNKSOCAEASYVWRHKY 1478
Db SLKPIGNIVWICCAFFIIFGILGVQLFKGKFFVCGEDTRNITNKSOCAEASYVWRHKY 1467
1478 SLKPIGNIVWICCAFFIIFGILGVQLFKGKFFVCGEDTRNITNKSOCAEASYVWRHKY 1457

1479 NFDNLGQALMSLFLVASKDGVWDIMYDGLDVGVDQOQPTMHNHPWMLYFIFLILVAF 1538
Db NFDNLGQALMSLFLVASKDGVWDIMYDGLDVGVDQOQPTMHNHPWMLYFIFLILVAF 1527
1539 VLNMFGVVVENPHKCRQHOEBEABARRBEEKRLRLBKKRSEKQMAEAOCKPYSDYS 1598
Db VLNMFGVVVENPHKCRQHOEBEABARRBEEKRLRLBKKRSEKQMAEAOCKPYSDYS 1587
1599 RERLAVHHLCTSHYLDLFTITGIVGLNVVTMAHEVYQOQPOLDEALKINVIYFIVFVS 1658
Db RERLAVHHLCTSHYLDLFTITGIVGLNVVTMAHEVYQOQPOLDEALKINVIYFIVFVS 1647
1659 VFKLVAFAFRFRFQDRWNQDLALVLLSIMGITLBEIEVNLSPINPTIIRMRVLRIAR 1718
Db VFKLVAFAFRFRFQDRWNQDLALVLLSIMGITLBEIEVNLSPINPTIIRMRVLRIAR 1707
1719 VLKLLKMAVGMALHTVMQALPOVGNLGLLFWLFFIFAAALGVELFGDECDTHPCBG 1778
Db VLKLLKMAVGMALHTVMQALPOVGNLGLLFWLFFIFAAALGVELFGDECDTHPCBG 1767
1779 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSPRDCDOESTCYNTVISPFIYFVSFLTA 1838
Db LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSPRDCDOESTCYNTVISPFIYFVSFLTA 1827
1839 QFVLNVNVIIVLMLKHEESNKEAEAELEAELEEMKTLSPQHPSPGLSPFIMPVGEV 1898
Db QFVLNVNVIIVLMLKHEESNKEAEAELEAELEEMKTLSPQHPSPGLSPFIMPVGEV 1887
1899 NSTDSKPGAPHTTAHIGASGFSLEBHTMVHPPEVPVPLGPDLLTVRKSGVSRTHSLP 1958
Db NSTDSKPGAPHTTAHIGASGFSLEBHTMVHPPEVPVPLGPDLLTVRKSGVSRTHSLP 1944
1959 NDSYMRNCRNSTAERSLGHGWLKPAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGA 2018
Db NDSYMRNCRNSTAERSLGHGWLKPAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGA 2004
2019 PTWGAIPKLPPPGSRPIAQRRLRQAAIRTDSDVQGLSGREDLLESEVSPCLTRSSS 2078
Db PTWGAIPKLPPPGSRPIAQRRLRQAAIRTDSDVQGLSGREDLLESEVSPCLTRSSS 2064
2079 FWGSSIOVQORSIGIOSKYSKHIRLPACPLGPSWAKOPPETRSSI-ELDTLSWISGDL 2138
Db FWGSSIOVQORSIGIOSKYSKHIRLPACPLGPSWAKOPPETRSSI-ELDTLSWISGDL 2124
2139 L-PSSOEPLFPRDLKKCYSVETQSCRRRPFGLDFQRHRSIAVSCLDGSGQRLCPSPS 2197
Db L-PSSOEPLFPRDLKKCYSVETQSCRRRPFGLDFQRHRSIAVSCLDGSGQRLCPSPS 2184
2198 SLGGQPLGGPGSRPKKLSPPSISIDPPESQGGRRPPCSPGVCLRRRAPASDSKDPVSSP 2257
Db SLGGQPLGGPGSRPKKLSPPSISIDPPESQGGRRPPCSPGVCLRRRAPASDSKDPVSSP 2244
2258 LDTAASPSPKDITLSLGLSSDPTMDP 2286
Db LDTAASPSPKDITLSLGLSSDPTMDP 2273
2245 PDSMAASPSPKDVLSSGLSSDPAIDLDP 2273

RESULT 2
US-08-984-709A-50
; Sequence 50, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla
; STATE: California

COUNTRY: US
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/984,709A
 FILING DATE: 02-DEC-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 450-8400
 TELEFAX: (619) 587-5360
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2353 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 US-08-984-709A-50

Query Match 51.7%; Score 6221; DB 3; Length 2353;
 Best Local Similarity 56.6%; Pred. No. 0;
 Matches 1368; Conservative 209; Mismatches 530; Indels 310; Gaps 62;

QY	25	PPGRLARCTRRRNERAPGRDRP--VASRSTTCPGPGAGAGSTKDPGSDADSEAG	82
DB	19	PPGPAALVG-----ASPESGAPGREAGERSELGVSPSPAARGAELGA--DEEQR	69
QY	83	LPYPALAPVVFYLSQSRPSWCLRTVCNPFERVSMLVTLNCVTLGMRPCEDTACD	142
DB	70	VPYALAAVFCGLQTTTPRSWCLRLVCNPFVSHVSMVLMNCVTLGMRPCEDVECG	129
QY	143	SQRCRILOAFDDIFAFFAVMMVMVALGIFGKKCYLGTWNRLDFFIVLAGMLEYSLD	202
DB	130	SERCNILEAPDAFIAFAFVEMVIMKVALGLFGQCYLGTWNRLDFFIVVAGMWEYSLD	189
QY	203	LQNVSPSAVTVRVLRLRAINRVPMSRIILVTLPLMGNVLLCFFVFFIFGIVGV	262
DB	190	GHNVSLSAIRTVRLRLRAINRVPMSRIILVTLPLMGNVLLCFFVFFIFGIVGV	249
QY	263	QLWAGLIRNRCFLPENFSLPSVD-LEPYQOTENEDESPPICSPQRENGMRSCBSVPTLR	321
DB	250	QLWAGLIRNRCFLDFAVRNNLTFLPYQYQTEGEENPPICSSRRDNGMOKCSHIP---	306
QY	322	GEGGGPPCLSDYETYN-----SSNTTTCVNNNQYITNCAGEHPFKAINFQNGY	374
DB	307	GRELRMECTLGWEAYTQPAEGVGAARNACINNNQYVNCVSDSPHNGAINFQNGY	366
QY	375	AWTAIFOVITLEGWVDIMYFMDAHSYNTFYFILLIIVGSFFMINCLVVIATQFSETK	434
DB	367	AWTAIFOVITLEGWVDIMYFMDAHSYNTFYFILLIIVGSFFMINCLVVIATQFSETK	426
QY	435	QRESQLMREORVRLFNASTLASFSPGSCYEELLYLVILKCAARLAQVSPAIGVRA	494
DB	427	QRESQLMREORARHLSNDSTLASFSPGSCYEELLYLVILKCAARLAQVSPAIGVRA	486
QY	495	GLLSSPVARSGQEPQPSGSCSTRSHR-----LSVHLV-HHHHHHHHHYHLGNGTLRV	546
DB	487	RKKVDPASVQGGP-----GHRQRRAGHTASVHLVYHHHHHHHHHHYHSHGSPRR	538
QY	547	PRASPEIQDRDANGSRRLML--PPPTPTPGGPPGAEVSHGFYHADCHLE--PVRQCA	602

DB	539	PGPEFGACD-----TRLVRAGAPPSPSPGPGPP-DAESVHSIYHADCHIEGPOERARV	591
QY	603	PPPRCPSEASGR-TVSGSKV-YPTV-----HTSPPPPIIKDKALVEVAPSP----	646
DB	592	AHAATAAASLRLATGLTGMNYPTILPSGVSGKSTSPGPK-----GKWAGPPPGTG	644
QY	647	--GPETLTSENIPTGPFSSMHKLLETQSTGAC--HSS-----CKLSSPCS KADSGACGPD	697
DB	645	GHGPLSLNS---PDPEKIHVVGEHGLGQAPGLSGLSVPCPLPSP--FAGTILTCELK	698
QY	698	SCPYCART-GAGEPESADHVPDSDSEAVYEFYQDAQHSDLRDP-----	740
DB	699	SCPYCTRALEDPEGELSGESDSDGRCGYEFTQDVRHGDWMDTPRPRATDTPGPGGS	758
QY	741	HSRRQRSGLGPDAPSSVLAFWRLLCDTFRKIVDSKYFGRGIMTALVNTLSMGIEYHEQ	800
DB	759	PQRAAQRAAP-GEFGWMGRLWVTFSGKLRRTVDSKYFSRGIMVAILVNTLSMGIEYHEQ	817
QY	801	PEELTNALEISNIIVTSLFALEMLLKLLAVGPGFYKPNYNI FGVIVVISWEIVGQG	860
DB	818	PEELTNALEISNIIVTSMFALEMLLKLLACGPLGYIRPNYNI FGIIVVISWEIVGQAD	877
QY	861	GGLSVLRTFRLMRVLKLVRFALQRLVLMKTMNDVATFCMLIMLFI FIFSLGMHLF	920
DB	878	GGLSVLRTFRLRLVLKLVRFALRRQLVLVKTMDNVATCTLLMLFI FIFSLGMHLF	937
QY	921	GCKFASERD-GDTLPDRKNFDSLWAVTVFQIITQEDWNKVLNGMASTSSWALYPIA	979
DB	938	GCKFSLKTDGTVPDRKNFDSLWAVTVFQIITQEDWNVLYNGMASTSSWALYFEVA	997
QY	980	LMTFGNVVFNLLVAILVEGFAEGDATKSESEDPFSPVDGDRKKRLALVAL-----	1035
DB	998	LMTFGNVVFNLLVAILVEGFAEGDANRSDTDEKTSVHFEEDFHKLRLQTTTELKWC	1057
QY	1036	-----GEHAELKSLPLLIHTAATPMWHPKSSS-TGVGEALGSGRRRTSSGSABPGA	1089
DB	1058	LAVTPNGHLEGSGLSPLIMCTAATPMPTKXSPFLDAAPSLPDSRGSSSSGDPPLG-	1116
QY	1090	AHEMKPPGARSPPHSPFWSAASWTSRRSRNSRLGRAPSLKRSPSGERRSLLSGEGE	1149
DB	1117	---DQKPPASLRSPFCAPWGPSPGAWSSRRSSWSLGRAPSLKRSGCGERESLLSGEGK	1173
QY	1150	SQDEESSEEDRASPA--GSDHHRGSLERAKSSFDLPDTL-----OVPGLH-----R	1196
DB	1174	STDDE--AEDGRAAPGPRATPLRRAESLDRPLRPAALPTKCDRDQGVVVALESDPFLR	1231
QY	1197	TAGRSSASHPQDCKNGKSGASGLARTLRTDDPQLDGGDDNDDEGNLSKGERITQAVRSLP	1256
DB	1232	IDSHREDAEALDDSDSESCCLRLHKVLEPKPQ-----W-----	1265
QY	1257	ACCEERDSWAYIFPPQSRPRLIICRITTHKMPDHVVVLVIIFLNCITIAMERPKIDPHSA	1316
DB	1266	--CRSREANALYLFSPQNRFRVSCQVITHKMFHVVLVFIFLNCVTIALERPDIDPGST	1323
QY	1317	ERIFLTLSNIYFTAVFLAEMTVKVALGWCFGQAYLRSSNNVLDGLLVLSIVDILVSM	1376
DB	1324	ERVFLSVSNIFTAIFVAEMVVKVALGULSGHAYLQSSNNLLDGLLVLSIVDIIYVAM	1383
QY	1377	VSDSGTKILGMLRVLLRLRLRVLISRAQGLKLVVETLMSSSLKPIGNIWIWICCAFFII	1436
DB	1384	ASAGGAKILGLVAVLLRLRLRVLISRAQGLKLVVETLISSLRPIGNIWILICCAFFII	1443
QY	1437	FGILGVQLFKGPFVCGEDTRNITNKSOCABEASVWRHRYKYNFNDLQALMSLFLVASK	1496
DB	1444	FGILGVQLFKGPFYCEGPDTRNISTKAQCRAAHYRWRRKYNFNDLQALMSLFLVSSK	1503
QY	1497	DGWDIMYDGLDVGVDQOPIMNHNPMMLLYFTSFLIIVAFVVLNMFVGVVFNHFKCRQ	1556
DB	1504	DGWNIMYDGLDVGVDQOPVQNHNPWMLLYFTSFLIIVSFFVLNMFVGVVFNHFKCRQ	1563
QY	1557	HOBEERAREEKRRLRLEKRRSKEKQMAEACKPYSDYSRFRLLVHHLCTSHYLDLF	1616
DB	1564	HQAEERAREEKRRLRLEERRRSTFPS-PEAQRPIYADYSPTRRSIHSLCTSHYLDLF	1622


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QY 1082 SGSAEPGAHHEMKCPPSSARSSPHSPWSAASWTSSRSRNSILGRAPSLKRRSPSGERS 1141
Db 1049 SGSAEPGAA-HEMKSPPSARSSPHSPWSAASWTSSRSRNSILGRAPSLKRRSPSGERS 1107
QY 1142 LLSGQESQDEESSEEDRAGSAGDHRHRSGLEREAKSSFDLPTLQVPLGHRRTASGR 1201
Db 1108 LLSGQESQDEESSEEDRAGSAGDHRHRSGLEREAKSSFDLPTLQVPLGHRRTASGR 1167
QY 1202 SSASHQDCNGKSASGRRLARTLTDQDGLDGDNDDEGNL 1241
Db 1168 GSASEHQCNGKSASGRRLARLPDPPDGLDGDADDEGNL 1207

RESULT 4
US-09-404-650-2
; Sequence 2, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-650-2

Query Match 45.0%; Score 5409; DB 3; Length 2175;
Best Local Similarity 50.5%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 513; Indels 450; Gaps 64;

QY 51 ASRSTTCTCPGGAAGAGSTEKDPG--SADSAEGL-----PYPALAPVVFVLS 97
Db 5 ASPSSAAAP-AEPGVTTTQDGRSPSPSPGEEPLDGDADHVPHPDLAPATFCLR 63
QY 98 QDSRPRSWCLRTVCNPMFERVSMVLINCVTLGMFRPCEDIAQSRCLIQAFDFIF 157
Db 64 QTTSPRNCWICWNCNPFECVSMVLINCVTLGMVQCDDMDCLSDRCKILQVDFDIF 123
QY 158 AFFAVEMVVMVALGIFGKKCYLGDWTNRLDFFVIAGMLBYSDDLQNVSPSAVTRVRL 217
Db 124 IFFAMWVLMVALGIFGKKCYLGDWTNRLDFFVIAGMVEYSLDLQNLNSAIRTVRL 183
QY 218 RPLRAINRVPMSRLVTLTLLDTPMLGNVLLLCFFVRFIFGIVGVOLWAGLLNRCELPE 277
Db 184 RPLKAINRVPMSRLVTLTLLDTPMLGNVLLLCFFVRFIFGIVGVOLWAGLLNRCELPE 243
QY 278 NFSPLSVLPEYYOTENEDESPFCQPRENGMRSCRSVPTLRGEGGPPCSL----- 332
Db 244 NFITQGDVALPYPYQPEDEDEMPICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDV 300
QY 333 -DYETYNSSNWT--CYNNQYNTNCAGHNPKGAINFDNIGYAMIAFQVITLEGWV 389
Db 301 YDGAGQDNLNAGLCVNNWRYNVCRTGSANPHKGAINFDNIGYAMIAFQVITLEGWV 360
QY 390 DIMYFVMDAHSFYNFIPILLIIVGSFFMNLCLVLIATQFSEPKQRESQIMREORVFL 449
Db 361 EIMYVMDAHSFYNFIPILLIIVGSFFMNLCLVLIATQFSEPKQREHRLMLEQORYL 420
QY 450 SNASTLASFSEPGSCYBELLYLILKARLIAQVRSRAIGVRAGLLSGPVARSQGEQ 509
Db 421 S-SSTVASAEPGDCYEEIFQYVCHILRAK-----RALGQALQS----- 462
QY 510 PSGSCTRSHRLSVHLLVHHHHHHHHHNGTLRVRASPEIQDRDANGSRRLMLPPP 569
Db 463 -----RRQAL-----GPE-----APAP 474
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QY 570 STPTSGGPPRGAEVSHFYHADCHLEPVRCQAPPPRCPSEASGRVTGSGKYVPTVHTSP 629
Db 475 AKPGP-----HAK-----EPRHYQLCPQHSPLDA-----TPHT-- 502
QY 630 PPEILKDKALVERVAPSPGPPTLTSTFNIIPGPSSMHKLELTOSTGAC-HSSCKIISPCKS 688
Db 503 -----LVQ-----PIPALAS-----DPASCPCQHQHEDGRRPSGLS 534
QY 689 ADSGACGPDSPCYCARTGAGEPESADHVMPSDSEAVVEFTQDAQHSDLRDPHSRRORS 748
Db 535 TDSGQEGSGS---GSSAGGEDEA-----DGDGA---RSSDGGASSELGKEEEREEQ-- 579
QY 749 LGPDAEPSVLA--FWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTN 806
Db 580 ----ADGAVWLCDGVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTN 635
QY 807 ALEISNIVTSLFALEMILLKLVVGPFCYIKNPYINIFDVIVVIVISWIEVGGQGLSVL 866
Db 636 ILEICNVVFTSMFALEMILLKLAAGFLDYLRNPYNIFDSIIIVISWIEVGGQADGLSVL 695
QY 867 RTRFLMRVLKVRFLPALQRLVLMKTMNDVATFCMLLMFIFIFSLGMLHFGCKFAS 926
Db 696 RTRFLRLVLKVRFPALRRQLVLMKTMNDVATFCMLLMFIFIFSLGMLHFGCKFSL 755
QY 927 ERD-GDTLPDRKNFDSLWAIIVTFQILTOEDWNKVLVNGMASTSSWAALFYALMTFEN 985
Db 756 RTDGTDTVPDRKNFDSLWAIIVTFQILTOEDWNKVLVNGMASTSPWASLYFVALMTFEN 815
QY 986 YVLFNLLVAILVEGFOAEGDATKSEDEDFPSV-----DGDGDKKRLALVAL 1035
Db 816 YVLFNLLVAILVEGFOAEGDANRYSDEDDQSSNIEBPKLOEGLDSSGDPK--LCPIPM 873
QY 1036 GEHAELRKSLPLLIHT---AATPMSPKSSSTGVGEALGSGSRRTSSGSAEPGAH 1091
Db 874 TPNGHLDPSL--PLGGHLGPAGAAGA--PRLSLQDPMLVALGSRKSSVMSL---GEMS 926
QY 1092 HEMKCPSPASRSPSPWSAASWTSSRSRNSILGRAPSLKRRSPSGERRSLLSGE-QOES 1150
Db 927 YDQSLSSSRSSYYGPGWGRSAAMASRRSWN-----SLKHKPPSAEHESLLSAERGGGA 980
QY 1151 QDEESSEE--DRASPAAGSDH-----BHRGSLEREAKSSFDLPTLQVPG 1193
Db 981 RVCEVADEGPPRAAPLHTPHAHIIHGPHLAHRHRHRTLSLDNRSDSDVLAELVFAVG 1040
QY 1194 LHRTASGRSS--ASEHQDCNGKSASGRRLARTLTD-DPQLDGDNDDEGNLSKGERIQAW 1250
Db 1041 AHPEAMRAAGAPAGHEDCNGRMP--IAKDVFTKMGDRGDEDEEIDYTLCFVRKRM 1098
QY 1251 VRSRLPACCRERDSWYIIFPPQSRFLLCRHRITHKMFVHVVLVLIIFLNCITIAMERP 1310
Db 1099 IDVYKPDWCEVREDWSVYLFSPENRFRVLCQITIAHKLFDYVVLAFIFLNCITIALERP 1158
QY 1311 IDHSAERIIFLTLSNYIFTAVELAEMTKVVALGWCFCQAYLRSSNNWLDGLVLVLSVI 1370
Db 1159 IEAGSTERIIFLTNSYIIFTAIFGEMTLKVSVGLYFGEQAYLRSSNNWLDGLVLFVSII 1218
QY 1371 DILVMSVDSGTKILGMLRLVRLRLRLRLVRSAGQLKLVVETLMSLKPIGNIIVIC 1430
Db 1219 DIVVLSASAGAKILGVLRLVRLRLRLRLVRSAPGLKLVVETLMSLKPIGNIIVIC 1278
QY 1431 CAFFIIFGILGVOLFKGKFPVCOGEDTRNITNKSQCAEASRYVRHRYKYNFDNIGQALMSL 1490
Db 1279 CAFFIIFGILGVOLFKGKFYHCLGVDTNRITNRSDCMAANYRWHHRYKYNFDNIGQALMSL 1338
QY 1491 FVLASQDGVNDINVDGLDVGVDQOQPMNHNPMMLLYFISFLIIVAFVULMVGUVVEN 1550
Db 1339 FVLASQDGVNINMYNGLDVAVDQOQVTHNHPMLLYFISFLIIVSFVFLNMFVGVVVEN 1398
QY 1551 FHKCRHQHEBEEARRREKRLRLEKKRSKEQMAEAOCKPYYSYRFLRVHHLCTS 1610
Db 1399 FHKCRHQHEBEEARRREKRLRLEKKR-----KAQRLPYIATYCHTRLLIHSWCTS 1451
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[illegible]

RESULT 6

US-09-404-650-4

: Sequence 4. Application IIS/09404650

Patent No. 6309858

TELEPHONE NO. 0302838
; GENERAL INFORMATION:

APPLICANT: Dietrich, Paul S.

APPLICANT: McGovern. Joseph G.

INVENTOR: JOSEPH G. ...
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS: COMPOSITIONS THEREOF.

; TITLE OF INVENTION: AND USES

FILE REFERENCE: R0043B-REG sequence listing

CURRENT APPLICATION NUMBER: US/09/404,650

; CURRENT FILING DATE: 1999-09-23
; CURRENT FILING DATE: 1999-09-23

NUMBER OF SEO ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

SEO ID NO 4

; LENGTH: 2188

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; TYPE: PRT

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ORGANISM: Homo sapiens

US-09-404-650-4

Query Match	44.9%	Score 5405	5	DB 3	Length 2198
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Best Local Similarity 50.3%: Pred No 0:
 44.3%, Score 3403.3; DB 3; Length 2188;

2000 Local Similarity 50.3%; FIED: NO: 0;
Matches 1225: Conservative 236: Mismatches 514: Indels 461: Cons 54

0v 51 ASRSSTCPGPGACAGCSTEKDBC - SANCSEACI

QY ST ASKRSITICPGGAAGAGSTIERDUG--SADSEAEGL-----PYPALAPWFFYLS 97

3 ASPFSSAAAF-AAEPGVITEQPGPRSPFSSPPGLEEPLDGADPHVPHPDLAIAFFCLR 63

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DB 64 QTTSPRNWCICKMVCNPNWFECVSMVLNLCVTLGMYQPCDDMDCLSDRCKILQVFDFF 123

QY 158 AFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAMLEYSLDLQNVFSFAVRTVRVL 217

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QY 218 RPLRAINRVESMRILVTLLDITLPLMLGNVLLCCFFVFFIFGIVGVQLWAGLLNRNRCFLPE 277

US-09-935-541-4
; Sequence 4, Application us/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-4

Query Match 44.9%; Score 5405.5; DB 4; Length 2188;
Best Local Similarity 50.3%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;

QY 51 AGRSTTCGPGAAGAGSTKDPG--SADSEAEGL-----PYPALAPVVFYLS 97
DB 5 ASPPSSAAAP-AAEPGVITTEQGPSPSPSPGLEEPLDGDADPHVPHDLPALIAFFCLR 63

QY 98 QDSRPSRLRVCPWPFRVSMVILLNCVTLGMPRPCEDIACQRCRILOAFDDFIF 157
DB 64 QTSRPNCKIKVCPWPFECVSMVILLNCVTLGMVYQPCDDMDCLSDRCIKILOVEDDFIF 123

QY 158 AFFAVEMVVMVALGIFGKKCYLGTWRLDFFIAGLMLEYSLDLQNVSPSAVTVRL 217
DB 124 IFFAMEMVLMVALGIFGKKCYLGTWRLDFFIAGLMLEYSLDLQNVSPSAVTVRL 217

QY 218 RPLRAINRVPSMRILLVTLTLPLMGNVLLLCFFVFFIFGIVGVLWAGLNRNCFLEPE 277
DB 184 RPLKAINRVPSMRILLVTLTLPLMGNVLLLCFFVFFIFGIVGVLWAGLNRNCFLEPE 243

QY 278 NFSPLSLVDLPYQYQTEDEDSPPFCSPQPNRGMKSCSVPTLRGEGGGPPCSL----- 332
DB 244 NPTQGDVALFPYQYQTEDEDSPPFCSPQPNRGMKSCSVPTLRGEGGGPPCSL----- 300

QY 333 -DYETYNSSNTT--CVNNQYTYNCSAGBNPKGAINFONIGYAMTAIQVITLEGWV 389
DB 301 YDFGAGRQDLNASGLCVNNRYVVCRTGSANPHKGAINFONIGYAMTAIQVITLEGWV 360

QY 390 DIMYFMDAHGFYFIPIILLIIVGSPFMNLCVLIATQFSETKQBSQLMREORVRL 449
DB 361 EIMYVMDAHGFYFIPIILLIIVGSPFMNLCVLIATQFSETKQBSQLMREORVRL 420

QY 450 SNASTLASFSPGSCYELLKYLVIILKAARLIAQVSRAGLLSSPVARSQGPQ 509
DB 421 S-SSTVASIAPGDCYBEIYOYVCHILKAKR-----RALGLYQALQS----- 462

QY 510 PSGSCTSRHRLSLVHLVHHHHHHVHLNGTLRVPRASPEIQDRDANGSRRLMLPPP 569
DB 463 -----RQAL-----GPE-----APAP 474

QY 570 STPTSPGPPRGAHSVHSHYHADCHLBFVRCAQPPRCPSPASGRVTGSGKVPYVHTSP 629
DB 475 AKGPP-----HAK--EPRHYQLCPQHSPLDA-----TPHT-- 502

QY 630 PPEILDKALVEVAPSPGPTLTSTFNPDPGFSSMHKLLTQSTGAC-HSSCKTSSPCSK 688
DB 503 -----LVQ-----BIPATLAS-----DPASCPQCHEDGRPSGLGS 534

QY 689 ADSGACGPDSCPYCARTGAGEPESADHMPDSDSEAVYETQDAQHSDLDHPHSRRQRS 748
DB 535 TDSQEGSGS-----GSSAGGEDEA-----DGGGA-----RSSDGAASELGEKEEBEQ-- 579

QY 749 LGPDAPSSVIA--FWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIYHPEBELTN 806
DB 580 ----ADGAVWLCDGVWRETRAKLRGIVDSKYFNKRGIMAILVNTVSMGIEHHEQPELTN 635

QY 807 ALEISNIVTSLFALEMLKLLVYGPYIKNPNYFDGVIVIVISVWEIVQGGGGLSVL 866
DB 636 ILEICNVVFTSMFALEMLKLLAAGFDYLRNPNYFDGIIVISVWEIVQGGGGLSVL 695

QY 867 RTERLMRVLKLVRFLPALORQLVLMKTMNDVATFCMLLMFLFIFISILGMHIFGCKFAS 926
DB 696 RTERLMRVLKLVRFLPALORQLVLMKTMNDVATFCMLLMFLFIFISILGMHIFGCKFAS 755

QY 927 ERD-GDTLPORKNFDSLLWAIIVTFQILTQEDWNKVLVYNGMASTSWAALFYIALMTFGN 985
DB 756 RDTGDTVPDRKNFDSLLWAIIVTFQILTQEDWNKVLVYNGMASTSWAALFYIALMTFGN 815

QY 986 YVLFNLLVAILVEGFOAGDATKSESEPDFPSPV-----DGDGRKKRLALVAL 1035
DB 816 YVLFNLLVAILVEGFOAGDANRSYDEQSSNIEEFKLOGLDSSGDPK--LCPIDM 873

QY 1036 GBHAELRKSLLPLLIHT----AATPMSPKSSSTGVGEALGSGSRRTSSSGSAEPGAAH 1091
DB 874 TPNCHLDPSL--PLGCHLGPAGA--PRLSLQPDMLVALGSRKSSVMSL---GRMS 926

QY 1092 HEMKCPSPNARSPHSPWSAASWTSSRSRSLGRAPSLKRRSPSGERSLLSGE--GQBS 1150
DB 927 YDORSLSSRSRYYPGWSAAWASRRSSWN-----SLKHKPPSAEHSLLSABERGGA 980

QY 1151 QDEESSSE--DRASPAGSDH-----RHGSLERAKSFDLPDILVPG 1193
DB 981 RVCEVADEGPRAAPLHPHAAHLLHGGPHLAHRHRRHRTLSLDRNSVDLAELVPAVG 1040

QY 1194 LHRTASGRSS--ASBHDQCNKGSASGLARTLTD-DPQLQDGDNDNENSGKGRIOAW 1250
DB 1041 AHPRAAWAAGAPAGHEDCNGRMP--JAKOVFTKWGDRGDEGEDEEIDYTLCFRVRKM 1098

QY 1251 VSRSLPACCRERDSWAIIPPOSRPRLCHRIITHKMFHDVVLVIFLNCITTIAMERP 1310
DB 1099 IDVYKPDCEVREDMSVYLFSPENRFRVLCOTIIAHKLFVYVLAFLFNCITTIALERPQ 1158

QY 1311 IDHSAERIIFUTLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLASSWNVLDGLLIVSI 1370
DB 1159 IEAGSTERIFUTVSNYIFTALFVGBMTLKVVSLGLYFGEQAYLASSWNVLDGLVFSII 1218

QY 1371 DILVSMVSDGSKILGLMLRVLRLTLRLPLRVISRAOGLKLVWETLMSLKPIGNIVIC 1430
DB 1219 DIVVSLASAGGAKILGLVRLRLTLRLPLRVISRAOGLKLVWETLMSLKPIGNIVIC 1278

QY 1431 CAFFIIFGILGVLFKGFVFCQGEDTRNTKSDCAEASVYRWVYRKHYNFNDLQALMSL 1490
DB 1279 CAFFIIFGILGVLFKGFVFCQGEDTRNTKSDCAEASVYRWVYRKHYNFNDLQALMSL 1338

QY 1491 FVLASKDGVDMYDGLDVGVDQOPIMNHNPMMLLYFISFLLVAFVLMNMFVGVVEN 1550
DB 1339 FVLASKDGVNIMYNGLDVAVDQOPVTHNPMMLLYFISFLLVAFVLMNMFVGVVEN 1398

QY 1551 FHKCRHQEBEERREKRLRLEKKRSKEKQMAEQAQCPYSDYSRFRLLVHLLCTS 1610
DB 1399 FHKCRHQEBEERREKRLRLEKKR-----KAQRLPYATYCHTRLLIHSWCTS 1451

QY 1611 HYLDLFTITVIGLVNVTNAMEHYQQOILDEALKICNYIFTVIFVFSFKLVAFARFR 1670
DB 1452 HYLDLFTITVIGLVNVTNAMEHYQQOILDEALKICNYIFTVIFVFSFKLVAFARFR 1511

QY 1671 FQDRWQOLDLAILLSIMGITLLEIEVNLSPINPTIIRMRVLRIRARVLRKLMVGMVR 1730
DB 1512 FQDRWQOLDLAILLSIMGITLLEIEVNLSPINPTIIRMRVLRIRARVLRKLMVGMVR 1571

QY 1731 ALLHTVQALPQVGNLGLLFFIIFALGVLEFGDCEDETHPCBGLGRHATFNFGM 1790
DB 1572 ALLDTVVQALPQVGNLGLLFFIIFALGVLEFGDCEDETHPCBGLGRHATFNFGM 1631

QY 1791 AFLTLFRVSTGDNWNGIMKDPDRDC--DQESTCVNTV--ISPIYFVSVLTAQFVLNVVVI 1847

Db	1632	APLTLFQVSTGDNMNGIMKOTLRDCTHDSRCLSLQVSPFLYFVSFLTAQFVLINVV	1691	Db	63	TTSPRNWCKVCPWFECVSMVLVLLNCVTLGMQPCDDMECLSDRCKILQVDFDFFI	122
Qy	1848	AVLMKHLESNKEAEAELEAELEEM-KTLSPQHPGLSP	1889	Qy	159	FPAYEMVYKVALGIFGKKCYGLDWTNRDLDFVIAGMLEYSLDQNYVSFAVRVRLR	218
Db	1692	AVLMKHLDNSKEAQDAEMDAELEMAHGLGPGPLPTGSPGAPGRPGGAGGGDTE	1751	Db	123	FFAMEMVYKVALGIFGKKCYGLDWTNRDLDFVIWAGMVEYSLDQNLNLSAIRVRLR	182
Qy	1890	FW-----FWEG-VNSTDSPKPGAPHTTAHGAASG-----	1920	Qy	219	PLRAINRVPMSRILVTLTLLDPLMIGNVLLCFFVFFIFIGVIGVQVWAGLNRFLPEN	278
Db	1752	GGLCRRCYSPAQENLWDSVLIIDKLEGEITIIDNLSGSIFH---HYSSPAGCKKCHH	1808	Db	183	PLKAINRVPMSRILVNLVLLDPLMIGNVLLCFFVFFIFIGVIGVQVWAGLNRFLPEN	242
Qy	1921	-----PSLEHPTWVP-----HPEEVFV-PLG	1940	Qy	279	FSLPLSVDLPEYQYOTENEDSFICSPQRENMRSCSVPTLRGGGGGPPCSL-----	332
Db	1809	DKQEVOLABTEAFSLNDRSSILLGDDLSLDDFTACFPGRKDSKGELDPFPMRVGDLG	1868	Db	243	FTIQGDVALPPYQYDEEDMPFICSLTDGNGIMGHEIPPLKEQ---GRECLSKDDVY	299
Qy	1941	POLLTVRKGVGTRTHSLPN-DSYMCRCNGSTARSGLHRGMWGLPKAQSGLSVHSOPADT	1999	Qy	333	DYETYNSSNTT--CVNNYOYTNCSAGHNPFKGAINFNDNIGYAWIAIPQVITUEGWD	390
Db	1869	ECFFPLSSTAVS-----PDPENFLCEMEIEIPFNV--RSW--LKHDSSOAPSPSPDAS	1919	Db	300	DFGAGRODLNAGSLCVNNWRYNVCRTGNANPHKGAINFNDNIGYAGIVIFQVITUEGWD	359
Qy	2000	SCILQIPKDVHY-----LLQPHGAPTGAIPKLPFG-----RSLAQRPLRQAART	2048	Qy	391	IMYFVMDAHSFYNYFYFILLIIVGFFFMINCLVVIATOFSETKQRESOLMBEORVRES	450
Db	1920	SPLLPMPAEFPFAVSASQKPEKGTGTLPKIALQGSWASURSPVNCTLLRQATGSD	1979	Db	360	IMYVMDAHSFYNYFYFILLIIVGFFFMINCLVVIATOFSETKQREHRLMLEQORYLS	419
Qy	2049	DSLVDQGLGREDLLSEVSGPCLTRSSGFWGSSIQVQORSIGOSKYSKHIRLPAPCP	2108	Qy	451	NASTLASFPSPGSCYEELKLYILRKAARLAQVSRAGVRAIGVAGLSSFPVARSQGPQ	510
Db	1980	TSLDAS-----PSSAGSLQTTLEDLSLTSLSRERLGPAPAP	2018	Db	420	SSTVASYPGPGDCEEIFQYVCHILRKAAR-----RALGLYQAL-----	458
Qy	2109	GLEPWSWAKOPPETRSSLDELDELTSWISGDLPLSPSQBEPLPPLRKKYCVETOSCRRP	2168	Qy	511	SGSCTSRHRLSVHLLVHHHHHHHHYHLNGTLPVPRASPEIQDRDANGSRRLMPPPS	570
Db	2019	G-----PRAGLSPAARRRL-----SLRGRGL	2039	Db	459	-----QNRQA-----MGPGT-----PAPA	473
Qy	2169	FWLDEORRHIAVCLDGSOPRLCPSPSL-----GGQPLGGPGRPKKLGPPSI	2220	Qy	571	TPTPSGPPRGAEVSHSFYHADCHLPVRQAPPPPCPSEASGRTVSGKVYTVHTSPP	630
Db	2040	FSLRGLRAHORSHS--SGGSTSPCTHDSMDPSDEGRGAGGGAGSHSETLSLSL	2097	Db	474	KPGP-----HAK--BFSCKLCPRHSPLD-----TPHT-----	500
Qy	2221	S---IDPPESQGRSPPCSPGVCLRR-----RAP---ASDSK	2250	Qy	631	PEILKDAIVEAVSPGPPTLTSTFNPPGPFSSMHKLLTQSTGACHSSCKISSPCSKAD	690
Db	2098	TSLFCPPP-----PPAPGTLTARKESTSSLAAPGRPHAAALHAGLARSPWAADRSK	2151	Db	501	-----LVQ-----PISAIL-----	509
Qy	2251	DPVSSPLDSTAASPKKDTLSLSGLSDPTMDP	2286	Qy	691	SGAGCPDSCPYC-----ARTGAGEPESADHVMPPDSDSEAVYFTQDAQH	734
Db	2152	DPGRAPLPGGLGFLAPPQPL-----PGELEP	2179	Db	510	--ASDPSSCPCHQHEAGRRPSGLGSTDSGEGSGGSAB---AEANGDGL-QSSEGDVS	563
RESULT 8				Qy	735	SDLRDPHRRRQSLGPDAPSSVLA-----FWRLICDTRKIVDSKYFGRGIMAILVN	789
US-09-404-650-5				Db	564	SD-----LGKEEQEDGAARLCGVWRETRKXKLRGIVDSKYFARGIMAILVN	611
; Sequence 5, Application US/09404650				Qy	790	TLSMGIEYHQBELTNALREISNIVFTSLFALEMLKLIVGPGFYIKPNYINIPDGVIIV	849
; Patent No. 6309858				Db	612	TVSMGIEHHQPEELTNILICNVVFTSMFALEMLKLAAAGLFDYLRPNYINIFDSIIVI	671
; GENERAL INFORMATION:				Qy	850	ISVMEIVGQGGGLSVLRTFLMRVLKLVFLPALQOLVLMKTMONVATFCMLMLFI	909
; APPLICANT: Dietrich, Paul S.				Db	672	ISIWEIVGQADGGLSVLRTFLRLVLRVLPALRRQVVLVLMKTMONVATFCMLMLFI	731
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;				Qy	910	FIFSILGMHLPGCKFASERD-GDTLPDRKNFDSLMLVTVVFOILTQEDMKNVLYNGMAS	968
; FILE REFERENCE: R0043B-REG sequence listing				Db	732	FIFSILGMHLPGCKFASERD-GDTLPDRKNFDSLMLVTVVFOILTQEDMKNVLYNGMAS	791
; CURRENT APPLICATION NUMBER: US/09/404,650				Qy	969	TSSWAALYFTALMTFGNVVLFNMLVAILVEGFOAEGDATKSESPDFPSPVDG-----	1022
; CURRENT FILING DATE: 1999-09-23				Db	792	TPWASLYFVALMTFGNVVLFNMLVAILVEGFOAEGDANRSCSDQSSNLEEFDKLPE	851
; NUMBER OF SEQ ID NOS: 12				Qy	1023	--DGDGRKRLALVALGEHAELRKLPLLIH--TAATPMHPSKSSITGVGEALGSGRR	1078
; SOFTWARE: PatentIn ver. 2.0				Db	852	GLDNRDLKLCPIPMTPNGHLDPSL--PLGAHLGPAGTMTAPRLSLQDPDLVALDORR	909
; SEQ ID NO 5				Qy	1079	TSSSGSAPGAHHEMKCPGASRSPHSPWASASWTSSRRSRSLGRAPSLKRSPSGE	1138
; LENGTH: 1835				Db	910	SSVMSL---GRMSVQDRSLSSRSYYGFWRSRGTWASRRSWN-----SLKHKPPSAE	960
; TYPE: PRT				Qy	1139	RRSLISGEGQS--QDEESSEE--DRASPAAGSDH-----RHRGSLREA	1179
; ORGANISM: Rattus sp.				Db			
US-09-404-650-5				Qy			

Query Match 44.4%; Score 5345; DB 3; Length 1835;
Best Local Similarity 55.4%; Pred. No. 0;
Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;
Qy 43 PRSRDSPVNASSTTCCPGAGAGAGSTEKDPGASDAEAG-----LPYPALAPVVFYLSQ 98
Db 8 PSSAAAPAPEGITQPGP-----RPPSPPGLEEPLGNTGTPVPHDLPAPVAFCLRQ 62
Qy 99 DSRPRSWCLRTVCNEFWERVSMVLVILLNCVTLGMFPCRDIACDQRCLIOAFDDFIFA 158

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Db 961 HBSLSGEGGSCVRACAREAPRTTAPLHAPHAAHHGPHLAHRRHRRRTLSLDT 1020
QY 1180 KSSFDLPDTPQVGLHRTAS--GRSSASBHDGNGKSGASGRARTLTD-DPQLDGDND 1236
Db 1021 RUSVDLGELVPVGAHRAWAGAGAPGHEDCNGRPN--IAKOVFTKMDRRDRGEDE 1078
QY 1237 DGNLSKGERIQAWVRSLPACCRERDSWASYIFPPQSRFLRCHRIITHKWFHDHVLVI 1296
Db 1079 EBIDYTLCPVRKMDIVYKPDWCEVREDWSVLFSPENKFRILCQIIIAHKLFDYVVLAF 1138
QY 1297 IFNCITITAMEPKIDPHSAEIRIFLTSNYITAVFLAEMTKVVALGWCFCGEAYLRSS 1356
Db 1139 IFNCITITALERPOEAGSTERIFLTVSNYIFAITFVGMETLKVWSLGLYFGEQAYLRSS 1198
QY 1357 WNVLDGLVLSVIDILVSMVSDSGTKILGMLRVLRLTLRLPLRVISRAQKLVWETL 1416
Db 1199 WNVLDGLVLFVSIIDIVSVASAGAKILGVLRLVRLTLRLPLRVISRAQKLVWETL 1258
QY 1417 MSSLKPIGNIVVICAPFIIFGILGVQLFKGFFVCOGEDTRNITNKSDCAEASRYVRH 1476
Db 1259 ISSLKPIGNIVLICCAFFIIFGILGVQLFKGFFVCOGEDTRNITNRSDCVAANYRVWH 1318
QY 1477 KYNFNLGAALMSFLVASKGMDIMYDGLDAGVDQOPIMNHPNMLLYPISFLIIVA 1536
Db 1319 KYNFNLGAALMSFLVASKGMDIMYDGLDAGVDQOPIMNHPNMLLYPISFLIIVS 1378
QY 1537 FVLNMFVGVVVENPHKCRQHEEAREARRRLEKRRLEKRRLEKRRLEKRRLEKRR 1596
Db 1379 FVLNMFVGVVVENPHKCRQHEEAREARRRLEKRRLEKRRLEKRRLEKRRLEKRR 1431
QY 1597 YSRFRLVHHICTSHYLDLFTVIGLVNVTNAMEHYQQPQLDBALKICNYIFTVFVF 1656
Db 1432 YCPTLAIHMSCTSHYLDLFTVIGLVNVTNAMEHYQQPQLDBALKICNYIFTVFVL 1491
QY 1657 ESVFKLVAFARFRFORWOLDIAIVLLSTMGITLBEIEVNLSPINPTIIRMRVLR 1716
Db 1492 EAVLKLVAFLRFRFORWOLDIAIVLLSTMGITLBEIEVNLSPINPTIIRMRVLR 1551
QY 1717 ARVLKLMVAGMRALLHTVMOALPOVGNLGLLEMLFFIFAALGVLEFGLECDTHPC 1776
Db 1552 ARVLKLMVAGMRALLHTVMOALPOVGNLGLLEMLFFIFAALGVLEFGLECDTHPC 1611
QY 1777 EGLRHATFNFGMAFLTLFRVSTGDNWNGIMKDPDRDC--DQESTCYNTV--ISPIYFVS 1833
Db 1612 EGRSRHATFNFGMAFLTLFRVSTGDNWNGIMKDPDRDC--DQESTCYNTV--ISPIYFVS 1671
QY 1834 FVLTAQVFLVNVAVIYMKHLESNKAEBAEAELEEMKTLSPQPHSPGSPFLWP 1893
Db 1672 FVLTAQVFLVNVAVIYMKHLESNKAEBAEAELEEMKTLSPQPHSPGSPFLWP 1713
QY 1894 GVBGVNSTDKPKGAPHTTAAHGAAGSFLSHPTMVPHPPEVPV--LGPOLLTV----- 1946
Db 1714 -AHGLGPCGPGCG-----PCPCPCPCGAPRLPTSSPGAGP 1750
QY 1947 RKSQVSRTHSLPNDNSYMCN--GSTAERSLGHGMLGPKAQSGLSIVHSOPADTSCILQL 2005
Db 1751 RKSQVSRTHSLPNDNSYMCN--GSTAERSLGHGMLGPKAQSGLSIVHSOPADTSCILQL 1801
QY 2006 PKDV-HYLLQPHG 2017
Db 1802 SGSVFHHYASPDG 1814

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RESULT 9

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US-09-935-541-5
; Sequence 5, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing

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; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1835
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-935-541-5

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Query Match 44.4%; Score 5345; DB 4; Length 1835;
Best Local Similarity 55.4%; Pred. No. 0;
Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

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QY 43 PRSRDPSVARSSTTCPCGGAAGAGSTEKDCSADSEAG-----LPYPALAPVVFYLSQ 98
Db 8 PSSAAAPAPFGITQPGP-----RSPPPSPGLEPLEGTPDPVHPDLAPVAFCLRQ 62
QY 99 DSRPSWCLRTVCNPFWRVSRVSMVLINCVLTIGMERPCEDIACDSQRCRILQAFDFTFA 158
Db 63 TTSRPNWCICKWCPNPFVPCVSMVLINCVLTIGMYQPCDDMECLSDRCKILQVDFDFIPI 122
QY 159 FFAVMVVMVALGIFGKKYCHLGTWNLDPFIVTIAGMLEYSLDLQNVSPSFAVTRVLR 218
Db 123 FFAMVMLKMYALGIFGKKYCHLGTWNLDPFIVMAGMVEYSLDLQNLNSAIRTVRVR 182
QY 219 PLRAINRVPSRMLVTLTLLDTPMLGNVLLCCFFVFTFEGIVGVQLWAGLNRCLFLEN 278
Db 183 PLKAINRVPSRMLVTLTLLDTPMLGNVLLCCFFVFTFEGIVGVQLWAGLNRCLFLEN 242
QY 279 FSLPLSVLDEPYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 332
Db 243 FTIQDVALPYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 299
QY 333 DYETYNSSNTT--CVWNQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 390
Db 300 DFGAGQDLNASGLCVNWNRYNVCRTGNANPHKGAIFDNIGYAGIVIFQVITLEGWVE 359
QY 391 IMYVMDAHFYNYFIYFILLIIVGSFMINCLVVIATOFSETKQRESQMLRORVPLS 450
Db 360 IMYVMDAHFYNYFIYFILLIIVGSFMINCLVVIATOFSETKQRESQMLRORVPLS 419
QY 451 NASTLASFSBPGCYEELLKYLKAAARLAAQVSRRAIGVRAGLSSPVARSQSPQP 510
Db 420 -SSTVASAEPGDCYEBIFQVYCHILKAKR-----RALGLYQAL----- 458
QY 511 SGSTRSHRSLVHHLVHHHHHHHHVHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPS 570
Db 459 -----QNRQA-----MGFGT-----PAPA 473
QY 571 TPTPSGPPRGAHSVHGFYHADCHLBPVRCQAPPPCPSPSEASGRVSGKVYTVHTSPP 630
Db 474 KPGP-----HAK-----EPHCKLCRHSPLD-----PTPHT--- 500
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Db 501 -----LVQ-----PISAIL----- 509
QY 691 SGACGPDSCPYC-----ARTGAGEPESADHVMPSDSDSBAVYFTQDAQH 734
Db 510 --ASDPSCPHCOHEAGRRPSGLGSTDSQEGSGSGSAB---AEANGDGL-QSSEGGVS 563
QY 735 SLLRDPHSRRRQSLGPDAPSSVLA-----FWLICDTRFKIVDSKYFGRGMAILVN 789
Db 564 SD-----LGKEEEDQEDGAARLQGVNRETRKRLRGIVDSKYFNRGMMAILVN 611
QY 790 TLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLVYGFPGYKPNYINEDGVIV 849
Db 612 TVSMGIEHHEQPEELTNALEISNIVFTSLFALEMLKLVYGFPGYKPNYINEDGVIV 671
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Db	1714	-AHGLGPCGPGC-	PCPCPCPCACAGPRLTSSPGAPG	1750
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Db	1751	RSGGAGAGG-DTSHLCRHCYSAQETL	W-----LDSVSLIKDSLEGELTIIDNL	1801
Qy	2006	PKDV-HYLLOPHG	2017	
Db	1802	SGSVFHHVSPDG	1814	
RESULT 10				
US-09-268-163-4				
; Sequence 4, Application US/09268163B				
; Patent No. 6353091				
; GENERAL INFORMATION:				
; APPLICANT: Lipscombe, Diane				
; APPLICANT: Schorge, Stephanie				
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF				
; FILE REFERENCE: B1055/7000				
; CURRENT APPLICATION NUMBER: US 09/268,163B				
; CURRENT FILING DATE: 1999-03-12				
; EARLIER APPLICATION NUMBER: US 60/077,901				
; EARLIER FILING DATE: 1998-03-13				
; NUMBER OF SEQ ID NOS: 28				
; SOFTWARE: FastSeq for Windows Version 3.0				
; SEQ ID NO 4				
; LENGTH: 2343				
; TYPE: PRT				
; ORGANISM: Homo sapiens				
US-09-268-163-4				
Query Match 14.0%; Score 1678; DB 3; Length 2343;				
Best Local Similarity 23.3%; Pred. No. 4.5e-126;				
Matches 625; Conservative 354; Mismatches 828; Indels 872; Gaps 81;				
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Db	32	PGPGGLQPGQVLYKQSIQAQARTMALYNPI	PVQKNCFTVNRSLFVSEDNVVRKAKRI	91
Qy	110	VCPNPFERVSMVLNLCVLTGMFERPCEDI	ACQSRCLIQAPDD---FIFAFVAVEMV	166
Db	92	TEPPPEYMLATIANCIVLAL	---EQHLPDGTKTPMSERLDDTEPYGIFCFEAGI	147
Qy	167	KWVALG-IFGKCYLGDWTNRDLFFVIAGMLEYS	---LDLQNVFSAVTVRVLPLRA	222
Db	148	KIIALGFGVFKHGSYLRNGWVMDVFWVLLTGILATAGTDFDLR	---TLRAVRVLRLPKL	202
Qy	223	INRVPMRILVTLTLLDTPMLGNVLLCPFVPIFGTVGVQLWAGLLRNRCFLPENFSLP		282
Db	203	VSGIPSLQVVLKSIKMAWVELLQIGLLLFAILMFAILGLEFYNGFKHACF	-----P	255
Qy	283	LSVDLEPVYQYTENEDESPFCISQPRENGMRSCTVPTLRGEGGGPPCSDLTYNTSSSN		342
Db	256	NSTDAEPV	-----GDFPCGKEAPARLCEGD	280
Qy	343	TTCVNMNOYITNCAGEHNPKGAINFDNTIGYAWIAIFQVITLEGWIDMYFWD-AHSF		401
Db	281	TEC---REYWP	-----GPNFGITNFDNLIFALLTVFCITMEGWTDILYNTNDAAGT	330
Qy	402	YNFYIFILLIIVSGFFMINI.CLVVIAITQFSETKRES	-----OLMREQVRFLSNASTL	455
Db	331	WNWLYIFPLIIIGSFFMLNLVGLSGEFAKEREVENRRRAFLKLRQQOIE	-----	382
Qy	456	ASFSEPGSCYBELKYLIVYLKKAARLQAQVSRAIGVRAGLLSSPVARSGOEPQSGCT		515
Db	383	-----RELNGYLEWIFKAEVMLAED	-----RNAEKSFLDVLK	417
Qy	516	RSRRRLSVHHLVHHHHHHHHVHLNGTLRVPRA	SPETQDQDANGSRRLMLPPSTTPPS	575
Db	418	RAATKKSRNDLIH	-----AEEGEDRFAD	440
Qy	576	GGPRGAESVHSFYHADCHLEPVRVCQAPP	PRCPSEASGRTVSGSGKVVYPTVHTSPPEILK	635

; Sequence 2, Application US/08713118		
; Patent No. 6040436		
; GENERAL INFORMATION:		
; APPLICANT: Franco, Rodrigo		
; APPLICANT: Sun Chen, Ai Ru		
; APPLICANT: Suey, David J.		
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL		
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS		
; NUMBER OF SEQUENCES: 6		
; CORRESPONDENCE ADDRESS:		
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.		
; STREET: Two Militia Drive		
; CITY: Lexington		
; STATE: MA		
; COUNTRY: USA		
; ZIP: 02173-4799		
; COMPUTER READABLE FORM:		
; MEDIUM TYPE: Floppy disk		
; COMPUTER: IBM PC compatible		
; OPERATING SYSTEM: PC-DOS/MS-DOS		
; SOFTWARE: Patent in Release #1.0, Version #1.30		
; CURRENT APPLICATION DATA:		
; APPLICATION NUMBER: US/08/713,118		
; FILING DATE: 16-SEP-1996		
; CLASSIFICATION: 435		
; ATTORNEY/AGENT INFORMATION:		
; NAME: Mata, Elizabeth W.		
; REGISTRATION NUMBER: 38,236		
; REFERENCE/DOCKET NUMBER: ACC96-01		
; TELECOMMUNICATION INFORMATION:		
; TELEPHONE: 617-861-6240		
; TELEFAX: 617-861-9540		
; INFORMATION FOR SEQ ID NO: 2:		
; SEQUENCE CHARACTERISTICS:		
; LENGTH: 2337 amino acids		
; TYPE: amino acid		
; TOPOLOGY: linear		
; MOLECULE TYPE: protein		
; US-08-713-118-2		
Query Match 13.9%; Score 1677; DB 3; Length 2337;		
Best Local Similarity 23.4%; Pred. No. 5,4e-126;		
Matches 627; Conservative 350; Mismatches 829; Indels 868; Gaps 82;		
QY	59	PGCAAGAGSTKDPGSADSEAGLPYPALAPV-----VFFYLSQSRSPRSCWCLRT 109
Db	32	PGPGGLPGQGVLYKQSIQARMTALYNPIPVKQNCFTVNRSLVFSESDNVVRKYAKRI 91
QY	110	VCNPFWRVSMVILLNCVILGMPCEDTACDSQRCRIIQAEDD---FIFAPFAVEMV 166
Db	92	TEWPPPEYMLATIIANCIVLAL-----EQHLPGDKTPMGERLDDTTPYFIGFCFAGI 147
QY	167	KWALG-IFGKCKYLGDTWNRDLFFVIAGMLEYS---LDLQNVSFSAVRTVRLRLRA 222
Db	148	KIALGFVFKGSLRGNWVMDFFVVLTLGATAGTDFDLR-----TLRAVRVLRPLK 202
QY	223	INRVPSMRILLTLDDLPMLGNVLLLCFFVFFIFGIVGVQLWAGLNRNCFLPENSLP 282
Db	203	VSGPISLQVVLKSIWKAMVPLLIQIGLLFFAILFAIGLEFYMGKFKHACF-----P 255
QY	283	LSVDLEPYQYOTENEDSEFFICSQPRENGMRSCRVPTLRGCGGGPCCSLDIYETNSSN 342
Db	256	NSTDAEPV-----GDFPGKEAPARLCEGD 280
QY	343	TTCCVNNWQYITNCASAGEHNPKGAINFDNIGYAMIAIPQVITLEGWIDIMYVMD-AHSF 401
Db	281	TEC-----REYWP-----GNFGIINPDNILLFAITVFQCITMEGWTDLIXNTNDAAGNT 330
QY	402	YNFIYFILLIIVGFFMNLCLVIVATQFSETKQRES-----OLMRQVRVRLSNASTL 455
Db	331	WNWLYFTPLIIIGFFMLNLVLGVLSGFBKEREVENRRAFLKLRQOOIE----- 382
QY	456	ASFSPGSGCYBELLKVLVYLKKAARLQAQVSRGAIQVSRAGLLSPVARSQGPQPSGCT 515

Db	383	-----RELNGYLEWIFKAEVMLAEE-----RNAEKSFLDVVK 417
QY	516	RSRRLSVHHLVHHHHHHHHHNGTLRVPASPEIQDRDANGSRRLMLPPPTPTPS 575
Db	418	RAATKKSNDLIH-----AEEGEDFAD----- 440
QY	576	GGPPRGAESVHSFYHADCHLEPVRCAQPPPCPSBASGRTVGSKVYPTVHTSPPEILK 635
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QY	636	DXALVEVAFSPGPPTLTSTFNIPPPFSSMHKILETQTCACHSSCKIISPCSKADSGAGC 695
Db	441	-----LCAVGSFFARAS----- 452
QY	696	PDSCEYCARAGAGEPESADHVMFSDSEAVVEFTQDAQHSDLDRPHSRRRQSLGPDABP 755
Db	453	-----LKSGKTESSYF-----RRKEK----- 469
QY	756	SSVLAFWRLICDTRFKIVDSKYFGRGIMIAILVNTLSMGIYEHQEPEELTNALEISNIVF 815
Db	470	--MFRFF-----IRRMVKAQSFYVWVLCVVALNTLCVAMVHNPRLTTLTYAEFVF 521
QY	816	TSLFALEMLLKLIVYGPFGYIKNPYINPFIQVIVIVISVWEIVGQ-----OGGLSVLRTFR 870
Db	522	LGLFLEMSLKMVGLGPRSYFRSSFCDFGVIGSVFVWMAAIKPGSSFGISVLRLR 591
QY	871	LMRVLKLVRFLPALORQLVVLAKMTDNNVATFCMLLMFLFIFISILGMHLFGCKFASERG 930
Db	582	LLRIFKVTYSSRLNVVSLNLSMKSIISLFLFLFVIVPALLQMLFGGQFNQDET 641
QY	931	DTLPDRKNFDSLLWAIWTVFQILUTQEDWNKVLNMG-----ASTSSWAALYFIATMTFNG 985
Db	642	PT-----TNEDTPAALTTFVQILTGEDWNAVWVHGIESQGVSKMGFSFYFVLTLFGN 697
QY	986	YVLFNLLVAILVEGFOAGDAIKSESEPDFFSPVDGDKRKLALVALGEAEARKSL 1045
Db	698	YTLNVFLATAVDNLANAQELTKDEEBEAA-----NOKLALQAKAEV--SP 746
QY	1046	LPPLIHTAATPMSPHKSSSTGVGEA----- 1071
Db	747	MSAANISIAARQNSAKARSVWEQASQLRQNLASCEALYSEMDPEERLRFATTHRR 806
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Db	807	PMKTHLDRPLVVELGRDGARGVGGKARPEAAEAPEGVDPRRHRHRDKDTTAAAGQ 866
QY	1098	-----PSARSS-----PHSPWSAASSWTSRRSSNLSGRAPSLKRRSPSGERSL 1142
Db	867	DRAEAPKAESGEPGAREPRPRSHSKEAA--GPPEARSEGRGP-----GPEGRRHH 919
QY	1143	LSGEGQSODEE-----ESSEDRASPAGSDHRRHSLE---REAKSSFDLEDTL 1189
Db	920	RRGSPEAAERPRHRAHRHQDFESKACAKGERARRHGGPPRAGPRAESG----- 972
QY	1190	QVPG-LHRTASGRSSASE--HQCNGKSASGRIA-----RTLRTDDQLDGDNDDE 1238
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QY	1239	GNLSKGERIAQWVRSRLPACCRER-----DSW----- 1265
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QY	1266	-----SAYIFPQSRFRLLCRI 1283
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QY	1284	ITHKQFHVHVLVILNLCITIAMERPKIDPHSAERIFLTLSNYIFTAVELAEWTKVVAL 1343
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QY 1457 TRN--ITNKSDCAEASYR--WVRHKYNFDNLGQALMSLFVLASKDGNVDIMYDGLDVGVD 1513
Db 1322 CRGOVLDEKEEVEAQPQWKYDHYDNVWALLTLFTVSTCEGPMVLKHSVDATYEE 1381
QY 1514 QOPIHNNPWWLLYFISPELLIIVAFVFLNMFVGVVNFHKKOHQEBEAREERKRLR 1573
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QY 1574 LEKKERSKEKMAEQAQCKPYSDYR--PRLLVHLCTSHYLDLRTITGIVGLNVVTMAE 1631
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QY 1692 LEEEBVNLSPINPTIIRIMVLRITARVLKLLKMAVGRALLHTVQALPQVGNIGLLFM 1751
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Db 1663 LSNQACDQANATECGSFAYFYFVSFIFLCSFLMLNLFVAVIMDNFYLTRDSSILGPH 1722
QY 1853 HLEB----- 1856
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QY 1936 VPUL-GPDLTLTVKSGVSRTHSLPNDSYMCMNGSTAESLGRGWGLPKQAGSGSILSVHS 1994
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Db 1946 -----PHEA-----RPLERGHSTELPVGSRGALAVDVQMOS 1977
QY 2050 -----SLDVGLGSRDILLSEVGPSCPLTRSSSFWGSSIQVQSGSIGSKV 2097
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QY 2192 LCSPSS-----SLGGQFL-----GGPGSRPKKXLS- 2217
Db 2137 PKKPSLSHSHTSPTAGQEPHPQSGSVNGSPLLSTGASTPGRGRRQLQTPLTER 2196
QY 2218 PSTSIDPPES-----QSRPPCSPG-----VCLRRAPASD-----SKDP 2252
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RESULT 12
US-09-452-007-2
; Sequence 2, Application US/09452007
; Patent No. 6140485
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Suey, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/452,007
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,118
; FILING DATE: 16-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-452-007-2

Query Match 13.9%; Score 1677; DB 3; Length 2337;
Best Local Similarity 23.4%; Pred. No. 5.4e-126;
Matches 627; Conservative 350; Mismatches 829; Indels 868; Gaps 82;
QY 59 PGGAAGAGTEKDPGASDSEAEGLPYALPV-----VFFVLSQDSRPSRSCIRT 109
Db 32 PGFGGLQPGQGVLYKQSIQAQRARTMALYNPIPVKQNCFTVNRSLFVSEDNVVRKAKRI 91
QY 110 VCPNPFERSVMLVILLNCVTLGMFRCEDIACDSQRILQAFDD---FIFAFVEMVV 166
Db 92 TEWPPPEYMLATIIANCIVLAL---EQHLPGDKTPMSERLDDTPEYFIFGIFCFEAGI 147
QY 167 KVALG-IFGKKCYLGDWTNRRLDFFVIAGMLEYS---LDLQNVSAVRTVVLRLPRA 222
Db 148 KIIALGFVHKSYLNGWNVDFVVLIGILATAGTDFDLR-----TURAVELRLPKL 202
QY 223 INRVPMRLVLLDITLPLMLGNVLLLCFFVFFIFGIVGVQLWAGLLRRCFLPNFSLP 282
Db 203 VSGIPSLQVVLKSIKMAVPLLIQGLLFFAILMLFAIIGLEFYMGFKHACF-----P 255
QY 283 LSVDLPEYPTQTENEDESFPICSPQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSN 342

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281 TEC-----REYWP-----GPNFGITNFDNIFAILTVQCITMEGWTDILYNTINDAAGT 330 Db
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383 -----RELNGYLEWIFAEVWLAEB-----SNABEKSPLDLK 417 Db
516 RSHRLSVHLLVHHHHHHHHHLLGNTLRVPASPEIQDORDANGSRRLMLPPPTPTPS 575 Qy
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696 PDSCPCYARTGAGEPESADHVPDSDSEAVYFTQAOHSDLRDPSHRQRORSLGPDABP 755 Qy
453 -----LKSCKTESSVF-----RRKEK-----469 Db
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470 -----IREMKAQSPYVWVLCVVALTLCVAVHYNQPRITTLIYFAEFVF 521 Db
816 TSLFALMLLKLIVGPGFYKPNYINIFDGVIVVISWVEITVGQ-----QGGGLSVLRTFR 870 Qy
522 LGLFLEMSLKMVGLGRSFRSPNCDFGVIVGSVFVWMAAIKPGSSFGISVLRALR 581 Db
871 LMRVLKVLRLPALQORLVVLMKTMONVATFCMLLMFLFIFISLGMHLFGCKFASERDG 930 Qy
582 LLRIKFKVTKWSSRLNVLVSLNMSKSIISLFLFLFIVVFPALLGMQLFGGQNFQDET 641 Db
931 DTLPDRKNPDLWAIWTVFOILTQEDWNKVLNMG-----ASTSSWAALYFIALMTFGN 985 Qy
642 PT-----TNFDTFFAAILTVFOILTGEDWNAMVTHGIESQGVGKMGSESSFYFIVLTLFGN 697 Db
986 YVLNLIIVALLVEGFOAEGDATKSESEDPFSPVDGDRKRLALVALGEHAERKSL 1045 Qy
698 YTLNVLALAVDNLANAQELTKDEEBEBA-----NOKLALQAKAEVAEV--SP 746 Db
1046 LPPLIIHTAATPMSPKSSSTGVGEA-----1071 Qy
747 MSAANISIAARQQNSAKARSWVEQASCLRLQNLARASCEALYSMDPEERLRFATTHRR 806 Db
1072 -----LGSGSRRTSSSGSAEPGAA-----HH-----EMKCP-----1097 Qy
807 PMKTHLDRLLVLVGLDGDGAPGVGGKARPEAAEPAGVDPPRHHRHHRDKOKTFAAGDQ 866 Db
1098 -----PSARSS-----PHSPWSAASWTSRRSRNSLGRAPSLKRRSPGERRSL 1142 Qy
867 DRABAPKAESGEPGAREPRPHRSKKEA--GPPEARSRGRGP-----GPEGRRHH 919 Db
1143 LSGEGQSODE-----ESSEDRASPAGSDHHRGSLE-----REAKSSFDLPDLT 1189 Qy
920 RRGSPBEEAERPRHRAHRHQDPKSCAGAKGBRRARRHGRPPAGPREASG-----972 Db
1190 QVPG-LHRTASGRSSASE--HODCNGKASGRLA-----RTLRTDDPOLDGDNDDE 1238 Qy
973 EEPARRHARKAQAPEAVEKETTEKATEKEAEIIVEADKEKELRNHQPREPHCDLETS 1032 Db
1239 GNLKGERIQAVRSRLPACCR-----DSW-----1265 Qy
1033 GTVTVGP-----NHTLPSTCLQVEQPEDADNQNRVTRMGSPQPPDNTIIVHIVMLTG 1086 Db

1266 Qy
1087 PLGEATVPSGNDVLESQAEKGKEVEADDVNRSGPRPIVPSYSSMFCLSPTNLLRRFCHYI 1146 Db
1284 ITHKMFHDHVLIVILNCITITAMERPKIDPHSABRIFLTLNYSITAVFLAEMTVKVVVAL 1343 Qy
1147 VTMRYFEVILVIALSSIALAAEDP-VRTDSPRNALKYLDYIFGTFTFEMVJRMIDL 1205 Db
1344 GWCGEQAYLSSNNVLDGLLVLSIDILVSMV--SDSGTKILGMLRLVRLTLRPLRV 1402 Qy
1206 GLLHPGAYFDLWNILD-----FIVVSGALVAPFSGSGKGDINTIKSLRVLRLPLKT 1261 Db
1403 ISRAOGLKLVVETLMSLSKPIGNIVVICAPFIIIFGILGVQLFKGKFFVCOQE-----D 1456 Qy
1262 IKRLPKLKAVIDCVNSLKNVLNILLIVYMLFEMFIFAVIAVQLFKGFFYCTDESKELED 1321 Db
1457 TTN--ITNKSOCABEASYSR-WYHKNFNDLGOALMSLFLVASKDGMVDIMYDGLDVGVD 1513 Qy
1322 CRGOYLDYEKEEVEAQRQWKYDHYDNLWALLTFTVSGEGWPVLKHSVDATYEE 1381 Db
1514 QOPIVNNHPMLLYFISLIIIVAFVLMNVGVVVENFHKCRQHOEEEEEAREERKLR 1573 Qy
1382 QPSPGIRMELSIFVIVVVFVFPFVNI FVALIITF-----QEGDKVME-----CS 1431 Db
1574 LEKRRSKEKQMAEAOCKEYYSYDSR--FRLVHHLCTSHYLDLDFITGVLGNVVTAME 1631 Qy
1432 LEKNERACIDFAISAKPLTRYMPQNRQSQYKTWTFVSPPEYFETAMIALNTVVLMMK 1491 Db
1632 HYQOQILDEALKICNYIPTVIVFESVEKLVAFARREFQDRWNQOLDLAIVLISIMGIT 1691 Qy
1492 FYDAPYEYELMKCLNIVFTSMFMECVLIKILAFGLNIFRDANNVDFVTVLGSLTDL 1551 Db
1692 LEEIEVNLSPNPTIIRTVRLRLARVLKLMKMAVMEALLHTVMQALPOVGNLGLFEM 1751 Qy
1552 VTEIANF--IN--LSFLRFRARLIKLRQGVTRILLWTFVQSFKALPYVCLLIA 1605 Db
1752 LIAFFIFAALGVELFGLECDETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD- 1810 Qy
1606 MLFFVIAIIGMVGFNIALDDD--TSINRHNFTFLQALMLLFRSATGEAMHEIMLSC 1662 Db
1811 -PSRDCQD--STCYNVTIVSPYFVSFVLTAQVPLVNVVIAVLN-----K 1852 Qy
1663 LSNQACDEQANATECGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPH 1722 Db
1853 HLEE-----1856 Qy
1723 HLEDEFIRWAEYDPAACGRISYNDMEMLKHMSPPLGLGKKCPARVAYKELVRMNMPISN 1782 Db
1857 -----SNKEAKEEABIEAEL-----ELEMKTLS--POPH 1883 Qy
1783 EDMTVHTSTLMALIRTALEIKLAPAGTKHQCDALRKEISVWVANLPKOTLDLLVPPH 1842 Db
1884 SP-----LGSPF---LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTVMVHPPEV 1935 Qy
1843 KPDEMTVGKYAALMIPDFYKQNKTRDQMOQAPGLSQMGPSVLF---HPLKATLQTO 1899 Db
1936 PVPL-GPDLTLTVRKSGVSRTHSLPNDSYMCNRNSTAERSLGHGWGLPKQSGSILSVHS 1994 Qy
1900 PAVLRGARVFLRQKSSIT---SLNNGAIQNESGIKESV---SWGTRQDA-----1945 Db
1995 QPADTSCIOQLPKDVHVLQPHGAPTGAIPKLPPOGSRPLAQORPLRQAIRTD-----2049 Qy
1946 -----PHEA-----RPPLERGHSTELPVRSGSALAVDVQMOS 1977 Db
2050 -----SLDVQGLSREDLLSEVGSPSCPLTRSSSFWGSGSIOVQORSIOQSV 2097 Qy
1978 ITRRGPGEGEPQGLUESQ---RAASMPRLAAETQPVTDASPMKESITLQAPRG-----2029 Db
2098 SKHRLPAPCFGLEPSWAKDPPETRS-----SLELDTLSWISGLLPL 2140 Qy
2030 -THLCSITP-----DRPPPSQASSHHHHHRRRRDRKQSRLEKGPSLS-ADMDGAP 2079 Db


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/
/  ZIP: 92101-2926
/  COMPUTER READABLE FORM:
/  MEDIUM TYPE: Diskette
/  COMPUTER: IBM Compatible
/  OPERATING SYSTEM: DOS
/  SOFTWARE: FastSeq Version 1.5
/  CURRENT APPLICATION DATA:
/  APPLICATION NUMBER: US 08/223,305C
/  FILING DATE: April 4, 1994
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER: 07/868,354
/  FILING DATE: April 10, 1992
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER: US 07/745,206
/  FILING DATE: 15-AUG-1991
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER: US 07/620,250
/  FILING DATE: 30-NOV-1990
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER: US 07/482,384
/  FILING DATE: 20-FEB-1990
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER: US 07/603,751
/  FILING DATE: 04-APR-1989
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER: WO PCT/US89/01408
/  FILING DATE: 04-APR-1989
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER: US 07/176,899
/  FILING DATE: 04-APR-1988
/  ATTORNEY/AGENT INFORMATION:
/  NAME: Seidman, Stephanie L.
/  REGISTRATION NUMBER: 33,779
/  REFERENCE/DOCKET NUMBER: 52516 (P519739)
/  TELECOMMUNICATION INFORMATION:
/  TELEPHONE: (619)238-0999
/  TELEFAX: (619)238-0062
/  INFORMATION FOR SEQ ID NO: 47:
/  SEQUENCE CHARACTERISTICS:
/  LENGTH: 2339 amino acids
/  TYPE: amino acid
/  STRANDEDNESS: single
/  TOPOLOGY: linear
/  MOLECULE TYPE: protein
/  FRAGMENT TYPE: internal
/  US-08-223-305C-47

Query Match      13.98; Score 1676; DB 2; Length 2339;
Best Local Similarity 23.4%; Pred. No. 6.5e-126;
Matches 627; Conservative 350; Mismatches 826; Indels 876; Gaps 82;

QY 59 PGGAAGAGSTEKDPGSADSEAEGLPYPALAPV-----VFFYLSQDSRSPRSWCLRT 109
D 32 PGFGGLPGQGVLYKQSIQARATMALYNPIYKQNCFTVNRSLFVPSEDNVVRKYAKRI 91
QY 110 VCNPTWTERVSMVILLNCVTGLMFRPCEDIACDSQRCLIAFD-----FIFAFVAVMVV 166
D 92 TEMPPFENMILATIIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIFCFEAGI 147
QY 167 KMVALG-IFGKKCYLGDWTNRLDFFIVIAGLMYS---LDLQNVSTSAVTVTVRLPLRA 222
D 148 KITALGFVFKHGYLRNGMVMDFVVLVTGILATAGTDFDLR-----TLRAVRLRLPKL 202
QY 223 INRVPSMRILVLLDLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLP 282
D 203 VSGIPSLQVVLKSIKMAKMPVLLQIGLLFFAILMFAILGIEFTMGFKHACF-----P 255
QY 283 LSVLDLEPYQOTENEDESPPFICSPRENGMRSCSVPTLRGEGGGPPCSLDIYETYNSSN 342
D 256 NSTDAEPV-----GDFPCGKEAPARLCEGD 280
QY 343 TTCVNNNQYNTNCSAGEHPFKAINFDNIGYAWIAIFQVITLEGWVDIMYFMD-AHSF 401
D 1143 LSQGEQESODEE-----ESSEDRASPAAGSDHRRGSLG---REAKSFFDLPTDL 1189
D 920 RRGSPPEAAERPRRHRAHRHQDPKCEKAGKERRARRHRRGPRGPRAGSAG- 972
QY 1190 QVPG-LHRTASGRSSASE--HQDCNGKASGRLA-----RTLTDQDQDGDNDDB 1238
D 973 EBFARRHFAHKAQAHAHAVEKETTEKATEKAEIIVEADKEKELNHQHPREPHCULETS 1032
QY 1239 GNLKGERIQAVRSELPAACBER-----DSW----- 1265
D 1033 GIVTVGP-----MHTLPSTCLQKVEEQPEDADNQRNTRMGSQDPDNTIVHIPVMLTG 1086
QY 1266 -----SAYIFPQSFRLCHRI 1283
D 1087 PLGEATVPSGNVDLESQAEKGKKEVEADDMRSGPRPIVPSYSSMFCLSPTNLLRRFCHYI 1146
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QY 2187 GQPRLCPSPS-----SLGQPL-----GGPSREPK 2213
 Db 2134 GGREPPKPKSLSSGHTSPTAGQEPHPQSGSVNGSPLLSTSGASTPGGRRQLPQT 2193
 QY 2214 KLSP-PSISIDPPES-----QGRPPCSPG-----VCLRRAPASD----- 2248
 Db 2194 PLTPRSITYKTANSSPIHFAGQOTSLPAFSGRLSGLSEHNALLQDPLSLOPLAGSR 2253
 QY 2249 -SKPSSVSPLDSTAASPSKPKDLSL-----SGLSS 2279
 Db 2254 IGSDDYLQRLDSEASVHALPEDITLPFEAVATNSGRSS 2292

 RESULT 15
 US-09-268-163-6
 ; Sequence 6, Application US/09268163B
 ; Patent No.: 6353091
 ; GENERAL INFORMATION:
 ; APPLICANT: Lipscombe, Diane
 ; APPLICANT: Schorge, Stephanie
 ; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
 ; FILE REFERENCE: B1055/7000
 ; CURRENT APPLICATION NUMBER: US/09/268,163B
 ; CURRENT FILING DATE: 1999-03-12
 ; EARLIER APPLICATION NUMBER: US 60/077,901
 ; EARLIER FILING DATE: 1998-03-13
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 2339
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-268-163-6

 Query Match 13.9%; Score 1674; DB 3; Length 2339;
 Best Local Similarity 23.4%; Pred. No. 9.4e-126;
 Matches 627; Conservative 350; Mismatches 826; Indels 876; Gaps 82;

 QY 59 PGFAGAGAGSTKDPGASDSEAGLPYPALAPV-----VFFYLSQDSRPSRCLRT 109
 Db 32 PGPGGLQPGQVLYKQSIQAQARTMALYNPIPVKQCNFTVNRSLFVSEDNVVRKAKRI 91
 QY 110 VCMPTFERSVLMVILLNCVTILGNFRPCEDIACSQRILQAFDD--PIFAFFAVEMV 166
 Db 92 TEMPPPEYMLATIIANCIVLAL---BOHLPDGDTPMSERLDDTEPYFIFGICFEAGI 147
 QY 167 KVALG-IFGKKCYLGDWTNRLDFFIVTIGMLEYS---LDLQNVSPSAVTRVRLPLRA 222
 Db 148 KIITALGFVHKGSYLRGNWVMDVFWVLGILATAGTDFDLR---TLRAVRLPLKL 202
 QY 223 INRVPMRILVTLTLLDPLMLGNVLLCFFVFFIFGIVQVLWAGLLRNCFLPENFSLP 282
 Db 203 VSGIPSLQVVLKSIKMAWVLLQIGLLFFAILMFALIGLEFYMGKFKACF-----P 255
 QY 283 LSVDPLEPYOTENEDSPFCISQPRENGMESCVRPLTRGEGGGPPCSLDYETYNSSN 342
 Db 256 NSTDAEBV-----GDFCCKEAPARLCEGD 280
 QY 343 TTCVNMNYVTCNSAGEHNPKGAINPDNTIGYAWIAIFQVITLLEGWVDIMYFVMD-AHSF 401
 Db 281 TEC---REYWP-----GNFGITNEDNILFALLTVFCITMEGWTDLTYNTNDAAGT 330
 QY 402 YNFYIFILLIIVSGFFMINICLVVIATQFSETKQES-----QLMEQORVFLSNASTL 455
 Db 331 WNWLYFIPLIIGSFFMLNLVGLVSGFAKEREVENRFAFLKLRQQOIE----- 382
 QY 456 ASFPESCSVEELLKYLVLKARLAQVRAIGVRLAGLLSPVARSQEPQSGSC 515
 Db 383 -----RELNGYLEWIFKAEVWLAED-----RNAEKSPLDVLK 417
 QY 516 RSHRRLSVHLLVHHHHHHHHHGLNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPS 575
 Db 418 RAATKSKNDLIH-----AEEGEDRFAD----- 440

QY 1284 ITHKOFDHHVAVIIFLNCITIAMERPKDIPSAERIFLITLNYIFTAVFLAEMTVKVAL 1343
 Db 1147 VTRMFEVILVIALSSIALAAEDP-VRTDSPRNALKYLDYFTGFTFEMWIKMIDL 1205
 QY 1344 GWCQGEQAYLRSSNNVLDGLLVISVIDILSMV-SDSGTKILGMLRVLRLRLRLR 1402
 Db 1206 GILLHPGAYFRLWMILD-----FIVSGALVAFSGSKGKDINTIKSLRVLRLPLKT 1261
 QY 1403 ISRAQGLKLVVETLMSLLPKIGNIVVIVICAFPIIFGILGVLPKGFVFCQGE-----D 1456
 Db 1262 IKRLPKLKAFCVNVSLKVNILILVYMLFMFIFAVIAVOLFKGKFFVCTDESKELERD 1321
 QY 1457 TRN--ITNKSOCAEASYR-WRHKYNPNLGOALMSFLVSLKQDGVIMVDGLDVGVD 1513
 Db 1322 CRGQYLDYEKEBEAQPQKWKYDEHYDNVLMWALLTFTVSTGEGPMVLKHSVDATVEE 1381
 QY 1514 QOPIMNHPMMLLYFISLILVAFVLMNMFVGVVENFKHQHQBEEBARREERKLRR 1573
 Db 1382 QGSPGYNELSIYVYVYVFFVFFVNFVLIITF-----QEQDKVMSL-----CS 1431
 QY 1574 LEKKERSKEKQMAEAQCKPYSDYSR--FRLVHHLCTSHYLDLFTIGVIGLVNVTMAME 1631
 Db 1432 LEKNERACIDFALSAPLTRYMPQNRQSFQYKTWTFVVSPPPEYFIMAMIALNTVVLMMK 1491
 QY 1632 HYQQQLIDALKICNIYITVIVFVSFKLVAFAPRRFQDRWQOLDLAILVLSITGIT 1691
 Db 1492 FYDAPYEYELMKCLINIVFTSMFMECVLKIIAFGLNLYFRDANNVDFVTVLGSITDL 1551
 QY 1692 LBEIE-----VNLSPINPIIRIMRVLRIRVILKLLKMAVGRALLHTVMQALPOVGNL 1746
 Db 1552 VTEIAETNNFINUS-----FLRLFRAALIKLIRQYTRILLWTIFVQSFKALPY 1602
 QY 1747 GLIFMLLFFIFALGVLEGLDCEHPCEGLGRHATFRNFQMAFLTFPRVSTGNWNG 1806
 Db 1603 CLLIAMFLFIYIIGQVFGNIALDDD--TSINRHNFRITFQALMLLFRSATGEAWHE 1659
 QY 1807 IMKD--PSRDCDE--STCVNTVLSPTFYFVSFVLTAQFVLNVNVIAMV----- 1851
 Db 1660 IMLSCLSNACDQANATECGSDFAFYFVSFIFLCSFLMLNLFVAVIMDNFYLTRDSS 1719
 QY 1852 ---KHLEE----- 1856
 Db 1720 ILGPHLDEIRVWAEYDPAACGRI SYNDMPFEMLKMSPLGLGKCPARVAVKRLVRN 1779
 QY 1857 -----SNKEAKEAELEAEL-----ELEMKTL- 1879
 Db 1780 MPISNEDMTVHTTSTLMALIRTALEIKLAPAGTKHQCDAAELRKEISVVMANLPKRTLDL 1839
 QY 1880 -POPHSP-----LGSPP-----LWPGVEGVNSTDPKPGAPHTTAHIGAAGSFLSLEHTMVP 1930
 Db 1840 LVPPHKPEDEMTGVKYAALMIFDYKQNTTRDQMOQAPGLSQMGVSLF---HPLKAT 1896
 QY 1931 HPEVVPVL-CPDLLTVRKGSVRTHSLPNDSYNCRNGSTAERSLGRHGLPKAQSGSI 1989
 Db 1897 LEQTOPAVLARGARVFLRQKST---SLNGGALQNOESGIKESV---SWGTQRTQDA-- 1947
 QY 1990 LSVHSQPADTSCILQLPRDHYLLQHPGAPTWGAIPKLPPGSRPLAQRPLRQAARTD 2049
 Db 1948 -----PHEA-----RPPLERGHGSTEIPVGRSGALAVD 1974
 QY 2050 -----SLDVOGLGSRDLLESEVSGPSCPLTRSSSFWGGSSIQVQORSG 2092
 Db 1975 VQMSITTRGDPGPOPLESGQ---RAASMPRIAAETQPTVDASPKRSISLTAQPRG 2031
 QY 2093 IQSKVSKHIRLPAPCPGLEPSWAKDPPETRS-----SLDLETLSWIS 2135
 Db 2032 -----THLCSSTP-----DRPPSPQASSHHHHHRRRRRDRKQKRSLEKGPSLS-AD 2076
 QY 2136 GDLLPSSQEBFLP-----RDLKKCYSVETQSCRRRRFGFWLDEORRHSIAVSCULDS 2186
 Db 2077 MDGAPSSAVGFLPPGEGTGCRRERERRQGRGSRQERRQPSSSSEKQRF---YSCDRF 2133

QY	576	GGPPRGAEVSHFYHADCHLEPVRCQAPPPRCPEASGRVSGKVYPTVHTSPPEILK	635	QY	1457	TRN--ITNKSDCAEASYR-WVRHKYNFNDLGOALMSLFLVASKDGWVDIMYDGLDAVGD	1513
Db	441	-----	440	Db	1322	CRGQYLDYKEBEVEAQPRQWKYDHYDNVWALLTLFTVSTGEGPMVLKHSVDATYEE	1381
QY	636	DKALVEVAPSPGPTLTSENIPGPSSMHKLLTOSTGACHSSCKISPCSKADSGAGC	695	QY	1514	QOPIMNHNPMWLLYFISFLLIYAVFVLNMFVGVVVENFHKCHQHOEEBAAREERLRR	1573
Db	441	-----	452	Db	1382	QGPSFCYRMELISFYVVFVVFVFFVNFVLIITF-----QOQGVKWE-----CS	1431
QY	696	PDCPCYARTGAGEPESADHVPDSDSEAVYFTQDAQHSLDRDPSRRQRSLGPDAPF	755	QY	1574	LEKKRSKEKOWAEQAACKPYYSYDYSR--FRLLVHHLCTSHYLDLFTTIGVGLNVVTMAME	1631
Db	453	-----	469	Db	1432	LEKNERACIDPAISAKPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVLMWK	1491
QY	756	SSVLAFWRLICDTRFKYDVKYFGRGIMTALVNTLSMGIHYEHOPEELTNALET-SNIVF	815	QY	1632	HYQQOQILDEALKICNYIFTVIFVESVFKLVAFAPRFRFPQDRWNQOLDIAIYLLSIMGIT	1691
Db	470	--MFRFF-----	521	Db	1492	FYDABEYELMLKCLINIVFTSMFSMECVLKIIAFGLVNYFRDAMNVDFTVLGSIITDIL	1551
QY	816	TSLEFALEMLKLLVGPFGYIKNPYINFDGVIVVLSWWEIVQ-----QGGGLSVLRTRF	870	QY	1692	LEEIE-----VNLSLPINPTIIRIMRVLRIARVLKLLKXAVGMRRALLHTVMQALPOVGNL	1746
Db	522	LGLFLETSLKMYGLGPRSYFRSSCFDFGIVGVSEFVWMAAIKPGSSSFGISVLRLR	581	Db	1552	VTEIAETNNFINLS-----FURLPRAAKLILKLRQGYTIRILLMTFVQSFKALPYV	1602
QY	871	LMRVILKLVFLPALQORQLVLMKMTMDNVATFCMLMLFIFIFISILGMHLFGCKEASERDG	930	QY	1747	GILFMLLPFIPAALGVELFGDLCEDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNG	1806
Db	582	LLRIFKVTKYSSLRNLVSVLNSMKSIISLLFLFLFIVFALLGMLFGGQFNQDET	641	Db	1603	CLLIAMLFPIYAIIGMQVFGNIALDODD--TSINRHNFRFQLQALMLLFRSATGEAMHE	1659
QY	931	DTLPDRKNFDSLMAIVTVFOILTQEDWNKVLYNGM-----ASTSSWAALYFIALMTFGN	985	QY	1807	IMKD--PSRDCQOE--STCYNTVVISPIYFVSFVLTAQFVLNVNVIJAVLM-----	1851
Db	642	PT---TNFDTFPAAILTVFOILTGEDWNAVMYHGIESQGGVSKGMFSFVIVLTLFGN	697	Db	1660	IMLSCLSNQACDEQANATECGSDFAYFYFVSFIFLCSPLMLNLFVAVIMDNFEYLTRDSS	1719
QY	986	YVLENLLVAIVLEGFQAEGDATKSESEDPFSPVSDGDRKKRLALVALGEHAELRKS	1045	QY	1852	-----KHLEE-----	1856
Db	698	YTLNWFIAIADNLIANAQELTKOEEEMEEAA-----NOKLALQAKEVAEV--SP	746	Db	1720	ILGPHHLDEFIRVWAEYDPAACGRISYNDMEFEMIKHMSPPGLGKCKPCPARVAYKRLVMN	1779
QY	1046	LPPLIIHTAATPMSPKSSSTGVGEA-----	1071	QY	1857	-----SNKEAKEAELEAEL-----ELEMKTLS--	1879
Db	747	MSAANISIAARQQNSAKARSVWEQASQLRIONLRASCEALYSEMDPEERLRFATTHLR	806	Db	1780	MPISNEDMTVHTSTLMALIRTALIEIKLAPAGTQHQCDAELRKEISVWVANLQKTLIDL	1839
QY	1072	-----LGCSRTSSGSAEPGAA-----HH-----EMKCP-----	1097	QY	1880	-POHSP-----LGSPP-----LWPGVEGVNSTDSKPGAPHTTAHIGAAGSFSLEHTMVP	1930
Db	807	PDMKTHLDRPLVWELGRDARGPVGGKARPEAAEAPGVDPPRHHHRHRODKTTPAAGDQ	866	Db	1840	LVPHPKDEMTVGKYYAALMIFDFYKQNKTTDQMQOAPGLSQMPVSLF---HPLKAT	1896
QY	1098	-----PSARSS-----PHSPWASASWTSSRSNLSGRAPSLKRRSPSGERRSL	1142	QY	1931	HPEEVPVPL--GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGRHGLPKAQSGSI	1989
Db	867	DRAEAPKAEGEPGARBERPRPHRSHKEAA--GPPEARSGRGRGP-----GPEGGRHH	919	Db	1897	LEQTQPAVLGARVFLRQKST---SLNNGGAIQNOESGKESV---SWGTOQTODA--	1947
QY	1143	LSGEGQESQDEE-----ESSEDRASPAGSDHHRGSLR---REAKSFDLPDTL	1189	QY	1990	LSVHSQPADTSCILQLPKDVHYLLQPHGAPTWCAGAIKPLPPGSRSLAORPLRQAARTD	2049
Db	920	RGSPSEAEAREPRHRAHRHQDPSKACAKGERRARHRGRAGPREAESG-----	972	Db	1948	-----PHEA-----RPLERGHSTEIFVGRSGALAVD	1974
QY	1190	QVFG-LHRTASGRSSASE--HQDCNGKSASGRLA-----RTLRTDDPQLGDGDDNDE	1238	QY	2050	-----SLDVQGLGREDLLSEVSGPSCPLTRSSSFWGSSSIQVQQRSG	2092
Db	973	EEPARRHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKELRNHQPREPHCDLETS	1032	Db	1975	VQMSITRRGPDGEPQPGLESQG---RAASMPRLAAETQVTDASPMKRSISTLAQPRG	2031
QY	1239	GNLSKBERIAQWVRSRLPACCRER-----DSW-----	1265	QY	2093	IQSKVSKHIRLPAPCPGLEBPMWAKDPPETRS-----SLELDELSWIS	2135
Db	1033	GTVTVGp-----MHTLPSTCLOKVEEQBEDADNQNRVTRMGSPDPNTIVHIPVMLTG	1086	Db	2032	-----THLCSTTP-----DRPPSQASSHHHHRRCHRRDRDKORSLEKGPSLS-AD	2076
QY	1266	-----		QY	2136	GDLPLSQBEPLFP-----RDLKKCYSVETQSCRRRPGFWLDEQRHRSIAVCLDS	2186
Db	1087	PLGEATVPSGNVDLESQAEGKEVEADVMRSGPRPIVPSYMFCLSPNTLLRRFCHYI	1146	Db	2077	MDGAPSSAVGGLPGCEGTPGCRERERQGRSQRERRQPPSSSSSEKORF---YSCDRF	2133
QY	1284	ITHMFDHVVLIIFNCITIAMERPKIDPHSAERIFLTLNSYIFTAVFLAEMTVKVVVAL	1343	QY	2187	GSQPRLCPSPS-----SLGGQPL-----GGPGSRPKK	2213
Db	1147	VTRYFEVILVIALSSIALAAEDP-VRTDSFRNNALKYLDVIFTGVTFEFVMIKIDL	1205	Db	2134	GREPPKPKPSLSSHTSPSTAGCEPGHPQGGSVNGSPULLSTSGASTPCRGRRLPQT	2193
QY	1344	GMCFGCQVILRSWNVLDGLLVLSVIDILVSV--SDSGTKILGMLRVLRLLRPLRV	1402	QY	2214	KLSP--PSISIDPPES-----QGRSPPCSRG-----VCLRRRAPAD-----	2248
Db	1206	GLLLHPGAVFRDLWNLTLD-----FIVVSGALVAFAPSGSKGKOINTIKSLRVLRVLRPLKT	1261	Db	2194	PLTPPSITYKTANSPIHFAGAQTSLPAFSPGSRGLSEHNALLQORDPLSQPLAPGSR	2253
QY	1403	ISRAOGLKLVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCOGE-----D	1456	QY	2249	-SKDPSVSPSLDSTAASPPKDDTLSL-----SGLSS	2279
Db	1262	IKLPLKKAIVFCVNSLKNVILNIVYMLFMPFIAVIAVOLFKGKFFYCTDESKELEDR	1321	Db	2254	IGSDPVLGORDSEASVIALPDTLITFEAVATNSGRSS	2292

us-09-611-257a-24.ra1

Mon Nov 22 06:47:52 2004

Search completed: November 18, 2004, 13:35:56
Job time : 78.6868 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:32:41 ; Search time 180.328 Seconds
(without alignments)
4491.206 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVPCVTPPLRGSR.....KKDTLSGLSDPTDMDPZ 2287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11542.5	96.0	2425	10 US-09-383-894-4	Sequence 4, Appli
2	11532	95.9	2374	10 US-09-383-894-2	Sequence 2, Appli
3	10806.5	89.8	2243	16 US-10-408-765A-625	Sequence 625, App
4	10732.5	89.2	2377	17 US-10-757-262-16	Sequence 16, Appl
5	6222	51.7	2353	16 US-10-408-765A-1128	Sequence 2, Appli
6	5409	45.0	2175	9 US-09-935-541-2	Sequence 2, Appli
7	5409	45.0	2175	14 US-10-425-800-2	Sequence 2, Appli
8	5405.5	44.9	2188	9 US-09-935-541-4	Sequence 4, Appli
9	5405.5	44.9	2188	14 US-10-425-800-4	Sequence 5, Appli
10	5345	44.4	1835	9 US-09-935-541-5	Sequence 5, Appli
11	5345	44.4	1835	14 US-10-425-800-5	Sequence 19, Appli
12	3950	32.8	1853	9 US-09-030-482B-19	Sequence 6836, Ap
13	3553	29.5	1657	14 US-10-369-493-6836	

14 1680.5 14.0 2264 15 US-10-627-370-2 Sequence 2, Appli
15 1678 14.0 2327 17 US-10-736-883-38 Sequence 38, Appli
16 1678 14.0 2343 13 US-10-033-026-4 Sequence 4, Appli
17 1676 13.9 2339 15 US-10-375-253-12 Sequence 12, Appli
18 1674 13.9 2339 13 US-10-033-026-6 Sequence 6, Appli
19 1674 13.9 2339 17 US-10-736-883-32 Sequence 32, Appli
20 1673 13.9 2331 17 US-10-736-883-44 Sequence 44, Appli
21 1662.5 13.8 2288 17 US-10-736-883-40 Sequence 40, Appli
22 1661 13.8 2333 17 US-10-736-883-28 Sequence 28, Appli
23 1647.5 13.7 2213 16 US-10-322-696-178 Sequence 178, Appli
24 1642.5 13.7 2237 15 US-10-375-253-14 Sequence 14, Appli
25 1642.5 13.7 2336 13 US-10-033-026-10 Sequence 10, Appli
26 1642.5 13.7 2336 13 US-10-033-026-8 Sequence 8, Appli
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35 1631 13.6 2181 13 US-10-029-413A-20 Sequence 20, Appli
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37 1631 13.6 2181 14 US-10-411-010-29 Sequence 29, Appli
38 1631 13.6 2181 16 US-10-322-696-54 Sequence 54, Appli
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43 1617.5 13.4 1969 10 US-09-457-571-16 Sequence 16, Appli
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45 1614.5 13.4 1977 10 US-09-919-039-367 Sequence 367, Appli

ALIGNMENTS

RESULT 1
US-09-383-894-4
; Sequence 4, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2425
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-383-894-4

Query Match 96.0%; Score 11542.5; DB 10; Length 2425;
Best Local Similarity 95.4%; Pred. No. 0;
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Db 133 WFERVSMVLILLNCVTLMGMPFPCEDIIACDSORCBILQAFDDFIEIAPFAVEMVVKMVALGI 192
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 Db 193 FGKCYLGDWTNRLLDFFVIAGMLEYSLDLQNVSFSAVRTVVRVLRPLRAINRVPMSRILV 252
 QY 234 TLLDITLMLGNVLLLCFFVFFIFGIVGVQVQWAGLLNRCLPENFSLPLSDLEPPYQT 293
 Db 253 TLLDITLMLGNVLLLCFFVFFIFGIVGVQVQWAGLLNRCLPENFSLPLSDLEPPYQT 312
 QY 294 ENEDESPTCSOPRENGRMSCRSVTLRGEGBGPPCSLDYETYNSSNTTCVNNQYIT 353
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 QY 534 HHYHILNGTGLVPRASPEIQDRDANGSRRLMLPPESTTPPGGPPRGAESVHSFYHADC 593
 Db 553 HHYHILNGTGLVPRASPEIQDRDANGSRRLMLPPESTTPPGGPPRGAESVHSFYHADC 612
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 Db 613 HLEPVRQAPPPCPSEAGRTVGSKVPTVHTSPPELKDHALVEVAPSPGPPTLTS 672
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 Db 1453 LVVETLMSLKPIGNIVVICCAFFIIFGILGVQVFKGKPFVFCQGBDTRNINKSCABAS 1512
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 Db 1513 YRWVHKNFNDLGOALMSLFVLASKDGVMDIMYDGLDAVGVDQOPIMNHNFMWLLYFIS 1572
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 Db 1573 FLLIVAFVFLNMVGVVVENFHKCFQHQBEEBARRRERKRLRLEKRRMLDDVIAAG 1632
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; Sequence 2, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2374
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-383-894-2

Query Match      95.9%; Score 11532; DB 10; Length 2374;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2206; Conservative 1; Mismatches 18; Indels 34; Gaps 2;

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Db 210 MLGNVLLCFVFFIFIGVGVQWAGLLRNRCFLPENFSLVDLEPPYQYOTENEDSPF 269

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Db 270 ICSPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYNTCSAGEHN 329

Qy 362 PFKGAINFDNIGYAWIAIFOVITLEGVVDIMYFMDAHSFNFIYFILLIIVGSFFMINL 421
Db 330 PFKGAINFDNIGYAWIAIFOVITLEGVVDIMYFMDAHSFNFIYFILLIIVGSFFMINL 389

Qy 422 CLVVIATQFSETKQRESQMRQVRFLSNASTLASPEGSCVCEELLKYLVTLRKAAR 481
Db 390 CLVVIATQFSETKQRESQMRQVRFLSNASTLASPEGSCVCEELLKYLVTLRKAAR 449

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Db 690 SNAVVEFTQAOHSDLRDPHSRRRQSLGPDAPPSVLAFWRLICDTFRKIVDSKYFGRG 749

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Db 1470 NFNLGQALMSLFLVASKDGVDDIMYDGLDAGVDQOPIMNHNPMWLLYFISFLLIIVAF 1529

Qy 1539 VLMNFVGVVVENPHKCRQHEEAEARRREKRLRLEKRR-----SKEQMAE 1587
Db 1530 VLMNFVGVVVENPHKCRQHEEAEARRREKRLRLEKRR-----SKEQMAE 1589

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Db 1590 AQCKPYSDYSRFRLLVHLLCTSHYLDLFTGTVIGLVNVTVMAMEHYQQOQILDEALKICN 1649

Qy 1648 YIFTVIFVESVFKLVAFARFFQDRWNQDLAIIVLLSIMGITLEEIEVNLSPINPTI 1707
Db 1650 YIFTVIFVESVFKLVAFARFFQDRWNQDLAIIVLLSIMGITLEEIEVNLSPINPTI 1709

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Db 1710 IRIMRVLRITARVLLKMLAVGNRALLHTVMQALPQVGNLGLLFLMFLFFIIFALGVLF 1769

Qy 1768 LECDETHPCGEGHATFRNFGWAFITLFRVSTGDNWNGIMKDPDRDCQESTCNTVVIS 1827
Db 1770 LECDETHPCGEGHATFRNFGWAFITLFRVSTGDNWNGIMKDPDRDCQESTCNTVVIS 1829
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 450 RLAQVSRAGVRAIGLLSPVARSQGPQSPSCSTRSHRRLSVHLLVHHHHHHHHVHLGN 509
 542 GTLRVPRASPEIOTDRDANGSRMLPPTSTPTPGGPPGAGSVHSFYHADCHLPRVQC 601
 510 GTLRVPRASPEIOTDRDANGSRMLPPTSTPTPGGPPGAGSVHSFYHADCHLPRVQC 569
 602 APPPCPCSEASGRTVSGSKVYPTVHTSPPEILKDKALVEVAPSPPTLTSENPDPGF 661
 570 APPPCPCSEASGRTVSGSKVYPTVHTSPPEILKDKALVEVAPSPPTLTSENPDPGF 629
 662 SSMKILLETQSTGACHSCIKISSPCSKADSGAGDSDSCPCYACARTGAGEPESADHMPDSD 721
 630 SSMKILLETQSTGACHSCIKISSPCSKADSGAGDSDSCPCYACARTGAGEPESADHMPDSD 689
 722 SEAVYFTQDAQHSDLRDPHSRRQSLGPDDEAPSSVLAFWRLICDTFRKIVDSKYFGRG 781
 690 SEAVYFTQDAQHSDLRDPHSRRQSLGPDDEAPSSVLAFWRLICDTFRKIVDSKYFGRG 748
 782 IMAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLIVGPPGYIKNPYN 841
 749 IMAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLIVGPPGYIKNPYN 808
 842 IFDGVIVISVMEIVQGGGLSVLRTFRLMRVILKLVRLPALOROLVLMKTMNDVATF 901
 809 IFDGVIVISVMEIVQGGGLSVLRTFRLMRVILKLVRLPALOROLVLMKTMNDVATF 868
 902 CMLLMFIFIFISILGMHFLGCKFASERDGTLDPRKNFDSLLWAIIVTFQILQEDMNKV 961
 869 CMLLMFIFIFISILGMHFLGCKFASERDGTLDPRKNFDSLLWAIIVTFQILQEDMNKV 928
 962 LYNMGASTSSWAALYFIATMTFGNYVLFNLVAILVEGFOAGDANKSESEPFPSVD 1021
 929 LYNMGASTSSWAALYFIATMTFGNYVLFNLVAILVEGFOAGDANKSESEPFPSVD 989
 1022 GDGRKKRLALVALGEHAELRKSLLPLIITHTAATPMHSPKSSSTGVEALGSSRTSS 1081
 989 GDGRKKRLALVALGEHAELRKSLLPLIITHTAATPMHSPKSSSTGVEALGSSRTSS 1048
 1082 SGSAEPGAAHEMKCPSPASRSPHS PWSAASWTSRSTRSSNSLGRAPSLKRSPSGRRS 1141
 1049 SGSAEPGAAHEMKCPSPASRSPHS PWSAASWTSRSTRSSNSLGRAPSLKRSPSGRRS 1107
 1142 LLSGEGQESQDEESSEEDRASPAGSDHHRGSLERAKSFDPLDPLVPLGHRHTASGR 1201
 1108 LLSGEGQESQDEESSEEDRASPAGSDHHRGSLERAKSFDPLDPLVPLGHRHTASGR 1167
 1202 SSASEHQCNGKSGASGLARLRTDDPOLGDDDDNDGNTSKGBRIQAWVRSLPACRE 1261
 1168 GSASEHQCNGKSGASGLARLRTDDPOLGDDDDNDGNTSKGBRIQAWVRSLPACRE 1227
 1262 RDSNSAVIFPQSRFRLLCHRIITHKMFDPHVVLVIIIFLNCITTIAMERPKIDPHSAERIFL 1321
 1228 RDSNSAVIFPQSRFRLLCHRIITHKMFDPHVVLVIIIFLNCITTIAMERPKIDPHSAERIFL 1287

1828 PIYFVSFVLTAQFVLVNVVIAVLAKMHLSEESKEAEELEAELEMKTILSPQHSPLG 1887
 1830 PIYFVSFVLTAQFVLVNVVIAVLAKMHLSEESKEAEELEAELEMKTILSPQHSPLG 1889
 1888 SPFLWPGVGVNSDTPKPGAPHTTAHGAASGFSLEHPTVPHPEEVVPLGPDLLTVR 1947
 1890 SPFLWPGVGVNSDTPKPGAPHTTAHGAASGFSLEHPTVPHPEEVVPLGPDLLTVR 1949
 1948 KSGVSRTHSLPNDVYMCNRNGSTAESRGLHGRWGLPKAQSGLTSLVHSQFADTSCILQPK 2007
 1950 KSGVSRTHSLPNDVYMCNRNGSTAESRGLHGRWGLPKAQSGLTSLVHSQFADTSCILQPK 2009
 2008 DVHYLLQPHGAPTGAIPKLPPLPPGRSPLAQRPLRQAARTDLSLVQGLGSRDILLSEVS 2067
 2010 DVHYLLQPHGAPTGAIPKLPPLPPGRSPLAQRPLRQAARTDLSLVQGLGSRDILLSEVS 2069
 2068 GPSCPLTRSSSSFWGSSIOVQORSIGIOSKVSXHIRLAPCPGLEFSWAKDPPETRSSL 2127
 2070 GPSCPLTRSSSSFWGSSIOVQORSIGIOSKVSXHIRLAPCPGLEFSWAKDPPETRSSL 2129
 2128 DTELWISGDLPLSPSOEELPRDLKCKYSVETQSCRRRPGFWMDEQRHRSIAVSCLDG 2187
 2130 DTELWISGDLPLSPSOEELPRDLKCKYSVETQSCRRRPGFWMDEQRHRSIAVSCLDG 2189
 2188 SQFRLCPSPSSILGGQPLGGGSRPKKLLGPPSISIDPPESQSRPPCSPGCLRRAPAS 2247
 2190 SQFRLCPSPSSILGGQPLGGGSRPKKLLGPPSISIDPPESQSRPPCSPGCLRRAPAS 2249
 2248 DSKDPSVSPFLDSTAASBPXKDTLSLGLSDPTDMDP 2286
 2250 DSKDPSVSPFLDSTAASBPXKDTLSLGLSDPTDMDP 2288

RESULT 3
 US-10-408-765A-625
 ; Sequence 625, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Baby, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 ; FILE REFERENCE: 660088.465
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 625
 ; LENGTH: 2243
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-625

Query Match 89.8%; Score 10806.5; DB 16; Length 2243;
 Best Local Similarity 93.3%; Pred. No. 0;
 Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;

62 GAAGAGSTEKDPGSADEAGLPPALAPVVFYLSQDSRSPRCLRTVCNPFWRYSML 121
 30 GRPFGSAEKDPGSADEAGLPPALAPVVFYLSQDSRSPRCLRTVCNPFWRYSML 89
 122 VILLNCVTILGMRPCEDTACDSQRCRIIQAEDDIFAEFVEMVVMVALGIFGKCKYL 181
 90 VILLNCVTILGMRPCEDTACDSQRCRIIQAEDDIFAEFVEMVVMVALGIFGKCKYL 149
 182 DTNRDLFFIVIAQMLEYSLDLQNVFSVAVTVLRLPRAINRVPMSRIILVTLTLP 241

QY	422	CLVVIATQFSETKQRESQOLMEQVRVFLSNASTLASPSEPGSCYBELLKYLVIYLRKAAR	481	QY	1479	NFDNLGQALMSLFVLAASKOGWVDIMYDGLDAVGVDQOQIMHNPWMLLYFISFLLIVAFF	1538
Db	390	CLVVIATQFSETKQRESQOLMEQVRVFLSNASTLASPSEPGSCYBELLKYLVIYLRKAAR	449	Db	1468	NFDNLGQALMSLFVLAASKOGWVDIMYDGLDAVGVDQOQIMHNPWMLLYFISFLLIVAFF	1527
QY	482	RLAQSRAIGVRAGLLSVPARSQOEPOPSGSCPSHRRRLSVHLLVHHHHHHHHHVLGN	541	QY	1539	VLANFVGUVVENFHKCRHQHQBEEBARRRERKRLEKRR-----SKEKQWAE	1587
Db	450	RLAQSRAAGVRVGLLSPALFGGOETQPSSCSRSHRRLSVHLLVHHHHHHHHHVLGN	509	Db	1528	VLANFVGUVVENFHKCRHQHQBEEBARRRERKRLEKRRNLMLDDVIASSGSSASAASE	1587
QY	542	GTLRVRASPEIQDRDANGSRRLMLPPPTSTTPSGGPPRGAESVHSFYHADCHLEPVRCQ	601	QY	1588	AOCKPYSDYGRFRLLVHHLCTSHVLDLFTIGVIGLVVVTWAMEHYQOQIILDEALKICN	1647
Db	510	GTLRVRASPEIQDRDANGSRRLMLPPPTPALSGAPPGGAESVHSFYHADCHLEPVRCQ	569	Db	1588	AOCKPYSDYGRFRLLVHHLCTSHVLDLFTIGVIGLVVVTWAMEHYQOQIILDEALKICN	1647
QY	602	APPPRCPSEASGRTVGSQVYTVTTSPPPEILKOKALVEVAPSPPTLTSFNTPGPF	661	QY	1648	YIFTVIFVFEVSEVKLVAFAPRRFQODRWNLQDLAIIVLSIMGITLEEIVNLSIPINPTI	1707
Db	570	APPPRCPSEASGRTVGSQVYTVTTSPPPEILKOKALVEVAPSPPTLTSFNTPGPF	629	Db	1648	YIFTVIFVFEVSEVKLVAFAPRRFQODRWNLQDLAIIVLSIMGITLEEIVNLSIPINPTI	1707
QY	662	SSMHKLLTOSTGACHSSCKISSPCSKADSGACGPDSCPCYCARAGAGEVELADREMPDSD	721	QY	1708	IRIMEVIRIARVILKLMKAVGNRLLHTVMQALPOVGNLGLLFLMLFFIFAALGVLEFGD	1767
Db	630	SSMHKLLTOSTGACHSSCKISSPCSKADSGACGPDSCPCYCARAGAGEVELADREMPDSD	689	Db	1708	IRIMEVIRIARVILKLMKAVGNRLLHTVMQALPOVGNLGLLFLMLFFIFAALGVLEFGD	1767
QY	722	SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSPSVLAFWRLICDTFRKI VDSKYFGRG	781	QY	1768	LECDETHPCCEGLGRHATFRNFGMAFLTIFRVSTGDNWNGIMKDPDRDQDQESTCYNTVIS	1827
Db	690	SEAVYEFTQDAQHSDLRDPHS--RRQSLGPDAPSPSVLAFWRLICDTFRKI VDSKYFGRG	748	Db	1768	LECDETHPCCEGLGRHATFRNFGMAFLTIFRVSTGDNWNGIMKDPDRDQDQESTCYNTVIS	1827
QY	782	IMAILVNTLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN	841	QY	1828	PIYFVSFVLTAQFVLVNVVIAVIMKHEESKEAEAELEAELEMKTLSPQSPHPLG	1887
Db	749	IMAILVNTLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN	808	Db	1828	PIYFVSFVLTAQFVLVNVVIAVIMKHEESKEAEAELEAELEMKTLSPQSPHPLG	1887
QY	842	IFDGVTVLISVMEIVGQGGGLSVLRTFRLMRVILKLVRLPALQRLQVLMKTMNDVATF	901	QY	1888	SPFLMPGVEGVNSTQSPKGPAPHTTAHGAAGFSLEHPT-----	1927
Db	809	IFDGVTVLISVMEIVGQGGGLSVLRTFRLMRVILKLVRLPALQRLQVLMKTMNDVATF	868	Db	1888	SPFLMPGVEGVNSTQSPKGPAPHTTAHGAAGFSLEHPT-----	1927
QY	902	CMLLMFLIFISILGMHLFGCKFASBRDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV	961	QY	1948	KLMDLALAGPGQSPAPPSAPSLGGSDPQIPLAEMEALSLTSEIVSRPSCSLATDDSLDP	2007
Db	869	CMLLMFLIFISILGMHLFGCKFASBRDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV	928	QY	1928	-----MYPHPEEVVPVIGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSL	1974
QY	962	LYNGMASTSSWAALYFIALTFTGNYVLFNLLVAILVEGQAE-----	1003	Db	2008	DMHTLLLSALESNMOPHTTLP---GPDLLTVRKSGVSRTHSLFNDSYMCRNGSTAERSL	2064
Db	929	LYNGMASTSSWAALYFIALTFTGNYVLFNLLVAILVEGQAEISKREDAAGQOLSCIQLP	988	QY	1975	GHGWLCPKAQSGSILSVHSQPADTSCILQLPKDVHLYLQPHGAPTGAIPKLPPEGRSP	2034
QY	1004	-----GDATKSEBPDPFSPVSDGDRKKRLALVALGEHAELKSLPLLIHTAATPM	1058	Db	2065	GHGWLCPKAQSGSILSVHSQPADTSCILQLPKDVHLYLQPHGAPTGAIPKLPPEGRSP	2124
Db	989	VDSQGGDANKSEBPDPFSPVSDGDRKKRLALVALGEHAELKSLPLLIHTAATPM	1048	QY	2035	LAQPLRRQAAIRTDLDVQGLSREDLLSEVSGPCPLTRSSSFVGGSSIQVOQSRGQ	2094
QY	1059	SHPKSSSTGVGEALGSGSRSTSSGSAEPGAAHEMKCPARSASSHSPWSAASSWTSRR	1118	Db	2125	LAQPLRRQAAIRTDLDVQGLSREDLLSEVSGPCPLTRSSSFVGGSSIQVOQSRGQ	2184
Db	1049	SHPKSSSTGVGEALGSGSRSTSSGSAEPGAAHEMKCPARSASSHSPWSAASSWTSRR	1107	QY	2095	SKVSKHIRLPAPCPGLEPSWAKDPPTSRSLDLELDTLSWISGDL--PSSQEEPLFPRDLK	2153
QY	1119	SSRNSLGRAPSLKRSPSGERRSLSCGQESODEESSSEEDRASPGSDHRRHGSLERE	1178	Db	2185	SKISKHMTPPAPCPGPEPNWKGPPBTRSLDLELDTLSWISGDL--PSSQEEPLFPRDLK	2244
Db	1108	SSRNSLGRAPSLKRSPSGERRSLSCGQESODEESSSEEDRASPGSDHRRHGSLERE	1167	QY	2154	KCVSVETQSCRRRPGFWLDEQRHRSIAVSCLDGSGQPRLCPSFSSGLGQPLGPGSRPKK	2213
QY	1179	AKSSEFLDPTLQVPLHRTASGRSSASEHQDCNGKSASGRILARTLRTDDPQLDGDNDDE	1238	Db	2245	KCVSVETQSCRRRPGFWLDEQRHRSIAVSCLDGSGQPRLCPSFSSGLGQPLGPGSRPKK	2304
Db	1168	AKSSEFLDPTLQVPLHRTASGRSSASEHQDCNGKSASGRILARTLRTDDPQLDGDNDDE	1227	QY	2214	KLSPPSISIDPPPSQSGSRPPCSPGVCLRRRAPASDSDKDPVSSPLDSTAASPSKKTLS	2273
QY	1239	GNLSKGERIQAWVSRLPACCRERDSWASYIPPPQSRFLLICHRILTHKPFDPVVLVILF	1298	Db	2305	KLSPPSITIDPPPSQSGSRPPCSPGVCLRRRAPASDSDKDPVSSPLDSTAASPSKKTLS	2364
Db	1228	GNLSKGERVRAWIRARLPACCLERDSWASYIPPPQSRFLLICHRILTHKPFDPVVLVILF	1287	QY	2274	LSGLSSDPTDMDP	2286
QY	1299	LNCTIAMERKPIDPHSAERFLTLSNVIPTAVFLAEMTVKVALGCMFCGEOALYLRSSWN	1358	Db	2365	LSGLSSDPTADLDP	2377
Db	1288	LNCTIAMERKPIDPHSAERFLTLSNVIPTAVFLAEMTVKVALGCMFCGEOALYLRSSWN	1347				
QY	1359	VLDGLLVLSVIDILVMSVDSGTILGMLRVLRLRLTLRLRVLRSQAQGLKLVVETILMS	1418				
Db	1348	VLDGLLVLSVIDILVMSVDSGTILGMLRVLRLRLTLRLRVLRSQAQGLKLVVETILMS	1407				
QY	1419	SLKPIGNIVTCCAFFIIFGILGVOLFQKGFVCOGEDTRNITNKSQCAEASVWRHXY	1478				
Db	1408	SLKPIGNIVTCCAFFIIFGILGVOLFQKGFVCOGEDTRNITNKSQCAEASVWRHXY	1467				

RESULT 5
US-10-408-765A-1128
; Sequence 1128, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing

APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1128
LENGTH: 2353
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-1128

Query Match 51.7%; Score 6222; DB 16; Length 2353;
Best Local Similarity 56.7%; Pred. No. 0;
Matches 1370; Conservative 208; Mismatches 529; Indels 310; Gaps 62;

QY 25 PPGLPARGWTRRRMERAPRRDSP--VASRSSTTCPPGGAAGAGSTEKOPGSAADSEAG 82
Db 19 PGPAAALVG-----ASPESPGAGREARCSSELGVSPSPSPAARGAELGA--DEQR 69

QY 83 LPYPALAPVVFYLSQSRPSKWLRTVCNPFVRSMLVILLNCVTLGMFRPCEDIACD 142
Db 70 VPYPALAAATVFCGLQTTRPSRCLRLVCNPFVRSMLVILLNCVTLGMFRPCEDIACD 129

QY 143 SORCRILQAFDDIFAPFAVAVMVKWALGFGKCYLGDWNRDLDFIVIAAGMLEYSLD 202
Db 130 SERCNILEAFDAIFAPFAVAVMVKWALGFGKCYLGDWNRDLDFIVIAAGMLEYSLD 189

QY 203 LQNYFSAVTRVRLPLRALNRPVSMRILVTLTLDLPLMGNVLLLCFFVFFIFGIVG 262
Db 190 GHNVSLSAIRTVRLPLRALNRPVSMRILVTLTLDLPLMGNVLLLCFFVFFIFGIVG 249

QY 263 QMWAGLLNRCFLPENSLPUSVD-LBPYYTENEDESPPICSPQRENGMRSCRSVPTLR 321
Db 250 QMWAGLLNRCFLDPAFVRRNNLTFLRPYYQTEEGEENPFICSSRRDNGMKCSHIP--- 306

QY 322 GEGGGPPCSLDYETYN-----SSNTTCVMNNOYVYTCSCGEHPNPFKGAINFNIGY 374
Db 307 GRELRMPCTLGMAYTQPOAGVGGAARNACINNQQYVYVYTCSCGEHPNPFKGAINFNIGY 366

QY 375 AWIAIFQVITLEGWVDIMYFMDAHSFYNYFIYFILLIIVGSFMINCLVVIATQFSETK 434
Db 367 AWIAIFQVITLEGWVDIMYFMDAHSFYNYFIYFILLIIVGSFMINCLVVIATQFSETK 426

QY 435 QRSQMLREORVPLSNASTLASFSEPGSCYEELLLKYLVLILKAARRLAQVRAIGVRA 494
Db 427 QRSQMLREORVPLSNASTLASFSEPGSCYEELLLKYLVLILKAARRLAQVRAIGVRA 486

QY 495 GLLSSPVARQGPQPSGSCSTRSHR-----LSVHHIV-HHHHHHHHHYHNGTLRV 546
Db 487 RKVVDPSAVGQGP-----GHRQRRAGRHATASVHHHHHHHHHHYHSHGSPRR 538

QY 547 PRASPEIQDRDANGSRRLML--PPPTPTPSGPPRGAESVHGFIHADCHLE--PVRQA 602
Db 539 PGPEPGACD-----TRLVRAGAPPSPSPGRGP--DAESVHSIYHADCHIEGQERARV 591

QY 603 PPRCPSEASGR-TVCSGKV-YPTV-----HTSPPEILKOKALIVEAPSP--- 646
Db 592 AHAATAAASLRATGLGTNYPTILPSGVSGKGSSTPGPK-----GKAGGPPGTG 644

QY 647 --GPPTLTSPNIPPGPSSMKHLEQTQAC--HSS-----KISPSKADSGACGPD 697
Db 645 GHGFLSLS-----PDYEKIPHVHGHGLGQAPGHLGSLVPCPLPSP--PAGTLTCELK 698

QY 698 SCPYCART-GAGEPESADHVMPDSSEAVVEFTQDAQHSIDLDP----- 740
Db 699 SCPYCTRALEDPEGLSGESGSDGRGYVEFTQDVVRHGRWDPTPRPRATDTPGPGPS 758

QY 741 HSRORSLGPDAPESPSSVLAFWRLLICDTRKIVDSKYFQFGIMAILVNTLSMGIEYHEQ 800
Db 759 PORRAQORAP-GEPOWGRMLWTFSGKLERIVDSKYFSGRGMMAILVNTLSMGIEYHEQ 817

QY 801 PEELTNALEISNIVFTSLFALEMLKLIVYGPFGYIKPNYPNIPDGVIIVISVWEIVGQOG 860
Db 818 PEELTNALEISNIVFTSMFALEMLKLIVYGPFGYIKPNYPNIPDGVIIVISVWEIVGQAD 877

QY 861 GGLSVLRTRFRLMRVLKVRFLPALQOLQVLMKTMNDVATFCMLLMFLFIFISILGMHLF 920
Db 878 GGLSVLRTRFRLMRVLKVRFLPALQOLQVLMKTMNDVATFCMLLMFLFIFISILGMHLF 937

QY 921 GCKPASERD-GDTPDRKNFOSLLWAIIVTVFOILLTOEDWNVKLVYNGMASTSWAALYFIA 979
Db 938 GCKFSLKTDGTGTVDRKNFOSLLWAIIVTVFOILLTOEDWNVKLVYNGMASTSWAALYFVA 997

QY 980 LMTFGNYLVNLLVAILVEGFOAEGDATKSESEDPFFSPSDVDGDRKKRLALVAL---- 1035
Db 998 LMTFGNYLVNLLVAILVEGFOAEGDANRSDDEKTSVHFEEDFKURELQTTTELKMS 1057

QY 1036 -----GEHAELKRSLLPPLIITHAATPMHPKSSS-TGVGEALGSGSRRTSSSGSAEPGA 1089
Db 1058 LAVTPNGHLEGSGSLSPPLIMCTAATPMPTPKSSPFLDAFSLPSRSGSSSGDPPUG- 1116

QY 1090 AHHEMKCPSPARSPPSPKSAASWTSRRSRNSLGRAPSLKRRSPGSRSLLSGEGOE 1149
Db 1117 --DOKPPASURSPCAPWPGSGAWSSRRSSWSLGRAPSLKRRSGQCCGERESLLSGEGK 1173

QY 1150 SQDEEESSEEDRASP--GSDHRHRSGLEREAKSSFDLPDLT-----OVPLH---R 1196
Db 1174 STDDE--AEDGRAAPGPATPLRAESLDPRPLPAALPTTKCRDRDQGVVALPSDFFLR 1231

QY 1197 TASGRSASHEQDCNGKSASGLARTLTDDPQLDGDNDDEGNLSKGERIQAWVRSLP 1256
Db 1232 IDSHREDAAELEDDSDSCCLRLHKVLEPYKQ-----W----- 1265

QY 1257 ACCRERDSWAIYPPQSRRLCHRIITHKMFHVVIVIFLNCITIAMERPKIDPHSA 1316
Db 1266 --CNSRRAWALYLFSPQNRFRVSCQKVIHMKMFHVVIVIFLNCITIALERPIDPGST 1323

QY 1317 ERIFLTLSNIFTAVFLAETVKKVALGWCFGEOAYLRSSNNVLDGLLVLISVDILVSM 1376
Db 1324 ERYFLSVSNYIFTAIFVAMVMKVVALGSLSGEHAYLQSSNNLDDGLLVLISVDIVVAM 1383

QY 1377 VDSGTKILGMLRVLRLLRPLRPLRISRAQGLKLVVETLMSSLPKIGNIWIICAFPII 1436
Db 1384 ASAGGAKILGVLRLRLRLPLRPLRISRAQGLKLVVETLMSSLPKIGNIWIICAFPII 1443

QY 1437 FGLGVQLFKGKFFVCOGEDTRNITNKSDCABASYRWRHXYKYNFDNLGQALMSLFLVASK 1496
Db 1444 FGLGVQLFKGKFFVCEGPDTRNISTKAQCRAAHYRWVRKYKYNFDNLGQALMSLFLVSSK 1503

QY 1497 DGWVDIMYDGLDVGVDQOPIMNHNPMMLYFTISLIIIVAFVFLNMVFGVVVVENHCKRO 1556
Db 1504 DGWVIMYDGLDVGVDQOPVQNNHNMMLYFTISLIIIVSFFVLNMVFGVVVVENHCKRO 1563

QY 1557 HQEEERARRERKRLRLRKKRSKSKQMAEACKPYSDYSRFLLVHHLCTSHYLDLF 1616
Db 1564 HQEAEERARRERKRLRLRERRRRSTPPS-PEAQRRPYADYSPTRSIHSLSCTSHYLDLF 1622

QY 1617 ITGVIGLVNVTWAMEHVQOQILDEALKICNYIFTVIFVFSVFKLVAFARFRFFODRN 1676
Db 1623 ITFICNVNITMSMEHYNQKSLDEALKICNYVFTIVFVEAALKLVAFGRFRFFKDRWN 1682

QY 1677 QLDLAIVLLSIMGITLLEIEVENLSLPINPTIIRIMRVLRIRARVLKLLKXAVGNALLHTV 1736
Db 1683 QLDLAIVLLSIMGITLLEIEEMSAALPINDTIIRIMRVLRIRARVLKLLKXAVGNALLHTV 1742

QY 1737 MQALPQVGNLGLLFFMLFFIFAALGVFLGDECEDETHPCGEGRHATFRNFMATFLTF 1796
Db 1743 VOALPQVGNLGLLFFMLFFIYAALGVFLGDECEDETHPCGEGRHATFRNFMATFLTF 1802

QY 1797 RVSTGDNWNGIMKDSRDC---DQESTCVNTVISPIYFVSVFLTAQFVLVNVVIAVLMKH 1853

Db 1803 RVSTGDNWNGTMRKDTLRCSREDEKCHLSYLPALGPVFTVFLVQAQFVLVNVVAVLWKH 1862
Qy 1854 LEENKKAKEAEAELELEBMKTLSPQPHGLSPFLWPVGVEVNSTDSKPKGAPHTTA 1913
Db 1863 LEENKKAEDAELELEMA-----QPGSARRVDADRP-----1899
Qy 1914 HIGASGFLBHTMPVHPPEEVPVPLGPDLLTVRKSGVSRTHSPNDSYMCNGSTA---1970
Db 1900-----PLQSPSGARDAPNLVARKVSVSRMLSLPNDSSYMFPRVVPASAP 1943
Qy 1971-----ERSLHRGWGLPKAQSGLSVHSQADTSCILQPKDVH-----YLLQP 2015
Db 1944 HPRPLQEVEMETYGATP---LGSVASVHSPPAESCASLIQIPLAVSSPARGEPHALSP 2000
Qy 2016 HGAPTWGAIPKLPPGRSPLAQRRLRQAAIRTDLSLDVQGLSREDLLSEV-----SGPSC 2071
Db 2001 RGT-----ARSPSLRLLCRQEAHVHTDSLEGK-IDSPRTLDPAAPGKEKTPVR 2047
Qy 2072 PLTRSSSPWGGSSIQVQSRGTSQKV--SKH-----IRLPAPCGLEBPSWAKDPPEIRS 2123
Db 2048 PVTQ-----GSLQSPPRSPRPASVTRKHTFGQHCVSRRPAAPGGEAEASDP-----2096
Qy 2124 SLELOTELSWISGDLLP--SSQEPLEP-----RDLKKCVSVTQSCRRRPGFWLDE 2173
Db 2097---ADEEVSHITSSACFWOFTAEHPGPEASPVAGGERDURRLYSVDAQFLKPG-RADE 2152
Qy 2174 QRRHSIAVSCLSGSGQRLCPSPSSLGQPLGSP--GSRPKKLSPPSISIDPP--ESQGS 2230
Db 2153 QWRPSAE---LGSGE-----PGEAKAWG-PEAEFALGARRKKCMSPPCISVSPPEADEGS 2203
Qy 2231--RPPCSFG--VCLRRRAPA-----SDSKDPSVSPDLSTAAS-----PSPKKTLSL 2274
Db 2204 ARPSAAEGSGTTLRRRTPSCEATPHRDSLEPTGSGAGGDPAAKGERWGOASCRAEHLTV 2263
Qy 2275 SGLSSDPTDM-----DP 2286
Db 2264 PSFAFEPLDGVPSGDP 2280

RESULT 6

US-09-935-541-2
; Sequence 2, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: McGivern, Joseph G.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-2

Query Match 45.0%; Score 5409; DB 9; Length 2175;
Best Local Similarity 50.5%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 513; Indels 450; Gaps 64;

Qy 51 ASRSTTCPGGAGAGSTEDPG--SADSEAGL-----PYPALAPVVFYIS 97
Db 5 ASPSSSAAAP-AAPGGVTTTQPGRSPSPSPGEEPLDGDANPHVPHDLPAPFAFFCLR 63
Qy 98 QDSRPSRCLRTVCNPFWRVSMVLVILNCVTLGMFRPCEDIACQSRCLIQAFDDIF 157
Db 64 QTTSPRNWCIRKVCNPFWECSVMLVILNCVTLGMVQPCDDMDCLSDRCKILQVDFDIF 123

Qy 158 AFFAVEMVVKWALGIFGKKCYLGDWTNRDLFFIIVIAMLEYSLDLQNVSPSAVTRVRL 217
Db 124 IFFANEMVLKMWALGIFGKKCYLGDWTNRDLFFIIVIAMWEYSLDLQNLINLSAIRTVRL 183
Qy 218 RPLRAINRVPMSRILVTLTDLTMLGNVLLCFVFIPIGVGVQWAGLLRNRCPLPE 277
Db 184 RPLKAINRVPMSRILVTLTDLTMLGNVLLCFVFIPIGVGVQWAGLLRNRCFLPE 243
Qy 278 NFSIPLSVDLPEPYQTENEDESPTCSQPRENGMRSCRSVPTLRGEGGGGPPCSL-----332
Db 244 NFIQGDVALPYPYQPEEDEMPPFLCSLSDGNGIMGCHIEIPLKEQ---GRECCLSKDDV 300
Qy 333--DYETYNSSNTT--CVNWNQYTNCSAGEHNPFGKAINFONIGYAWTAIFOVITLEGW 389
Db 301 YDFGAGRODLNASGLCVNWNRYNVRTGTSANPHKGAINFONIGYAWTIVIFQVITLEGW 360
Qy 390 DIMYFVMDAHSFYNIYIFILLIIVGFSFMINLCVVIATQFSETKQESQMLREORVFL 449
Db 361 EIMYFVMDAHSFYNIYIFILLIIVGFSFMINLCVVIATQFSETKQERHRLMLRQRYL 420
Qy 450 SNASTLASFSBPGSCVEELLKYLVIILKAARLAQVSRRAIGVRAGLLSSPVARSQEPQ 509
Db 421 S-SSTVASAEBCDCYEHLFQVYVCHLRKAKR-----RALGLYQALQS-----462
Qy 510 PSQSCSTRSHRRLSVHLVHHHHHHHHYHGLNGTLRVPRASPEIQDRDANGSRRLMLPPP 569
Db 463-----RRQAL-----GPE-----APAP 474
Qy 570 SPTPTSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVSGKVVTVHTSP 629
Db 475 AKPGP-----HAK---EPRHYQLCPOHSELD-----THT--502
Qy 630 PREILLKDALVAVAPSGPPTLTSTFNIPPGPFSSMHKLETTQSTGAC-HSSCKISPCSK 688
Db 503-----LVQ-----PIPATLAS-----DPASCPCQCHEDGRPPSLG 534
Qy 689 ADGACGPDSCPYCARTGAGEPESADHVPDSDSEAVYEFTQDAQHSLDHPHRRRQRS 748
Db 535 TDSGQEGSGS---GSSAGGEDEA---DGDGA---RSSEDCASSELGKEEBEEQ--579
Qy 749 LGPDAPSSVLA--FWELICDTRKIVDSKYFGRGIMAILVNTLSMGIEHYHQPELTN 806
Db 580---ADGAVMLCGDVWRETRAKLURGIKDFYFRGIMAILVNTVSMGIEHYHQPELTN 635
Qy 807 ALSEINIVTSLFALEMLKLLVYGPFGYIKPNYINFDGVIVVISVWEIVGQGGGLSVL 866
Db 636 ILBICNVVFTSMFALEMLKLAAGFLDYLRNFYINFDISIIVISWEIVGQADGGLSVL 695
Qy 867 RTERLMRVLKVRFLPALQOLVLMKTMONVATFCMLLMFLIFISILGMHFGCKPAS 926
Db 696 RTERLLRVLKVRFLPALRQLVLMKTMONVATFCMLLMFLIFISILGMHFGCKPSL 755
Qy 927 ERD-GDTLPDRKNFDSLIIWAVTVFOILLTOEDKWKVLYNGMASTSSWAALYFIALMTFGN 985
Db 756 RTDGTDTVPDRKNFDSLIIWAVTVFOILLTOEDKWKVLYNGMASTSPWASLYFVALMTFGN 815
Qy 986 YVLFNLMLVAILVEGFOAGDANKSEDPDFPSV-----DGDGRKKLALVAL 1035
Db 816 YVLFNLMLVAILVEGFOAGDANKSYSDQSSNIIEBFDKLQGLDSSGDPK--LCRIPM 873
Qy 1036 GEHAELRKSLLPLLIHT---AATPMHSPKSSSTGVGEALGSGSRRTSSSGSAEPGAH 1091
Db 874 TPNGHLOPSL--PLGHLGPAGAAGPA--PRLSLQPDPMVALGSRKSSVMSL---GRMS 926
Qy 1092 HEMKCPSPASPHSPWASASTSRRSSRSLGRAPSLKRRSPSGRRSLLSGE-QGES 1150
Db 927 YDQSLSSSSSSSYGPMGRSAWASRSSWN-----SLKHKPSAEHSLISAERGGA 980
Qy 1151 QDEBESSEE--DRASPAGSDH-----RHRGSLEREAKSFPDPTQLVPG 1193
Db 981 RVCEVADEGPPRAAPLHTPHAHHTHHGPHLAHRRHRRRTLSLDNRDSVDLAEIAPVG 1040

1941 PDLTVKRGVGRTHSLPN--DSYMCNRNGSTAESRSLCHRWGLPKAQSGSILSVHSQPADT 1999 QY
1869 ECFPLSLSTAVS-----PDPEFLCEMBEIPFNFV--RSW--LKHDSQAAPPSPSPDAS 1919 Db
2000 SCILQPKDVHY-----LLPHGAPTWGAIPKLPPLPG-----RSPLAQRLRQAAIRT 2048 QY
1920 SPLPMPAEFFHPAVASQKPEKGTGTTPKIALQGSWASLRSFVNCVTLRLQATGSD 1979 Db
2049 DSLDVOGLGSRREDLLSEVSGFSCPLTRSSSSFWGSSIQVOQRSGIQSKVSKHRLPAPCP 2108 QY
1980 TSLDAS-----PSSAGSLQTTLEDLSLTSDFRRLGPPAPAP 2018 Db
2109 GLEPSWAKDPBETRSLDLTSLSWISGDLPLSSQEEPLFPRDLKCKYSVETQSCRRRPG 2168 QY
2019 G-----FRAGLSPAARRL-----SURGRL 2039 Db
2169 FWLDRQRHSIAVSCLDSSQPRLCFSPSSL-----GQPLGGQSGSRPKKLSPPSI 2220 QY
2040 FSLRGLRAHQHSHS--SGSTSPGCTHDSMDPSDEBGRGGAGGAGSEHSETLSLSL 2097 Db
2221 S----IDPPESQSRPPCSPGVCLRR-----RAP---ASDOK 2250 QY
2098 TSLFCPPP-----PPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAADRSK 2151 Db
2251 DPSVSPDLSTAAASPKKDTLSLSGLSSDPTMDP 2286 QY
2152 DPPGRAPLPMGLPAPPQPPL-----PGELEP 2179 Db

RESULT 9
US-10-425-800-4
; Sequence 4, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-425-800-4

Query Match 44.9%; Score 5405.5; DB 14; Length 2188;
Best Local Similarity 50.3%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;

51 ASRSTTCTPGGAAGAGSTEKDPG--SADSEAGL-----PYPALAPVVEFYLS 97 QY
5 ASPSSSAAAP-AAEPGVTTTQPGSPSPSPGEEPLDGADPHVHPDLAPAFCLR 63 Db
98 QDSFPRSWCLRTVCNPFERYSMVLILNCVTLGNFRCEDIACDSORCIIQAFDDIF 157 QY
64 QTTSPRNCICIKWNCNPFECVSMVLILNCVTLGNFYQCDMDCLSDRCKILQVDDIF 123 Db
158 AFFAVEMVVMVALGIFKKCYLGDWTNRDLFFIVIAQMLEYSLDLQNVFSARTVYL 217 QY
124 IFFAMEVLMKVALGIFKKCYLGDWTNRDLFFIVMAGNVEYSLDLQINLSAIRTVL 183 Db
218 RPLRAINVPMSRIILVTLITLPMLGVLILCFEVEFFIVGVQVLWAGLLRNCFLPE 277 QY
184 RPLKAINVPMSRIILVTLITLPMLGVLILCFEVEFFIVGVQVLWAGLLRNCFLPE 243 Db
278 NPSLPLSLDLEPYOTENEDESPFICSPQRENMGMSRCSVPTLRGEGGPPCSL----- 332 QY

244 NFTIQGVVALPPYQPBEDDEMPPICSLSGDNGIMGCHIEIPPLKEQ---GRECCLSKDDV 300 Db
333 -DYETYNSSNTT--CVNNWQYITNCAGAHNPFGKAINFNINIGYAMIAIPOVITLEGWV 389 QY
301 YDFGAGQDLNASGLCVNNWRYNVCRTGSANPKGAINFNINIGYAMIVIFQVITLEGWV 360 Db
390 DIMYFVMDAHSFYNYFIYFILLIIVGSPFMINLCLVITATQFSETKQESQIMRQVRFL 449 QY
361 EIMYVMDAHSFYNYFIYFILLIIVGSPFMINLCLVITATQFSETKQESQIMRQVRFL 420 Db
450 SNASTLASFSFGSCYBELLYVILKKAARRLAQVSRALGVRAGLLSSSPVARSGOBPO 509 QY
421 S-SSTVASYPGDCYEEIFQVCHILKAKR-----RALGLYQALQS----- 462 Db
510 PSGCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIODRANGSRRLMLPPP 569 QY
463 -----RQAL-----GPE-----AFAP 474 Db
570 STPTSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSSEASGRTVSGKVYPTVHTSP 629 QY
475 AKPGP-----HAK-----EPHYQLCPQHSPLDA-----TPHT-- 502 Db
630 PPEILKDKALVEVAPSPGPTLTSTFNIPGPPSSMHKLETTQSTGAC--HSSCKISPCSK 688 QY
503 -----LVO-----PIPALAS-----DPASCPCCQEDGRRPSGLGS 534 Db
689 ADSGAGCPDSCPYCARTGAGEPEESADHVMPSDSBAVEFTQDAQHSIDLDPHSRRQRS 748 QY
535 TDSGQEGSGS-----GSSAGGEDEA-----DGDGA---RSSEGDGASSELGEEEEQ-- 579 Db
749 LGPDABPSSVLA--FWRLICDTFRKIVDSKYFGRGIMIALVNTLSMGLEYHQPBELTN 806 QY
580 -----ADGAVMLCGDVWRETRAKLIGIVDSKYFNRGIMAILVNTVSGHIEHQPBELTN 635 Db
807 ALEISNIVETSLFALEMLKLLVYGPFGYKXPNYIFDGVIVVVISVWEIVGQCGGLSVL 866 QY
636 ILIEICNVFTSMFALEMLKLLAFGLFDYLRPNYIFDSIIVISLWELVQADGGLSVL 695 Db
867 RIFRLMRVLKLVFLPALQRLVLMKTMNDNVATFCMLLMFLFIFISILGMHFGCKEAS 926 QY
696 RIFRLMRVLKLVFLPALQRLVLMKTMNDNVATFCMLLMFLFIFISILGMHFGCKEAS 755 Db
927 ERD-GDTLPRKNFDSILWAIIVTVFQILLTQEDMKNVLYNGMASTSSWAALYFIATMTFGN 985 QY
756 RTDTGDTVPDRKNFDSILWAIIVTVFQILLTQEDMKNVLYNGMASTSSWAALYFIATMTFGN 815 Db
986 YVLNLLVAILVEGFOAEGDATKSESEDPFSPV-----DGDGDRKRLALVAL 1035 QY
816 YVLNLLVAILVEGFOAEGDATKSESEDPFSPV-----DGDGDRKRLALVAL 873 Db
1036 GEHAELRKSLLPPLIHT-----AATPMSPKSSSTGVGEALGSGSRRTSSGSAEPGAH 1091 QY
874 TPNGLDPSL--PLGGHLGPAGAAGPA--PRLSLQDPDMLVALGSRKSSVMSL---GRMS 926 Db
1092 HEMKCPPSARSSPHSPWSAASSWTSRRSSNSLGRAPSLAKERSPSGRRSLSGE-QGES 1150 QY
927 YDQRSLSRSSSYGPGWRSAAWASRRSWN-----SLKHPPSAEHSLLSERRGGGA 980 Db
1151 QDEESSEE--DRASPAAGSDH-----RHRGSLEREAKSSEFDPTLQVPG 1193 QY
981 RVCBAADGPPRAAPLPHTPAHHIIHGHPLAHRHRRRTLSLDRDSVDLAELVPAVG 1040 Db
1194 LHRITASGRSS--ASEHQDCNGKSASGLARTLRTD-DPOLDGDNDDEGNLSKGERIQAW 1250 QY
1041 AHPAAWAAAGPAPGHEDCNGRMP--IAKDVFTKMGDRGDRGDEBEIDYTLCFRVMK 1098 Db
1251 VRSILPACCRRDSSWAVIPPOGRFRLCHRIITHKMFDFHVLVIFLNCITIAMBRPK 1310 QY
1099 IDVTKPDWCEVREDWSVYLFSPENFRVLCOTIAHKLFDVVLAFILNCITIALERPQ 1158 Db
1311 IDPHSAERIFLTLNFIYFVAVFLAEMTVKVALGMCFOEQAYLRSSMNVLGGLVLSVI 1370 QY
1159 IEAGSTERIFLTVSNYIFTAIFVGMTLKVSLGLYFGQAYLRSSMNVLGGLVLSVI 1218 Db

510 --ASDPSCHQCHAEGRPSGLGSTDSQGGSGGSAE---AEANGDGL-QSSEGDVS 563
 735 SLDLPHSRQRSLGDAEPSSVLA-----FWRLICDTFKKIVDSKYFGGIMAILVN 789
 564 SD-----LGKEERQEDGAARLCGDVRETRKLRGIVDSKYFNKIMAILVN 611
 790 TSLMGIEVHGOPELTHNALETISNIFTSLFALEMLKLLVVGPGYIKNPNYINIGDVIV 849
 612 TVSMGIEHGOPELTHNALETISNIFTSMFALEMLKLLVVGPGYIKNPNYINIGDVIV 671
 850 ISWETIVCOQGGSLVLTFRMLRVLRFLPALORQLVVLMTKMDNVATFCMLLMFI 909
 672 ISWETIVCOQGGSLVLTFRMLRVLRFLPALORQLVVLMTKMDNVATFCMLLMFI 731
 910 FIFSLGMLHFGCKFASERD-GDTLPDRNFDSLLWAVTVFQIILTQEDWNVLYNGMAS 968
 732 FIFSLGMLHFGCKFASERD-GDTLPDRNFDSLLWAVTVFQIILTQEDWNVLYNGMAS 791
 969 TSSWAALFIALMTGNVLENLVAILVEGFOAGDATKSESEPDFTSPSDG----- 1022
 792 TTPWASLYFVALMTFNGYVFLNLLVAILVEGFOAGDANRSCDEQSSNLEEDKLUPE 851
 1023 --DGRKKEALVALGEHAELKSLPLLIH--TAATPMSPKSSSTGVGALGSGRR 1078
 852 GUNDRDLKLCIPMTPNGHLDPST--PLGAHLGPAGTGTAPRLSLQDPVVALDSRK 909
 1079 TSSSGSAEPGAHEMKPCPSARSSPHSPWSAASSWTSSRNSLGRAPSLKRRSPSGE 1138
 910 SSVMSL--GRXSYDQSLSSRSSYYPGWRSMTWASRRSWN-----SLKHKPPSAE 960
 1139 RSLLSGEGQES--QDEBSSEE--DRASPAGSDH-----RURGSLEA 1179
 961 HESLLSGEGGSCVRACEAREEAPTRTAPLHAPHAAHGHPLAHRHHRHTLSLOT 1020
 1180 KSFEDLPTLQVPLGERTAS--GRSSASHEQDCNGKSASGLRLTLTD-DPOLDGDND 1236
 1021 RUSVDLGLVVPVGAHRAARWAGQAPGHEDCNGRMPN--IAKDVFTKMDRRDRGEDE 1078
 1237 DEGNLSKGERIQAWVRSLPACRRDSWASAYIFPQSRRLIICHLIITHKMFHDVVLVI 1296
 1079 EEDYTLCTFRVRKMDVYKPDWCEVEDWSVLFSPENKERILCQIIAHKJFDYVVLAF 1138
 1297 IFNCTITAMERPKIDPHSAERIFLTLSNVIPTAFLAEMTKVVALGWCFCGQAYLRSS 1356
 1139 IFNCTITAMERPKIDPHSAERIFLTLSNVIPTAFLAEMTKVVALGWCFCGQAYLRSS 1198
 1357 WNVLDGLLVLISVIDILVSMVSDSGTKILGMLRLVRLTLRLPLVLSRAGGLKLVVETL 1416
 1199 WNVLDGLVLFVSIIDIVSVASAGAKILGLVLRVLRLLRLPLVLSRAGGLKLVVETL 1258
 1417 MSSLKPIGNIVVICAPFIIPGILGVOLFPGKFPVCGEDTRNITNKSDCAEASRYVRH 1476
 1259 ISSLKPIGNIVVICAPFIIPGILGVOLFPGKFPVCGEDTRNITNKSDCAEASRYVRH 1318
 1477 KYNFDNLGOALMSLFLVASKDGDWDIMYDGLDAGVDQOQPMNPNWMLLYFISFLIIV 1536
 1319 KYNFDNLGOALMSLFLVASKDGDWDIMYDGLDAGVDQOQPMNPNWMLLYFISFLIIV 1378
 1537 FVFLNMFVGVVVENPHKCRHQEERREARRREKRLRLEKRRKMKOMAEQCKPYSD 1596
 1379 FVFLNMFVGVVVENPHKCRHQEERREARRREKRLRLEKRRKMKOMAEQCKPYSD 1431
 1597 YSRFRLLVHHLCTSHYLDLFTGVTGLNVVTWAMEHYOQOILDEALKICNYFTVIVF 1656
 1432 YCPTRLTHSMCTSHYLDLFTGVTGLNVVTWAMEHYOQOILDEALKICNYFTVIVF 1491
 1657 ESVEKLVAFAPERFQDWNQDLALVLLSIMGITLIEEIVNLSLPINPTIIRIMRVLRI 1716
 1492 EAVLKLVAFLGRFRFDRNQLDLALVLLSIMGITLIEEIVNLSLPINPTIIRIMRVLRI 1551
 1717 ARVLKLLKVAAGMRALLHTVMOALPQVGNLGLFLMFLFFIAPALGVELFGDLECDTHPC 1776
 1552 ARVLKLLKVAAGMRALLHTVMOALPQVGNLGLFLMFLFFIAPALGVELFGDLECDTHPC 1611

1777 EGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPBDC-DOESTCYNTV--ISPIYFVS 1833
 1612 EGMSEHATFRNFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDETCUSSIQFVSLPLFVS 1671
 1834 FVLTAQVFLVNVVAVLAVLMLKLEESNKAKEAEAELEEMKTLSPQPHSLGSPFLWP 1893
 1672 FVLTAQVFLVNVVAVLAVLMLKLEESNKAKEAEAELEEMKTLSPQPHSLGSPFLWP 1713
 1894 GVEGVNSTDSKPCAPHTTAHGAASGFSLSHPTWVPHPEVVP-LQPDLLTV----- 1946
 1714 -AHGLGPCPCPG-----PCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPC 1750
 1947 RKSQVSRTHSLPNDSYMCRN-GSTAERSLGRHGLPKAQSGLSVHSQPADTSCILQL 2005
 1751 RSGGAGAGG-DTESHLCHCYSPAQETL-----W-----LDSVSLIKDSLEGELTIIDNL 1801
 2006 PKOV-HYLLQPHG 2017
 1802 SGSVFHYASPDG 1814

RESULT 11

US-10-425-800-5
 ; Sequence 5, Application US/10425800
 ; Publication No. US20030180886A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dietrich, Paul S.
 ; APPLICANT: McGivern, Joseph G.
 ; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
 ; TITLE OF INVENTION: AND USES
 ; FILE REFERENCE: R0043B-REG sequence listing
 ; CURRENT APPLICATION NUMBER: US/10/425,800
 ; CURRENT FILING DATE: 2003-04-29
 ; PRIOR APPLICATION NUMBER: US/09/404,650
 ; PRIOR FILING DATE: 1999-09-23
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 1835
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 ; US-10-425-800-5

Query Match 44.4%; Score 5345; DB 14; Length 1835;
 Best Local Similarity 55.4%; Pred. No. 0;
 Matches 1139; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

43 PRSRDSPVASRSSTTCPCGCAAGAGSTKDPGSDSEAG-----LPYPALAPVVFYLSQ 98
 8 PSSAAAPAPFPGITEQGP-----RSPPPSPGLEPTEGTPDVPHPDLAPVAFCLRQ 62
 99 DSRPSRCLRTVNCNPFERVSMLVLLNCVTLGMRFCEDIAQSQRILQAPDDIFA 158
 63 TTSRNCWIKMVCNPNWECVSMVLLNCVTLGMYQPCDDMECLSDCKILQVDFDIFI 122
 159 FFVEMVVKVVALGIFGKKCYLGDWNRDLFFVIAGLMLEYSLDLQNVSAVTVLRL 218
 123 FFAMEVVKVVALGIFGKKCYLGDWNRDLFFVIAGLMLEYSLDLQNVSAVTVLRL 182
 219 PLRAINVPNRILVTLVLLDTPMLGNVLLLCFFVFFIFGIVGVLWAGLRNRCFLPEN 278
 183 PLKAINVPNRILVTLVLLDTPMLGNVLLLCFFVFFIFGIVGVLWAGLRNRCFLPEN 242
 279 FSLPLSVLDLEPYOTENEDESPFICSPQRENGMRSRCSVPTLRGEGGGGPPCSL----- 332
 243 FTIQDVALPPYQPEEDEDEMFICSLTDGNGIMGCHIEIPPLKEQ---GRECCLSKDDVY 299
 333 DYETNVSSTNTT--CVNKNQYTCNAGEHNPFGAINFDNIGVATIAI FOVITLKGWD 390
 300 DFGAGQDLNAGSLGVNWNRYNVCRTGNANPHKGAINDNIGAGIVFIVITLEGWVE 359
 391 IMYFMDAHSFVNFYIFILLIIVGSFFMINCLLVVIATQFSETKQESQLMREQVRFLS 450

111 CNPFRVSMVLINLCVTLGMPFCPCDIACDQRCRILQAFDDDELFAFEAVMVVWMA 170
124 CT-WFECVSMVLINLCVTLGMPFCPCDIACDQRCRILQAFDDDELFAFEAVMVVWMA 182
171 LGIFGKCYLGDWNRLDQFVIVAGMLEVSLDLQWSPSAVTRVRLVPLRAINRVPMSR 230
183 LGIFGKCYLGDWNRLDQFVIVAGMLEVSLDLQWSPSAVTRVRLVPLRAINRVPMSR 233
231 ILVTLTLLDPLMGNVLLLCFFVFFIFGIVGVLWAGLLNRNCFIPENFSLVDLEPY 290
234 ILVNLTLTLLDPLMGNVLLLCFFVFFIFGIVGVLWAGLLNRNCFIPENFSLVDLEPY 293
291 YOTENEDSPPTCSOPRENKMSRCSVPTLREGGGGPPCSL-----DYETINSSNTT 344
294 YQPEBDDDEPFCISLGGINGMGCHIEPLKEQ---GRECCLSKDDVDFGAGRODLNAS 350
345 ---CVNNNOYTYNCSAGEHPPFGAIFNDNIGYAWIAIFOVITLEGWVDIMYFVMDAHSFY 402
351 GLCVNNRYNVCRTGSANPHKGAIFNDNIGYAWIAIFOVITLEGWVDIMYFVMDAHSFY 410
403 NFYIFLILII----- 412
411 NFYIFLILIISELILHVMPCDSFSTAQSPKCGDSLPGVAERSLLIRDSSSSVITDEAAA 470
413 ----- 412
471 MENLLAGTSKGDSEYLLRLAGSQVHSQAQOMLGRGLGPRSLTGTGEPHPSWSPAIRRNDP 530
413 -----VGSFFMNLCLVVIATOFSETKQRESQLMREORVRLFNASTLA 456
531 QCOPGQPLPHFMAQVQGVFFMNLCLVVIATOFSETKQREHLMLEQORYLS-SSTVA 589
457 SFSEPGSCYEELKYLYILRKAARLAQVSRRAIGVRAGLSLSPVARSQEPPOSSCTR 516
590 SYAEPGDCYEEIFQYVCHILRAK-----RALGLYQALQSRQALGPEAPAPA----- 638
517 SHRRLSVHHLVHHHHHHHHYHGLNGTLRVPRASPEIQDRDNGSRRLMPPSTPTPSG 576
639 -----KPGHAKPEPRH 649
577 GPPRGAESVHSFYHADCHLEPVRCQAPPPRCPEASGRVTVGSGKVYPTHTSPPPPEIKD 636
650 YPLTVVESILGROAEBCTL---RAAAHP-----SSGASHPGVGSSEAPELCPQ 694
637 XALVEVAP-----SPGPPTLSFMIPPGPFSSMHKLLTQSTGAC-HSSCKISPCSKADS 691
695 HSPLDATPHTLVQPIPATLAS-----DPASCPCQCHEDGRPRPSGLGSTDS 739
692 GACGPDSCPYCARTGAGEPESADHVMPSDSEAVVEFTQDAQHSDLRDPHSRRQRSLGP 751
740 QGEGSGS-----GSSAGGEDEA-----DGDGA---RSEDCASSELGKEEEBEQ----- 781
752 DAEPSSVLA--FWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIBYHEQPE----- 802
782 -ADGAVMLCGDVWRETRAKLGIIVDSKYFNRGIMAILVNTVSMGIEHQAASQAQPGA 840
803 -----ELTNAL-----ISNIV----- 814
841 CGRGONPDLMTLKAPLCHNVPSPGQVLSHPVTPHTAPWRMETGKGHCHEGPGQR 900
815 FTSIPALFEMILKLVYGFPGYIKPNYIFDGVIVISWEIVGQGGSLVRLTFRLMRV 874
901 SSDPFALEMILKLVYGFPGYIKPNYIFDGVIVISWEIVGQGGSLVRLTFRLMRV 960
875 LKLVRFALQRLQVLMKTMNDVATFCMLLMLEFIFPSILGMHFGCKPASERD-GDTL 933
961 LKLVRFALQRLQVLMKTMNDVATFCMLLMLEFIFPSILGMHFGCKPASERD-GDTL 1020
934 PDRKNFDSLLVAIVTFQILLQEDWNVLYNGMASTSSWAAALYFALMTFNGYVLFNLLV 993
1021 PDRKNFDSLLVAIVTFQILLQEDWNVLYNGMASTSSWAAALYFALMTFNGYVLFNLLV 1080
994 ALLVVEGFQAE-----GD 1005

1081 AILVEGFOAEVTVVLABEAPPQGLRKTGRGGGLDGGGLQFKLLAGNLSLKEGVADEVGD 1140
1006 ATKSESEBDFPSPV-----DGDGRKKRLALVALGEHAELKSLPLLIHT-- 1053
1141 ANRSYDEDESSNIEEDFKLOEGLDSSGDPK--LCPIPMTPNGHLDPSL--PLGGHLGP 1196
1054 -AATP-----MSHPKSSSTGVG-----BALGSGSRRTSSSGSA----- 1085
1197 AGNAGPAPRLSLOPDDPMLVALGSRKSSVMSLGRMSYDQSLVGGLRATAGVQAFAHLVP 1256
1086 BP-----GAHHHEMKCPFSARSSPHSPWSAASSWTSSRSNSLGRAPSLKRSRSGERR 1140
1257 QPWWCLMGADPNNGNSFQSSRSRSGYGPWGRSAAMASRRSSWN-----SLKHKPSABHE 1310
1141 SLLSGE-QESODESESEE--DRASPAGSDH-----RHRGSLREAKSS 1182
1311 SLLSBERGGGARVCVAADEGPPRAAPLPHAHVHHVHGHPLAHRHRRHRTLSLDNRDS 1370
1183 FDLPTLQVPGHLRTASGRSS--ASEHQDCNKSASGRILARTI--DDPQLDGGDDND- 1237
1371 VDLAEIVPAVGAHPRAAWRAAGPAPGHEDCNGRMP--IAKDVFTKMGDRGDRGEDEEI 1428
1238 -----EGNLSKGERIOAWVRSLPACCRERDSWSAYIFPPQSRFR-----LLC--- 1280
1429 DIVSGGAGBDTLTCFRVKMIDVYKPDWCVRREDMSVYLFSPENLRDLGWVLECOGK 1488
1281 -----HRIITHKMFHDVHLVILFNCITTIAMERPDKIDPHSABRIFLTLN 1325
1489 VGDVLVWVYQRRQRQTIIAHKLFDYVVLAFIFLNCITIALERPQIEAGSTERIFLTVSN 1548
1326 YIFTAVFLAEMTVKVVVALGWCQGEQAYLRSSNVLDGLLVLSVIDILVSMYSDSGTKIL 1385
1549 YIFTAIFVCEMTLKVVSLGLYFGEQAYLRSSNVLDGLVFLVSIIDIVVSLASAGAKIL 1508
1386 GMLRVLRILRTPLRVISRAOGLKLVAVETLMSLKPIGNIVVICCAFFIIFGILGVQLF 1445
1609 GVLRVLRILRTPLRVISRAOGLKLVAVETLMSLKPIGNIVVICCAFFIIFGILGVQLF 1668
1446 KGKFFVCQGEDTNIINKDKCAEASVYRWVRHKYFNFDNLGOALMSLFLVASKDQWIMYD 1505
1669 KGKFFVHCLGVDTNITNIRSDCMAANYRWVHHKYNFDNLGOALMSLFLVASKDQWIMYD 1728
1506 GLDAVGVQDQPIIMHNPMMLLYIFISLLIVAPFVLMFVGVVVENPHKCHQHEBEARR 1565
1729 GLDAVGVQDQPIIMHNPMMLLYIFISLLIVAPFVLMFVGVVVENPHKCHQHEBEARR 1788
1566 REEKRLARLEKKRSEKQMAEAOCKPYSDYSRFRLLVHHLCTSHVLDLFTIGVILNV 1625
1789 REEKRLARLEKKR-----KAQRLPYATYCHTRLLIHSMTCTSHYLDIFITFICLV 1841
1626 VTMAHEHYQOP 1636
1842 VTMSLEHYNQF 1852
RESULT 13
US-10-369-493-6836
; Sequence 6836, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21

Qy	66	AGSTKDPG-----SADSEAGLPYPALAPVFFYLQSDSRBRSCWLRVCN	112
Db	88	ASSSEASPSRWEGRQIEWNEEQIEESEE-LPYGCPAEPALRCFYQARPFRKALQWMS	146
Qy	113	PFPERVSMVLILNCVTLGMFRPCED-IACDSQRCRILQAFDDFIAFFAVEMVKNVAL	171
Db	147	PWFDRITMAVIMINCVTLGMFRPCEDGDCDTCYRCQILDIDNCIFVVFAFEMVIKMAL	206
Qy	172	GIFGKKCYLGTWNRLDFFIVIAQMLEYSLDQ--NVPSAVRTVRLPLRINRVPS	228
Db	207	GFYGFAPAAVMTWNRLDFFIVMAGIABFVUHEYIUGMINLTAIRTVRLPLRAVNRPS	266
Qy	229	MRILVTLTLLDPLMLGNVLLLCFFVFFIFGIVGQWAGLLRRCF--LPEPTS-----L	281
Db	267	MRILVTLTLLDPLMLGNVLLLCFFVFFIFGIVGQWAGLLRRCVNLKPTISENQSL	326
Qy	282	PLSYDLIPYQTEENDESDPFICSQPNRMRSCSVPTLRGEGGGPPCSLDIETYNSSS	341
Db	327	FNNVKLFRFYIPE-DTSLVETICQPDANGLHTCSNLPPTVD--GVKCNLTLDYDKVT	382
Qy	342	NTTCVNNQYYTNCISAG-----EHPFKGAINFONIGVAMTAIQVIT	384
Db	383	NDSCINNNIYNEQVNIYPSLMTIASCPIKVMQRNPFQSGVSFDNIGFAWIAFLVIS	442
Qy	385	LEGWVDIMYFVMDAHSFYNFIYFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREQ	444
Db	443	LEGWTDIMYVQDAHSFNNIYFVLLIIVGAFPMINCLVVIATQFAETKRRETERMLQE	502
Qy	445	RVPLSNASTLASGSEPG-----SCYEELLKVLVYIRKAARLQAQVSAIGVRAG	495
Db	503	RKMLLRNDSISCTGSEITGGASKEEGDTVYAAVFRFIGHTFRTRKAACKKYTAY-----	557
Qy	496	LLSSPVARSQEQPQSGSCSTRSHRRLSVHHLVHHHHHHHVLHNGTVLRVPASPEIQD	555
Db	558	-----MEERAERKSSERQORRSKL-----DMATLSRIEKAED	592
Qy	556	RDANGSRRLMLPPSTPTSGGPPRGAESVHSFYHADCHLEPVRQCAPPCPESEASGRT	615
Db	593	EE-----DETITRENGDDQIQEM-----	611
Qy	616	VSGGKYVPTVHTSPPPBEILKOKALVEAPSPGPPTLTSPNIPGPFSSMHKLTQTGTGA	675
Db	612	-GDGVRIKRVKIEEBPKI-----	628
Qy	676	CHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSDSEAYVEFTQDAQHS	735
Db	629	-----KIGNGNSNGPHYKHSSDEES-----DEDGEED	656
Qy	736	DLRDPHSRRRQSLGPDABPSSVLAFWRLICDTRFKIVDSKYFGSGIMTALIVLTLNGI	795
Db	657	QYVDGEAKKK-----STPSKI--WW--FRKIQKFVICDFTGILVAILVNLMSGV	706
Qy	796	EYHQEPELTNALIEISNIVFTSLFALEMLLKLVYGPFGYIKKNPNYINFDGVTWISVWEI	855
Db	707	EYHQEPELTVILEYSNLFATALFALEMLLKIIASGLFGYADGNLFDGGIIVALSVUEL	766
Qy	856	VGOQGGGLSVLRTFRMLRVKLVRFLPALQROLVLMKTMQNVATFCMLLMFLFIFISIL	915
Db	767	FOEGKGGLSVLRTFRLLRLKLVRFPALRYQLVVMRLTMDQNTVFFGLVLVFIIFSIL	826
Qy	916	GMLHFCCKFASERD-----GDTLP--DRKNPDSLILWAIIVTVFQILTQEDWNKVLYNGMASTS	970

APPLICANT: Castle, John C.
APPLICANT: Armour, Christopher D.
TITLE OF INVENTION: SPLICE VARIANT ISOFORMS OF HUMAN CALCIUM CHANNEL CACNA1B
FILE REFERENCE: RS0202Y
CURRENT APPLICATION NUMBER: US/10/627,370
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 2264
TYPE: PRT
ORGANISM: Homo sapiens
US-10-627-370-2

Query Match 14.0%; Score 1680.5; DB 15; Length 2264;
Best Local Similarity 23.9%; Pred. No. 1.2e-101;
Matches 623; Conservative 349; Mismatches 831; Indels 801; Gaps 82;

QY 59 PGPAGAGSTKDPGSDSEAEGLPYPALAPV-----VFFYLSQDSRPRSMCLRT 109
DB 32 PGPGLQPCORVLYKOSIAQARTMALYNPIPVKQNCFTVNRSLFVFSEDNVVRKAKEI 91
QY 110 VCNPFERSMVLINCVTLGMFRPCEDIACSQRILQAFDD---FIFAFFAVMVV 166
DB 92 TWPFPFYMILATIANCIVLAL---EQHLPDGDTPMSERLDDTEPYFIFGIFCPAEG 147
QY 167 KVALG-IFGKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSPSAVTVRVLPLRA 222
DB 148 KIIALGFVFKGSLRNGWNVDFVVLGTGILATAGTDFDLR-----TLRAVRVLRPLKL 202
QY 223 INRVPMRILVTLTLPLMLGNVLLCFVFFIFGIVGVOLWAGLLRNRCFLPENSFLP 282
DB 203 VSGIPSLVVYKSIKAMVPLLIQIGLLFPAILMFAIIGLETFMGFHKACF-----P 255
QY 283 LSVDLPEPYQYOTENEDSPFICSPRENGMRCRSVPTLRGEGGGGPPCSLDVETYNSSN 342
DB 256 NSTDAEPV-----GDFPCGKEADARLCEGD 280
QY 343 TTCVNNQYNTCSAGHNPFKGAINDNIGYAMIALFQVITLEGVVDIMYFMD-AHSP 401
DB 281 TEC---REYWP-----GNFGITNPDNIFLAILTVFCITWEGWTDILYNTNDAAGNT 330
QY 402 YNFIYFLLIIVGSEFFMINCLVVIATQFSETKORE-----OLMREORVRFLSNASTL 455
DB 331 WNNLYFPLLIIGSFEMNLVLGVLSGEFAKERVENRRAFLKLRQQOIR-----382
QY 456 ASFSEPGSCYEELKLYILKAAARLAQVRAIGVRAGLLSPVARSGOEPOPSGCT 515
DB 383 -----RELNGYLEWIFKAEVMALED-----RNAEKSPLDLVK 417
QY 516 RSHRLSVHLLVHHHHHHHHYHLGNGTLRVPRASPEIQORDANGSRRLMLPPSTPTPS 575
DB 418 RAATKKGSRNDLIH-----AEEGEDRFAD-----440
QY 576 GGPGRGAESVHSFVHADCHLEPVRCAQPPRCPCSEASGRIVGSGKVTYVHTSPPPRLK 635
DB 441 -----440
QY 636 DKALVEVAPSPGPPTLTSTFNIPPGPFSSMHKLELTQSTGACHSSCKISSPCSKADSGACG 695
DB 441 -----LCVAGSPPARAS-----452
QY 696 PDSPCYARTGAGPESADHVPDSDSEANVEFTQDAQHSDLRDPHRSRRORSILGPDAP 755
DB 453 -----LKSQGTSSSYF-----RRKEK-----469
QY 756 SSVLAFAWRLICDTPRKIVDSYVFGRGIMAILVNTLSMGIBYHQPDELTNALISNIVF 815
DB 470 ---MREFF-----IRRMVKAQSFYVVLVCVVALNLCVAMVHYNQPRLLTTLTYFAEFVF 521
QY 816 TSLFALEMLKLVVGPGRYKKNPNIYFDGVIVIVISWVEIVGQ-----QGGGLSVLRFR 870
DB 522 LGLFLEMLSLMYGLGRPSYFRSSFNCFDFGIVGSEFVVWAAIKPGSSFGISVLRALR 581

QY 871 LMRVLKLVRELPALQQLVLMKTMNDVATFCMLMLFIPIFISILGMHLFGCKFASERDG 930
DB 582 LLRFKVTYKWSLRLNVSLNSMKSIISLLELFLFVIVFALLGMQLFGQGFQDET 641
QY 931 DTLPRKNFDSLWAIIVTVFOILTQEDWKNVLYNGM-----ASTSSWAALFYALMTFGN 985
DB 642 PT---TNFDTPPAILTVFQILTGEDWNAVMYHGIESGGVSKGMFSFVIVTULFGN 697
QY 986 YVLENLVAILVEGFAEGDATKSEPDFSPSVDGDGDKRKRLLALVALGEHAELRKS 1045
DB 698 YTLNVLFLAIVDNLNANAQELTKDEEEMEEAA-----NQKALQKAEVAEV--SP 746
QY 1046 LPPLIHTAATPMSPKSSSTGVGEA-----1071
DB 747 MSAANISIAARQONSAKARSVWEQASQLRLQNLASCEALYSEMDPEERLEFATRHRL 806
QY 1072 -----LGSSSRRTSSSGSAEPGNA-----HH-----EMKCP-----1097
DB 807 PDMKTHLDRPLVVELGRDGAAGFVGKARPEAAEAPGVDPPRRHHRHDKKTPAAGDQ 866
QY 1098 -----PSARSS---PHSPWSAASSWTSRRSSNLGRAPSLKRRSPSGERRSL 1142
DB 867 DRABAPKAESGEPGAREPRPHRSKSEA--GPPEARSERGRGP-----GPEGRRHH 919
QY 1143 LSQEGQESQDEE-----ESSEEDRASAGSDHRRHRSLE---REAKSFDLPD 1189
DB 920 RRGSPPEAAAREPRHRAHRHQDPKCECAGAKERRARRHRRGFRAGPREAESG-----972
QY 1190 QVPG-IHRTASGRSSASE--HQDCNGKSASGLA-----RTLTDPOLDGDDNDE 1238
DB 973 EEPARRHRAHKAQPAHEAVEKETTEKATEKEAEIVEADKEKELRNHQPREPHCDETS 1032
QY 1239 GNLSKERIQAWRSRLPACCRER-----DSW-----1265
DB 1033 GTVTGVP-----MHTLPSTCLQKVEEQEDADNQNRNTRMGSQDPDPTIIVH 1086
QY 1266 -----SAYIFPPQSRFLLCHRI 1283
DB 1087 PLGEATVWPSGNVDLSQAEGKEVEADDVMSRGPPIVFPVSSMFCLSPTNLLRRFCHI 1146
QY 1284 ITHKMFHDVVLVIIFLNCITAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVAL 1343
DB 1147 VTMRYFEVILVIALUSSIALAAEDP-VRTDSPNNALKYLDYIFTCVTFEVMVIXMIDL 1205
QY 1344 GWCFGEQAYLRSMWNLDGLLVLSIVTDIIVSMV-SDSGTKILGLMLRVLRLTLRLPLRV 1402
DB 1206 GLLHPCAYFRDLWNILD---FIVVSGALVAFASGSKGKDINTIKSLRVLRLPLKT 1261
QY 1403 ISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVLPKGFVFCOGE-----D 1456
DB 1262 IKRLPKLKAVFDCVNSLKNVNLIVYMLFMFIFAVIAVOLFKGFYCTDSKELERD 1321
QY 1457 TRN--ITNKSDCAEASVR-WVRHKYFNDFNLGOALMSLFLVLSKDGWVDIMYDGLDAGVD 1513
DB 1322 CRQYLDYKEEVEEAQQRQWKYDFHYDNVLMWALLTLFTVSTGEGWMLKHSVDATYEE 1381
QY 1514 QQPMINHPWMLLYFISFLIVAFVFLNMFVGVVVENFHKCRQHQBEEERARRRERLRR 1573
DB 1382 QGSPGYMELSIYVVYVVFVFFVFVNIIFVALLIITF-----QEQGDKVMSE-----CS 1431
QY 1574 LEKKRREKQMAEQCKPYYSYR--FRLLVHHLCTSHYLDLFTTGVGLNVVTVWAME 1631
DB 1432 LEKNERACIDFAISAKELTRYMPQNRSQYKTVTFVVPSPFFEFIMAMIALNTVLMMK 1491
QY 1632 HYQPOQILDALKICNVIFTVIFVFSVFKLVAFAPRRFFQDRWNQDLDAVLVLSIMGIT 1691
DB 1492 FYDAPYVELMLKCLNIVFTSMFSECVLKIAGVNLNYFEDANNVDFEVTVLGSIIDIL 1551
QY 1692 LEEIE-----VNLSLPINPTIIRIMVLRIRVLRKLLKMAVGMALLHTVMQALPOVGNL 1746
DB 1552 VTEIAETNNFNILS-----FLRLFPRAARLLKLLRQGYTIRILLTTFVQSFKALPYV 1602

[illegible]

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RESULT 15
US-10-736-883-38
; Sequence 38, Application US/10736883
; Publication No. US20040214238A1
; GENERAL INFORMATION:
; APPLICANT: LIPSCOMBE, Diane
; APPLICANT: BELL, Thomas
; APPLICANT: THALER, Christopher
; APPLICANT: CASTIGLIONI, Andrew
; TITLE OF INVENTION: NOCICEPTIVE NEURON-SPECIFIC CALCIUM CHANNEL ISOFORM AND USES
; FILE REFERENCE: B0877.70026US00
; CURRENT APPLICATION NUMBER: US/10/736,883
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/443,474
; PRIOR FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 2327
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-736-883-38

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Query Match	14.0%	Score 1678;	DB 17;	Length 2327;
Best Local Similarity	23.2%;	Pred. No. 1.8e-101;		
Matches	620;	Conservative 378;	Mismatches 805;	Indels 872;
	Gaps	87;		
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QY	92	-VFFYLSQDSRPRSWCLRTVCNPMFERYSMLVILLNCVTLGMFRCEDEDIACDSQRCLILQ		-----EQLPDPDGTMPSE
Db	73	RSLSFVSEDNVVRKYAKRITWPFPEYMIATIANCIIVLAL-----		-----EQLPDPDGTMPSE
QY	151	AFDD---FIFAFFAVEMVVMVALG-IPGKKCYILGDTWNRLDFFTVIAGMLEYS---		-----LDL
Db	129	RLDDEPYFYGICFEAGIKIILGFVHKGSYLNRGNWVDFVVVLGILATAGTDFDL		-----188
QY	204	QNVSFSAVRVTVLRLPRAINRVSMRILLTVLLDITLMLGNVLLCLLPFFVFIQVGVQ		-----263
Db	189	R-----TLRAVRLRLPLKVSGLPSQVLVKSIMKAMVPLQLIGLLFFAILMFAIGLE		-----243
QY	264	LWAGLLNRRCFLPENSLPLSVDLERYVQTEDESPFICSQPRENGRSCSVETLRGE		-----323
Db	244	FYMGKTHKACF-----PNSDTDEPV-----		-----263
QY	324	GGGGPPCSLDYETNGSSNTTCVNMNOYITNCSEAGHNPPKGAINFOINIGYAWIAIFOVI		-----383
Db	264	--GDFPCGKDPAPQCDDGTEC-----REYWP-----		-----GPNFGITNFNILLFVTFVOCI
QY	384	TLGGWDIMYFVMD-AHSFYNFYIFILLIIVGSFFMINCLVITATOPSETKQRES-----		-----438
Db	312	TWEGWTDILYNTNDAAGTNWLIYFIPLIITIGSFFMLNLVLGSLVSGFAKERERVENRRA		-----371
QY	439	--QLMREQVRKFLSNASTLASFSEPGSCYBELLKLVVILRKAARRLAQVSRALCVRAGL		-----496
Db	372	FLKLRQQQIE-----RELNGYLEWIFKABEVMIAED-----		-----404
QY	497	LSPVARSQEPQPSGCTRSRHLRVSHVLVHHHHHHHHHHLGNGTLRVPRAPEIQDR		-----556
Db	405	-----KNAEKSPLDLVKRAATKTKSRNDLIH-----		-----AEEGEDR
QY	557	DANGSRRLMLPPSTPTSGGPPRGAEVSHSFYHADCHLEPVRCAQPPRCPSPASGRV		-----616
Db	438	-----FVDL-----		-----437
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Db	442	---CAVGPFFARAS-----		-----LKSGETESSYF-----
QY	737	LRDPHSRRRQSLGPDABPSSVLAEWRLLCDTFRKIVDSKYFGRGIMAILVNTLSMGIE		-----796
Db	465	-----RRKEK-----MFRFF-----		-----IRRMVKAQSFYVWVLCVVALNTLCVAMV
QY	797	YHEQPEELTNALEIGNIVFTSLFALEMLKLAVYGPFGYKPNYINFDGVIVVISWEIV		-----856
Db	503	HYNQPORLTTALYFAEFVFLGLFLETMSLKMVGLGRSYFRSFCDFPGVIVGSIPEV		-----562
QY	857	QQ-----QGGGLSVLRTFLMRVLKVLRFPLALQRLVLMKTMNDVATFCMLLMFIPI		-----911
Db	563	WAAIKPGTSFGISVLRALRLRLRIKVTYKNSLRNLVSLNSMKSIIISLLFLLFIVV		-----622
QY	912	FSILGMHLFGCKEASERDGLTPDKENFDSLILWAIIVTFQIILTQEDWNKVLNMG		-----966
Db	623	FALLGMQLFGGQFNQDETP-----TNEFDTFPAAILTVFQILTGEDWNAVYHGESQGG		-----678
QY	967	ASTSSWAALYFIALMTFGNYVFLNLLVAILVEGFAEGDATKSESEPDPFSPVSDGDGR		-----1026
Db	679	VSKGMFSSFFYIVLTLFGNYTLNVFLAIVDNLANAQLTKDEEMSEAA-----		-----729
QY	1027	KRLIALVALGEHAEKSLSLPLLIHTAATPMSPHKSSSTGVGEALGSGSR-----		-----1077

Db 730 NOKLALQKAEVAV--SPMSAANISIAAROONSAKARS--VWQASQALQONLRASCE 785
Qy 1078 -----RTSSSGSAGFAGAAH-----EMKCPSPASRSPHSPWSAAS 1113
Db 786 ALYEMDPEERLRVASTHRVAPDKMTHDRPLVWPGRDGLRPGVSGSKPEGTEATESA 845
Qy 1114 WTSRSSN-----SLGRAP-----SLKRRSPSGE-----1138
Db 846 DLPRHHRDRDKTSATAPAGGEQDRTSTGTAREERARPRSHSKETPGADTVQVCE 905
Qy 1139 ---RRSLLGEGESODEE-----ESSEEDRAS---PAGSDH--RHRG--SLEREA 1179
Db 906 RSRHRRGSPPEATEREPRHRAHRHAQDSKGTAPVLVPGERRAHRGPRGPREA 965
Qy 1180 KSSPD-----LPTQLVPGGLHRTASGRSSASE-----HQCNGKASAS 1216
Db 966 ENNEPFRHRAHVKVPTLOPPE--REAAEKESNAVEGDKETRNHOPKPHCDLEAIAVT 1024
Qy 1217 G-----RLARTL--RTDDPOLDGGDDND-----1237
Db 1025 GVGPLHMLPSTCLQVDEQEDADNQNVTRMGSPSPDSTTVHVPVTLTGPGETPVVP 1084
Qy 1238 EGNL-----SKGER-----TQAWRSRLPACCRERDSWSAYIIPPOSRFRILCHRIIT 1285
Db 1085 SGMNLEGQAGKKEAEADVLRRGPRPIVPS-----SMFCLSPNLLRRFCHYIVT 1137
Qy 1286 HKMFHVVIIVIFLNCITIAMBRPKIDPSAERIFLTSNYIFTAVFLAEMTVKVVALGW 1345
Db 1138 MYFEMVILVIALSIALAAEDP--VRTDSFRNALKMYDIYFTGVFTFEMVIMKIDLGL 1196
Qy 1346 CFGEQAYLRSSNVNLDGLVLSVIDI--LVSMVSDSGTKILGMLRLVRLRLTLRLPLRVIS 1404
Db 1197 LLHPGAYFRDLNMLDIFVVGSLVAFAPFSFGSGKGDINTIKSLRVLRVLRPLKTIK 1256
Qy 1405 RAQGLKLVVETLMSSLPGNIVVICAPFIIIFGILGVQLFKGKFFVCOGE-----DTR 1458
Db 1257 RLPKLKAVDCVNSLKNVNLILVYMLFMFIFAVIAVQLFKGFFVCTDESKELERDCR 1316
Qy 1459 N--ITNKSDCAEASR--VWRHKYNFNLGOALMSLFLVASKOQWDIMYDGLDVGVDQ 1515
Db 1317 GOYLDYEKEVEAQPRQWKQYDHYDNVNLWALLTLFTVSTGEGWPMVLKHSVDATYEEQ 1376
Qy 1516 PIMNHPWMLLYIFISFLIIVAFVFLANMFVGVVENFHKCRHQBEBEAREERKRLRLE 1575
Db 1377 PSECFRMEISIFYVYVFWPFFVFNIPFVLIITF-----QEQGKVMSE-----CSLE 1426
Qy 1576 KRRSEKQMAEACPKPYGYSR--FRLLVHHLCTSHYLDLFTIGVIGLNVVTMAEHY 1633
Db 1427 KNERACTDFALSAPKPLTRYMPQNKQSFQYKTWTFVVSPPFEYFIMAMIALNTVYLMKFY 1486
Qy 1634 QQPQILDEALKICNYIFTVIFVFSFKLVAFAPRRFFQDRWQOLDJAIIVLSIMGITLE 1693
Db 1487 DAPYEYELMLKCLNIVFTSMFSMECILKIIFAGVNLNYFRDANWVDFVTVLGSITDILVT 1546
Qy 1694 EIEVNLSPINPTIIRNVLRIARVLKLMAGMEALLHTVMOALPOVGNLGLLEFLL 1753
Db 1547 EIANNF---IN---LSFLRLFRARLKLJURGGVTIRILMTFVQSFKALPYVCLLAML 1600
Qy 1754 FFIFAAALGVLELFCEDCEHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKO--P 1811
Db 1601 FFYIATIGMQVFGNIALDDD--TSINPHNNFRITFLQALMLLFRSATGEAHMILMSCLG 1657
Qy 1812 SRQCD---QESTCNTVNTSPYFVSFVLTAQFVLNVVIAVLN-----KH 1853
Db 1658 NRACDPHANASEC--GSDFAFYFVSFIFLCSFLMLNLFVAVIMDNFVYLTDRSDSILGPHH 1716
Qy 1854 LEE-----1856
Db 1717 LDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPGLGKCPARVAYKXLRVNMNPIGNE 1776
Qy 1857 -----SNKEAKEAELEAELE-----ELEMKTLS--POPHS 1884

Search completed: November 18, 2004, 13:58:59
Job time : 208.328 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:21 ; Search time 50.7329 Seconds
(without alignments)
4337.375 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVRCVTPPLRGSR.....KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.79.*

1: Pirl.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11657	96.9	2254	2 T09053	low voltage-activa
2	3553	29.5	1657	2 T15038	hypothetical prote
3	1720.5	14.3	1810	2 T31092	probable voltage-g
4	1676	13.9	2339	2 A42566	omega-conotoxin-se
5	1655.5	13.8	2259	2 S29236	calcium channel pr
6	1653.5	13.7	2272	2 C54972	voltage-dependent
7	1652.5	13.7	1891	2 T43262	calcium channel al
8	1652.5	13.7	2178	2 S29237	calcium channel pr
9	1650.5	13.7	2288	2 S41080	calcium channel al
10	1642	13.7	2223	2 A47447	calcium channel pr
11	1640.5	13.6	2237	2 T45115	N-type calcium cha
12	1638	13.6	2251	2 B54972	voltage-dependent
13	1637.5	13.6	2270	2 A54972	voltage-dependent
14	1636	13.6	1993	2 T30902	sodium channel SCA
15	1632.5	13.6	2222	2 A37490	voltage-dependent
16	1632.5	13.6	2336	2 A45386	omega-conotoxin-se
17	1631	13.6	2181	2 A38198	calcium channel al
18	1628	13.5	1873	2 A30063	dihydropyridine re
19	1622	13.5	2161	2 JH0564	calcium channel al
20	1619.5	13.5	1911	2 T33048	calcium channel al
21	1616	13.4	1852	2 A37860	calcium channel pr
22	1614.5	13.4	1977	2 S54771	sodium channel alp
23	1613	13.4	2203	2 T42742	voltage-dependent
24	1610	13.4	2143	2 JH0427	voltage-dependent
25	1603	13.3	1610	2 A46227	probable voltage-d
26	1595.5	13.3	1783	2 T37258	calcium channel pr
27	1595	13.3	2166	2 S11339	voltage-dependent
28	1592.5	13.2	2139	2 A44467	
29	1587.5	13.2	1646	2 JH0422	

30 1587.5 13.2 1873 2 A55645 calcium channel, v
31 1585.5 13.2 2016 2 A38195 sodium channel pro
32 1580 13.1 1917 2 C88728 protein C48A7.1 fi
33 1577.5 13.1 1559 2 T30535 calcium channel al
34 1574 13.1 2171 2 S05054 calcium channel al
35 1573 13.1 2108 2 S72458 sodium channel pro
36 1567.5 13.0 1687 2 S41742 calcium channel al
37 1565 13.0 1957 2 S68453 sodium channel pr
38 1557.5 12.9 2220 2 A45290 sodium channel pr
39 1556 12.9 2019 2 A33996 sodium channel pr
40 1551.5 12.9 1840 1 CHRTM1 sodium channel pro
41 1549 12.9 1976 2 I56555 sodium channel pro
42 1546.5 12.9 1983 2 A60054 sodium channel pr
43 1546 12.9 2262 2 T30890 calcium channel al
44 1544.5 12.8 1951 2 S00320 sodium channel pro
45 1544.5 12.8 2005 2 A46269 sodium channel alp

low voltage-activated, T-type calcium channel alpha chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09053
R:Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox,
A:Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium
A:Reference number: Z16538; MUID:98154730; PMID:9495342
A:Accession: T09053
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2254 <PER>
A:Cross-references: UNIPROT:O54898; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g3
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Map position: 17
A:Note: CACNA1G
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C:Keywords: calcium channel; voltage-gated ion channel

ALIGNMENTS

RESULT 1

T09053

low voltage-activated, T-type calcium channel alpha chain - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09053

R:Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox,

A:Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium

A:Reference number: Z16538; MUID:98154730; PMID:9495342

A:Accession: T09053

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2254 <PER>

A:Cross-references: UNIPROT:O54898; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g3

A:Experimental source: strain Sprague-Dawley; brain

C:Genetics:

A:Map position: 17

A:Note: CACNA1G

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C:Keywords: calcium channel; voltage-gated ion channel

Query Match	96.9%	Score 11657;	DB 2;	Length 2254;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 2219;	Conservative	0;	Mismatches	6;
			Indels	0;
			Gaps	0;
QY	62	GAAGAGSTEKDPGSDSEAGLFPALAPVVFYLSQDSRPSRWCRLTVCNPFERSVSM	121	
Db	30	GROGPGSTKDPGSDSEAGLFPALAPVVFYLSQDSRPSRWCRLTVCNPFERSVSM	89	
QY	122	VILLNCVTILGMFRPCEDIAQDSORCRLQAFDDFIQAFFAVEMVVMVWALGIFGKCYLG	181	
Db	90	VILLNCVTILGMFRPCEDIAQDSORCRLQAFDDFIQAFFAVEMVVMVWALGIFGKCYLG	149	
QY	182	DTWNRDLDFIVTAGMLEYSLDQNVSFSAVRTVRVLRPLRINRVSFMRILVLLDITLP	241	
Db	150	DTWNRDLDFIVTAGMLEYSLDQNVSFSAVRTVRVLRPLRINRVSFMRILVLLDITLP	209	
QY	242	MLGNVILLCFVFFFIQVGVOLWAGLLNRCFLPNFSLPLSVLEPYQYQTEDESPF	301	
Db	210	MUGNVILLCFVFFFIQVGVOLWAGLLNRCFLPNFSLPLSVLEPYQYQTEDESPF	269	
QY	302	ICSPRENGMRSCRSVPTLRGGGGPPCSLDYETVNSSTTCVNNQYNTCSAGEHN	361	
Db	270	ICSPRENGMRSCRSVPTLRGGGGPPCSLDYETVNSSTTCVNNQYNTCSAGEHN	329	
QY	362	PPKGAINFDNIGYAWIAIQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFPMNL	421	
Db	330	PPKGAINFDNIGYAWIAIQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFPMNL	389	
QY	422	CLVVIATQFSEKQESQIMREQVRFLSNASTLASFSEPGSCYEELKYLVYILRKAAR	481	

390 CLVVIATQFSETKORESQLMREQVRFLSNASTLASFSEPCSCYEELLKYLVIILRKAAR 449 Db
482 RLAQVRAIGVRAGLLSPVARSQOEQPSGSTRSHRRLSVHLLVHHHHHHHHYHLGN 541 Qy
450 RLAQVRAIGVRAGLLSPVARSQOEQPSGSTRSHRRLSVHLLVHHHHHHHHYHLGN 509 Db
542 GTLRVPASPEIQDRDANGSRLLMPPSTPTPGGPPRGAEVSHSFYHADCHLEPVRCQ 601 Qy
510 GTLRVPASPEIQDRDANGSRLLMPPSTPTPGGPPRGAEVSHSFYHADCHLEPVRCQ 569 Db
602 APPRCPEASGRVVGSKVYPTVHTSPPELKKALVEVAPGPPPTLTSFNIPGPF 661 Qy
570 APPRCPEASGRVVGSKVYPTVHTSPPELKKALVEVAPGPPPTLTSFNIPGPF 629 Db
662 SSMHKLITQGTGACHSSCKISSPCSKADSGACGDCPCYCARTGAGPEPEADHWMPDS 721 Qy
630 SSMHKLITQGTGACHSSCKISSPCSKADSGACGDCPCYCARTGAGPEPEADHWMPDS 689 Db
722 SEAVYFTQDAQHSDLRPHRRRORSLGPDAPSSVLAFWRLICDTERKIVDSYFGRG 781 Qy
690 SEAVYFTQDAQHSDLRPHRRRORSLGPDAPSSVLAFWRLICDTERKIVDSYFGRG 749 Db
782 IMATILVNTLSMGIEYHQPEELTNALRISNIVETSLFALEMLLKLIVGPGYIKNPYN 841 Qy
750 IMATILVNTLSMGIEYHQPEELTNALRISNIVETSLFALEMLLKLIVGPGYIKNPYN 809 Db
842 IFDGVIVISVWEIVGQGGGLSVLTFRLMRVLKLVRLPALQRLVLMKTMONVATF 901 Qy
810 IFDGVIVISVWEIVGQGGGLSVLTFRLMRVLKLVRLPALQRLVLMKTMONVATF 869 Db
902 CMLLMFIFIFSLGMLHPCGFASERDGTLPDRKNFDSLAIWIVTFQIILTQEDWNKV 961 Qy
870 CMLLMFIFIFSLGMLHPCGFASERDGTLPDRKNFDSLAIWIVTFQIILTQEDWNKV 929 Db
962 LYNMGASTSSWAALFYALMTFQNYVLFNLLVAILVEGFAEGDAKSESEPDFSPSYD 1021 Qy
930 LYNMGASTSSWAALFYALMTFQNYVLFNLLVAILVEGFAEGDAKSESEPDFSPSYD 989 Db
1022 GGDGRKRLALVALGHAELRKSLLPPLIHTAATPMHPSKSSSTGVGALGSGSRRTSS 1081 Qy
990 GGDGRKRLALVALGHAELRKSLLPPLIHTAATPMHPSKSSSTGVGALGSGSRRTSS 1049 Db
1082 SGSAEPGAHHKPCPSARSPHSPWASSTSRSSNSLGRAPSLKRRPSPGERRS 1141 Qy
1050 SGSAEPGAHHKPCPSARSPHSPWASSTSRSSNSLGRAPSLKRRPSPGERRS 1109 Db
1142 LLSGEGQESODEESSEEDRASPGSDHRRGSLEREAKSSFDLPDLTQVPGHLRTASGR 1201 Qy
1110 LLSGEGQESODEESSEEDRASPGSDHRRGSLEREAKSSFDLPDLTQVPGHLRTASGR 1169 Db
1202 SSASEHQDCNGKSGASGLARTLRTDDPOLGDDDDNDGNTSKGERIQAWVRSLPACC 1261 Qy
1170 SSASEHQDCNGKSGASGLARTLRTDDPOLGDDDDNDGNTSKGERIQAWVRSLPACC 1229 Db
1262 RDSWSAVIFPPQSRFRLLCHRIITHKMFHDHVLVILFNCITIAMERPKIDPHSAERIFL 1321 Qy
1230 RDSWSAVIFPPQSRFRLLCHRIITHKMFHDHVLVILFNCITIAMERPKIDPHSAERIFL 1289 Db
1322 TLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSNVLDGLLVLISVIDILVMSVSDS 1381 Qy
1290 TLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSNVLDGLLVLISVIDILVMSVSDS 1349 Db
1382 TKILGMLRVLLRLTLRPLRVISRAQGLKLVETLMSSLKPDIGNIVTCACFFIIFGLG 1441 Qy
1350 TKILGMLRVLLRLTLRPLRVISRAQGLKLVETLMSSLKPDIGNIVTCACFFIIFGLG 1409 Db
1442 VOLPKGKFFVCOGEDTRNITNKSDCAEASYRWHRKYNFDMGQALMSLFLVASKGQWVD 1501 Qy
1410 VOLPKGKFFVCOGEDTRNITNKSDCAEASYRWHRKYNFDMGQALMSLFLVASKGQWVD 1469 Db
1502 IMYDGLDAVGVDQOQIMNHNPMWLLYFISFLIIVAFFVLNMFVGVVVENFHKRQHQBEE 1561 Qy
1470 IMYDGLDAVGVDQOQIMNHNPMWLLYFISFLIIVAFFVLNMFVGVVVENFHKRQHQBEE 1529 Db

1562 EARRRBEKRLRRLEKKERSKEKQMAEAQCKPYYSYDSYRFRLLVHHLLCTSHYLDLFTITGVI 1621 Qy
1530 EARRRBEKRLRRLEKKERSKEKQMAEAQCKPYYSYDSYRFRLLVHHLLCTSHYLDLFTITGVI 1589 Db
1622 GLNVVTVAMHYQOQIILDEALKICNVIFTVIFVFESVEKLVAFARFRFFQDRWNQDLDA 1681 Qy
1590 GLNVVTVAMHYQOQIILDEALKICNVIFTVIFVFESVEKLVAFARFRFFQDRWNQDLDA 1649 Db
1582 IVLUSIMGITLLEEVNLSLPINPTIIRIMRVLIARVLKLLKMAVGMREALLHTVMOALP 1741 Qy
1650 IVLUSIMGITLLEEVNLSLPINPTIIRIMRVLIARVLKLLKMAVGMREALLHTVMOALP 1709 Db
1742 QVGNLGLLFFMLFFIFAALGVLELFCDETHCEGLGRHATFRNFGAFLLTFRVSTG 1801 Qy
1710 QVGNLGLLFFMLFFIFAALGVLELFCDETHCEGLGRHATFRNFGAFLLTFRVSTG 1769 Db
1802 DNWNGIMKDPDRDCDOESTCYNTVISPFIYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEA 1861 Qy
1770 DNWNGIMKDTLRDCDOESTCYNTVISPFIYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEA 1829 Db
1862 KEEAELEAELEEMKTLSPQPHSPPLGSPFLWPGVEGVNSTSPKPGAPHTTAHIGAASGF 1921 Qy
1830 KEEAELEAELEEMKTLSPQPHSPPLGSPFLWPGVEGVNSTSPKPGAPHTTAHIGAASGF 1889 Db
1922 SLEHPTMVPHPBEVVPVPLGPDLLTVRKSGVGRTHSLPNDSYMCRNGSTAERSIGHRGWGL 1981 Qy
1890 SLEHPTMVPHPBEVVPVPLGPDLLTVRKSGVGRTHSLPNDSYMCRNGSTAERSIGHRGWGL 1949 Db
1982 PKAQSGLSVHSQADTSCTILOPKDVHYLLQPHGAPTGWGAI PKLPPPPGRSPFLAQRPRLR 2041 Qy
1950 PKAQSGLSVHSQADTSCTILOPKDVHYLLQPHGAPTGWGAI PKLPPPPGRSPFLAQRPRLR 2009 Db
2042 ROAAITRTDLSLDVQGLSGREDLLSEVSGPCPLTRSSFWGSSIQVQORSQISQSKVSKHI 2101 Qy
2010 ROAAITRTDLSLDVQGLSGREDLLSEVSGPCPLTRSSFWGSSIQVQORSQISQSKVSKHI 2069 Db
2102 RLPAPCPGLEPWAQDPPETRSLELDTLSWISGDLIPSSOEELPFPDLKKCYSVETQ 2161 Qy
2070 RLPAPCPGLEPWAQDPPETRSLELDTLSWISGDLIPSSOEELPFPDLKKCYSVETQ 2129 Db
2162 SCRRRPGFGLDQRRHSIAVCLDSGQPLCPSPSSLGQPLGPGSPKPKKLSPSPSIS 2221 Qy
2130 SCRRRPGFGLDQRRHSIAVCLDSGQPLCPSPSSLGQPLGPGSPKPKKLSPSPSIS 2189 Db
2222 IDPPEQSGRPPCSPGVCLRRAPASDSDKPSVSSPLDSTAASPKKOTLSLSGLSSDP 2281 Qy
2190 IDPPEQSGRPPCSPGVCLRRAPASDSDKPSVSSPLDSTAASPKKOTLSLSGLSSDP 2249 Db
2282 TDMDP 2286 Qy
2250 TDMDP 2254 Db

RESULT 2

T15838
hypothetical protein C54D2.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C:Accession: T15838
R:Minx, P.
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1657 <MIN>
C:Cross-references: EMBL:U37548; NTD:g1017804; PID:g1017809; PIDN:AAA79201.1; CESP:C54D2.5
A:Gene: CESP:C54D2.5
A:Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; 334/2; 370/2; 439/3; 470/3; 511/3
C:Superfamily: sodium channel protein

Query Match	29.5%;	Score 3553;	DB 2;	Length 1657;
Best Local Similarity	42.2%;	Pred. No. 1.3e-217;		
Matches 800;	Conservative 234;	Mismatches 436;	Indels 426;	Gaps 42;
QY	66	AGSTKDPG-----SADSEAGLDPYALAPVVFYLSQDSRPSWCLRTVCN	112	
Db	88	ASSSEASPSRWGRQIEWGNEEQIEESE-LPYGFABPALRCFCYQARPPRKALQWMS	146	
QY	113	PMFERVSLVILNLCVTLGMPRPCEB-IACDSQRCRILQAEDDFIAPFAVMVVMVAL	171	
Db	147	PMFDRIITWAVIMNCVTLGMVAPCEBGGDDCYRCQILDOIIDNCIFYFAFEMVKTAL	206	
QY	172	GIFGKKYIGDTWNBLDFFIIVIAGLMYSLDIQ--NVFSFASVTRVRLRLRAINEVPS	228	
Db	207	GFYGPAAVSDTNRLDFFIVMAGIAEFVLYLGGNINLTARTVRLPLRAVNRIPS	266	
QY	229	MRILVTLTLLDTLPMIGNVLLLCFFVFFFIIGVGVQLWAGLLNRNCF--LPENFS----	281	
Db	267	MRILVNLTLTLLPMIGNVLLLCFFVFFFIIGVGVQLWAGLLNRNCLNPKTISENQAL	326	
QY	282	PLSVLDPEYYOTENEDESPFICSPRENGMRSCRSVPTLRGEGGGGPPCSLDIETYNSSS	341	
Db	327	FNNVKLTFRFYIPE-DTSLLEYICSPDANGLHTCSNLPYTVD---GVKCLNTLDEYDKVT	382	
QY	342	NTTCVNNQYTYNCSAG-----EHNPFKGINFDMIGYAWIAIFOVIT	384	
Db	383	NDSCINNNIYYNECOVNIYPSLMTIAISCFIKWQRPFGSVSFDNIGFAWIAIFLVIS	442	
QY	385	LEGWVDIMYFMDAHSFNFYIFILLIIVGSFFMINICLVVIATQPSETHKQESQLMRQE	444	
Db	443	LEGWTDIMYVQDHAHSFNNYIFVILLIVIGAFFMINICLVVIATQFAETKRTERMLQE	502	
QY	445	RVRELSNASTLASPSPEG-----SCVEELIKYLVILRKAAARLAQVSAIGVRAG	495	
Db	503	RKMILLNRDSISCTSEIGGASKEEGTVAAVFRFIGHTFRRTKRAAKKYTAY-----	557	
QY	496	LLSFSVARSGQEPQPSGCTSRHRLRSVHHLVHHHHHHHHYHLGNTLRVPRASPEIOD	555	
Db	558	-----MEERAERKSSERQQRKSKL-----DDMATLSRIEKAED	592	
QY	556	RDANGSRRLMLPPSTPTSGGPPRGASVHSFYHADCHLEVPRCAPPQPPRCFSEASGRT	615	
Db	593	EE-----DETTITRENGDDQIEQN-----	611	
QY	616	VGSGKVYPTVHTSPPEILKDKALVEVAPSGPPTLTSENIIPGPSSMHKLELTQSTGA	675	
Db	612	-GDGVIRKRVKIEEPKI-----	628	
QY	676	CHSCKTISPCSKADGACGPDSCPYCARTGAGEPESADHVPDSDSEAVYEFTQAOHS	735	
Db	629	-----KIGNGNSNGPHYKSSDSEES-----DEDGEED	656	
QY	736	DLRDPHSRRRQRSIGDAPBSPSVIAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGI	795	
Db	657	QVYDGEBAKK-----STPSKL--WW--FREKIQKFVICDFTRGILVAILVNTLSMGV	706	
QY	796	EYHEQPEELTNALIEINIVFTSLFALEMLLKLVVPGVGIKNPNYNIIDGVIVIVISWEI	855	
Db	707	EYHQEQPEILTVILEYNSLFTALFALEMLLKLIASGLFGYLDAGNFDGGIVALSVEL	766	
QY	856	VGOQGGGLSVLRTFRIMRVKLVRFLPALQROLVVMKMTMNVATFCMLLMFIIFISIL	915	
Db	767	FOBKGGGLSVLRTFRLLRIKLVRFPALRYQLVVMRLTMDNVTVFFGLVLVFIIFSIL	826	
QY	916	GMLHFCCKEASERD---GDTLP--DRKNPDSLIIWAVTVFQILTQEDWNKYLYNGMASTS	970	
Db	827	GMLHFCCKFCVKEEKFGLGAKKCKERKNFDTLIWLIIIVFQILTQEDWNKVLFNMGMAQTN	886	
QY	971	SWAALFYIALMTFGNVYVLFNLVAILVGVGFQAGDATKSESEPPFSPVSDGDRKKRL	1030	
Db	887	PWAALFYVALMTFGNVYVLFNLVAILVGVGFQSEERKQLEADKARKQAVDEERKREL	946	

RESULT 3
T31092

probable voltage-gated sodium channel - Aiptasia pallida
C:Species: Aiptasia pallida
C:Date: 02-Sep-2000 #sequence
C:Accession: T31092
R:White, G.B.; Pfaehl, A.; Haddock, S.; Lamers, S.; Green,
submitted to the EMBL data Library, January 1998
A:Description: Structure of a putative sodium channel from
A:Reference number: Z20975
A:Accession: T31092
A:Status: preliminary; translated from GB/EMBL/DDAT

A;Molecule type: mRNA	
A;Residues: 1-1810 <WHI>	
A;Cross-references: UNIPROT:O44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AAB9	
C;Genetics:	
C;Superfamily: sodium channel protein	
Query Match 14.3%; Score 1720.5; DB 2; Length 1810;	
Best Local Similarity 25.8%; Pred. No. 6.2e-101;	
Matches 509; Conservative 342; Mismatches 694; Indels 429; Gaps 65;	
QY 110 VCNFWERVMVILLNCVTIGMPCEDIACDSQRCILQAFDFIF-APEAVEMVVKM 168	
DB 110 ITNQEFERFILLTIIVNCIFLAL-----RDPEQBPYFAAIYTFEMLKI 155	
QY 169 VAIG-IFGKKCVGLGTNRLOPFIIVIAGMLEYSLDONVSFAVRTVLRPLRAINVP 227	
DB 156 IAKGLVMEYAYLRDPKWLDFVVILGVTLVPNVANL--SGIRIFVLRALRTISAVE 213	
QY 228 SMRLVTLTLLDPLMGNVLLLCFFVFIPIGVQLWAGLIRNRCFIPENFSLPSVDL 287	
DB 214 GLKTVNALLSKMKLSVDLIITTFELCVFALVGMQLFVGSURNKCVLKPPIITDIDS 273	
QY 288 ----PPYQTEDEDESPFCSPRENGMESCVRPTLRGEGGGPPCSDIYETYNSSNT 343	
DB 274 FVTNESHVWHPTDTPITC-----GNSTSGCEPLNY-----306	
QY 344 TCVNWNYNTNCSAGBNPKGAINFDNIGYAMIAIFQVITLEGWVDIMFYMDAHSFYN 403	
DB 307 TCL-----ANIG-NNENYGYTNLDNFGWAVITAFQVLTLDYENVNYVLLSMGMY 357	
QY 404 FIYFILLIIVGFFMNLCLVIAIOTFSETKQRESQIMREQVRFLSNASTLASTSEPGS 463	
DB 358 IFYEFMVIFGFSYLLNLAVAVSY----QOEVLALQDRENYNNKLGVASLYSFGH 412	
QY 464 CYBELLYVILRKAARLAQVSRAGVRLG-LSSPVARSQEPQPSGSCSTRSHRLS 522	
DB 413 C-----VFKLNRNSKSTKSLASKCKMSFCVPCISGKQEHNG-----453	
QY 523 VHLVHHHHHHHHYHLNGTLRVPRASPE---IQDRDANGSRRLMLPPDPTTPPGGPP 579	
DB 454 ----HASDNESHASTG-GTIRVDSTAIEMKMLNDKNEVRTNGHSLPEPKT-----499	
QY 580 RGAESVHSFVHADCHLEPVRCQAPPCPSEASGRVGSKVYPTVHTSPPEILKDAL 639	
DB 500 ----SSFP-----SVSDN-----SIH-----IRNSS 518	
QY 640 VYVAPSGPPTLTSF--NIPPGFPSSMHKLETQSTGACHSSCKISGPCSKADSGACPD 697	
DB 519 TEVMPQ-----TSKFDNI-----LTKILDVKS-----SFLKLSAISEQSS-----555	
QY 698 SCPYCARTGAGEPESADHVMPDSDSEAVYFTQDAQHSILDRPHRRRQRSIGPDAPSS 757	
DB 556 -----TDGVNNEININQPKSVSFIARV-----LTPRGLARQSTSGSATHKT 601	
QY 758 VL---AFWRICDTFRKIVDSKYFGRGIMTALVNTLSMGLEYHQPELTNALEISNIV 814	
DB 602 ITKQDTKWNIRRMISKIVLHGMDTFTFTCMVNTLFLSLEYHNMSNYMLVEIGNKV 661	
QY 815 FTSIFALEMLLKLAVYGPFGYIKNPYNIFDGVIVISVWE-----IVGQQGGSLVLRTF 869	
DB 662 FTMVFLLEMLIKITAFGPKGYIKSEWNIFDGFIVISVMDLVMLVELLDHSDGLSVLRTF 721	
QY 870 RLMLVKLVRLPALQROLQVLVMTQNVATFCLMLLFIPIFSLGMHLFGCKFASERD 929	
DB 722 LLRVVFKLAQSQWQTMNMLLSIARSVQGLNLTIVLGIYVYMLAVGVQLFDQYTTKNF 781	
QY 930 GDTLPDRKNFUSLLWAVTVQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLF 989	
DB 782 NGDVP-RWNFTDFWHSFMMIFKVLGCE-WIEPLXDCMRASISWATLFTLIVIGNFLV 839	
QY 990 NLLVAILVEGFOAEG---DATKSESEPDPFSEVDGDRKRLALVALGEHAELRKS-- 1044	

RESULT 4
A42566

DB 840 NLFIALLLNAPARESELEQEAQKTKTKPSKFAQGV-----SKLSR-ALRFRSTVSKITQ 891	
QY 1045 LLPPLIHTAATPMWHPKSSSTGVGEALGSGSRRTSSGSAEPCAAHHEMKCPSPARSSP 1104	
DB 892 VLPTRVHD-----GENATGDK-----APTQNGL 917	
QY 1105 HSPMSAASSWTSRRSNSRSLGRAPSLKRRSPSGE-----RRSLSGEQSSQDEESSE 1158	
DB 918 ESKTSDSAISTSSNASNAMISAVTAFOQGNKKGKLNDRDTFRRLSLAIE-----965	
QY 1159 EDRASPAGSDHRRHGSLSEREAKSSFDLPDTLQVPLHRTASGRSSASHEQDCNGKSASGR 1218	
DB 966 -----TANSNTSNTNLAMAASST-----SIIGR 989	
QY 1219 LARTLRDTPDQDGDNDNDEGNLSKGERIQAWVRSLRPACCRERDSWAGYI-FFPQSRFR 1277	
DB 990 -----QDHGTSOPDPPTMEVDECCPWCNMKMTCCGICITR--WTASDGYRSWNL 1037	
QY 1278 LLCHRIITHKDFDVVLVIIIFLNCITIAIE-----RPKIDPHSAERIFLTLSNFIYAV 1331	
DB 1038 LAVKKEVBEHYFEWTLITAIIMASSIALTFEDINLPSRKL-----KEYLQVLTNFFAVT 1091	
QY 1332 FLAEMTVKVVVALGWCFCGEAYLRSSNVNLDGLLVLISVIDILVMSVDSGTK--ILGMLR 1389	
DB 1092 FSIEFLLKVLGL-----GVVSFRNCWCLDVLIIVFPV-----SSVIADSSNODSSLSLR 1143	
QY 1390 VLRLRLTLRLPLRVISRAQGLKLVLTMLSSLPKIPNIVVICCAPIIFIGILGVLPKGF 1449	
DB 1144 SLRTLRALPLRAISRWEGRVVVNSLLFAIPGIGNVLVCMVFWLIFSINGVQFEGGR 1203	
QY 1450 FVQCGEDTRN-----ITKSDCAEASVYWRHKYMFNDLQALMSLFLVLASQGVWDIMY 1504	
DB 1204 FKCVDNKNERLPISIVQNRSECIQGYRWNSDINFDNSLNGFMALFOVATEGMEVWR 1263	
QY 1505 DGLDAGVQDQOPIIMHNPMWLLYFISLILVAFVFLNMFVVVVENFHKCRQHEB-----1560	
DB 1264 DAVIDAREVQDSQSDGVNFSAYAYFVVFIIVGVSFTLNLFIGVIDFNRLKKYQDFGAL 1323	
QY 1561 ----EAPRREERKRLRLEKRSKEKQMAEACKPYYSYD-----SRPLLVLHLCSTHYL 1613	
DB 1324 DVLLTSPQRAWFTIRKAAATKPKKVISRSPENSEMAWLEFDVIHSSRFETLI-----1374	
QY 1614 DLPITGVIGLVNVTMAMEHYQQOILDEALKICNVYFTVIEFVESYFKLVAFAPRFFQD 1673	
DB 1375 -MEF---ICNLILWMIQHYGQKPAEQALMIINLFTGLTLEALIRVLRL-HYFRE 1429	
QY 1674 RWNQDLATVLLSIMGITLEEIEVNLSLPINPTIIRIMRVIRIARVLKLLKMAVGMALL 1733	
DB 1430 PMNVDFVIVVLSILGILIEHLEYELFITPSPF---VARVFRIGRLRFFYKGAIRRL 1486	
QY 1734 HTVQALPQVGNLGLLFLMLFFIFAALGVLFGLDECEHPCEGLGRHATERNFGWAF 1793	
DB 1487 FALIISLIPALLNIGALLFLTMFIYAIIGMSSFGYVK-----KTGALDSVVNFETFGNSML 1541	
QY 1794 TLPFRVSTGDNWNGIMKD---PSRDCOE-----STCVNTVSIPIYFVSFVLTAQFVLVN 1844	
DB 1542 LLFRLSTAGNDVNLKPLIKPPDCDKKUMCIPNGNCSTFWLAVVYFTTILFTFLIIN 1601	
QY 1845 VVIATVLMKHEESNKEAKEAEAEAELEEMKTLSPQHPSPLOGSPFLWPGEVGNSTDSP 1904	
DB 1602 MYTIIILNLSQAH-EQEEVGVTDLDMFY-----YHWERFD-----1638	
QY 1905 KPGAPHTTAHGAASGF--SLEHTVMPHPBE-----VVPVLGPDLLTVKRGVSRTH 1955	
DB 1639 -PGATQYIPH-SALSDFDVGLDHLRIPQPNKFACIMNLNIPKOG-----DRVH 1685	
QY 1956 SLFNDSYMCRN--GSTAERSLGHGRWGLPKAQSILSVHSQPADTSCIIQLPK 2007	
DB 1686 CFVNVQALVRVLGDIEDGLG-----SSSVAYTLMKSMXEQHCISTFPK 1730	

omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively spliced)
 C:Species: Homo sapiens (man)
 C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
 C:Accession: A42566
 R:Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McC
 Science 257, 389-395, 1992
 A:Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type
 A:Reference number: A42566; PMID:92335886; PMID:1321501
 A:Accession: A42566
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-2339 <WIL>
 A:Experimental source: IMR32, hippocampus
 A>Note: sequence extracted from NCBI backbone (NCBIP:109168)
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.9%; Score 1676; DB 2; Length 2339;
 Best Local Similarity 24.0%; Pred. No. 6e-98;
 Matches 638; Conservative 364; Mismatches 827; Indels 824; Gaps 88;

QY 59 PPGAGAGAGSTKDPGSDADSEAGLPYPALAPV-----VFYLSQDPRPSWCLRT 109
 DB 32 PPGGLOPQGVLYKQSIQAQARTWALNPVKNQCTVNSLSEVFSDDNVRKYAKRI 91
 QY 110 VCNPFERVSMLVLLNCVTLMFRPCEDIAQDSQRILQAFDD---FIFAFAVEMV 166
 DB 92 TEWPFPEYMIATIANCIVLAL-----EQHLPDGDKTPMSERLDDTEYFIFGICFEAGI 147
 QY 167 KWAALG-IFGKCVLGDWNRDLDFEIVAGLEVY---LDLQNVSFSAVRTVRLPRA 222
 DB 148 KIALGFVFKGSLRNQWNVDFVVLGTLAGTAGTDFDLR---TLRAVRVLRPLK 202
 QY 223 INRVPSMRILLTLTLPLMGNVLLLCFFVFFIGVGVOLMAGLLNRCLFENSLP 282
 DB 203 VSGIPSLQVVLKSMKAVPLQGLLFFALMFAIGLEFYMGKFKACF-----P 255
 QY 283 LSVLDPEYYQTENEDEFFICQSPRENGMRSCRSVPTLRGGGGPPCSDLYETNGSSN 342
 DB 256 NSTDAEPV-----GDFPCQKEAPARLCEGD 280
 QY 343 TTCVNNQYVYVNCAGEHNPFGKAINFDNICYAMIAIPOVITLEGWVDIMFYVMD-AHSF 401
 DB 281 TEC---REYVP-----GNFGITNFDNLIFAILTVFQCITWEGWTDILYNTDAAGT 330
 QY 402 YNFIYFILLIIVGSFMINCLVVIATQFSETKQES-----QLMEQQRVFLSNASTL 455
 DB 331 WNWLYFPLIIIGSFMLNLVLGSLGFEKAKERVENRRAFLKLRQOQIE----- 382
 QY 456 ASFSEPGSCVEELLKYLVIYLRKAARLAQVSRAGLSSPVARSQBPQPSGSC 515
 DB 383 -----RELNGYLEWIFKAEVMEVLABED-----RNAEKSPLDLVK 417
 QY 516 RSHRRLSVHLLVHHHHHHHHHGLNGTLVPRASPEIQDRDANGSRRLMLPPSTPTPS 575
 DB 418 RAATKSRNDLIH-----AEEGEDRFAD----- 440
 QY 576 GGPPRGAESVHGFYHADCHLEPVRCAOPPCPSASGRVVGSKVYPTVHTSPPEILK 635
 DB 441 ----- 440
 QY 636 DXALVEVAPSGPPTLTSFNIPGPFSMHKLESTQACHSSCKISSPCSKADSGACG 695
 DB 441 -----LCAVGSPPARAS----- 452
 QY 696 PDSCPCYARTGAGEPESADHVPDSDSEAVYFTQDAQHSDLRDPHRRQRSLGPDAP 755
 DB 453 -----LKGKTESSYF-----RRKE----- 469
 QY 756 SSVLAFWRLLCDTRKIVDSKYFGRGIMAILVNTLSMGIEYHQEPLEETNALEISNIVF 815
 DB 470 --MERFF-----IRRMWKAQSFYVVLVCVAINTLCVANVHYNQPRRTTTLTYFAEFVF 521
 QY 816 TSLFALEMLLKLVLVGPFGYIKPNYINFDGVIWISVMEIVG---QQGG--GLSVLRTR 870

DB 522 LGLEFTEMSLKYGJGPRSYFRSSNCFDFGIVGVSFEVWAAIKPGSGFISVLRLR 581
 QY 871 LMRVLKLVRFALPALQOLVVLMTKTDNVATFCMLMLFIFISILGMHLFGCKFASERDG 930
 DB 582 LURIFKVKYWSLNLVSVLSNKSIIISLLFLFVIFVALLGMQLFGGQFNQDET 641
 QY 931 DTLPRKNPDSLLMAIVTVFQILTQEDMNKVLNMG-----ASTSSWAAVFIATMTFCN 985
 DB 642 PT---TNFDTPPAAILTVFQILTGEDWNAVWYHGIESGGVSKGMFSSFYIVLTFGN 997
 QY 986 YVLFNLVAILVEGQAEGDATKSEBDFPSPVDGDRKKRLALVALGSHAEIRKSL 1045
 DB 698 YTLNVFLAIAVDNLANAQELTKDEEMEEAA-----NOKLALOKAVEAEV--SP 746
 QY 1046 LPPLIHTAATPMSPHKSSSTGVGBA----- 1071
 DB 747 MSAANISIAARQNSAKARSVWEQASQIRLQNLASCEALYSEMDPEERLRFATRHLR 806
 QY 1072 -----LGSGRRTSSSGSAEPGAA-----HH-----EMKCP----- 1097
 DB 807 PMDKTHLDRPLVWELGRDARGPVGGKARPEAAEAPGVDPPRRHHRDOKTPAAGDQ 866
 QY 1098 -----PSARSS-----PHSPWSAASWTSRRSRNSLGRAPSLKRRSPSGERSL 1142
 DB 867 DRAPKAAESGEPGARBEPRPHRSHSGKEAA--GPPEARSEGRGP-----GPEGRRHH 919
 QY 1143 LSGGQESQDDE-----ESSEDRASPAGSDHHRGSLE-----REAKSSFDLPDL 1189
 DB 920 RRGSPSEAAERPRHRAHRHQDESKCAGAKGERARHRRGPPRAGPREAESG----- 972
 QY 1190 QVPG-LHRTASGRSSASE--HQDCNGKSASGLA-----RTLRTDDPOLDDGDDNDE 1238
 DB 973 EEPARRHRAHKAQPAHEAVEKETTEKEATEKEAIVEADKEKELRNHQPREPCDLETS 1032
 QY 1239 GNLSKGERIQAVRSRLPACRRER-----DSW----- 1265
 DB 1033 GTVTGVP-----MHTLPSTCLOKVEQPEDADNORNVTRMGSPQDPNTIVHIPVMLTG 1086
 QY 1266 -----SAYIFPQSRFLLCHRI 1283
 DB 1087 PLGEATVVPVSGNVDLSQAQKEVADVWRSGPRPIVPSNMFCLSPNLLRRFCHI 1146
 QY 1284 ITHMFDHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNVIPTAVFLAEMTVKVAL 1343
 DB 1147 VTRVFEVILVIALSSIALAAEDP-VRTDSPPNNALKYLDVIFTGVTFEVMVIMIDL 1205
 QY 1344 GWCFGEQAVLRSSNVLDGLLVLSVIDILVSV--SDSGTKILGMLRVLRLRLRPLRV 1402
 DB 1206 GLLHHPGAYFRDLWNILD---FIVVSGALVAFAPSGSKGDKINTIKSLRVLRLPLKT 1261
 QY 1403 ISRAQGLKLVETLMSLKPIGNIVVICCAFFIIFGILGVOLPKGKFFVCGE-----D 1456
 DB 1262 IKRLPKLKAIVFCVNSLKNVNLIVMLFPIFAVIAVQLFKGKFFCTDESKELED 1321
 QY 1457 TRN--ITNKSDCAEASYR-WVRHKYNFDNLGALMSLFLVASKDQGVNDIMYDGLDVGVD 1513
 DB 1322 CRGGVLDYEKEVEAQPRQWKYVDHYDNVALLTLFTVSTGEGPWLKHSVDATYEE 1381
 QY 1514 QOPIMNHNPMWLLYIFISFLLIVAFVFLVMFVGVVVENFHKHQHQBEEBARREKRLER 1573
 DB 1382 QQSPGMYRMEUSIFVYVVFVFPFVFVFIIVFALIIITF-----QBQDKVNSE---CS 1431
 QY 1574 LEKRSRSEKQMAEAOCKPYYSYSR--FRLAVHLCTSHYLDLFTITGVIGLVNVTNAME 1631
 DB 1432 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKWTFTVVSPPFEYFIMAMIALNTVVLMMK 1491
 QY 1632 HYQQOILDEALKICNYIFTVIFVESVEKLVAFAPRRFFODRWNLQDLAIVLLSIMGIT 1691
 DB 1492 FYDAPYVELMLKCLINIVFTSMFSECVLKIIAFGLVNYFRDAMNVDFVTVVLSITDIL 1551
 QY 1692 LEEIE-----VNLSLPINPTIIRINRVLRLVRLKLLQKAVGMRLALLHTVMOALPQVGNL 1746

[illegible]

RESULT 5

S29236

calcium channel protein BII-1, brain - rabbit

C:Species: *Oryctolagus cuniculus* (domestic rabbit)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S29236

R:Niidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.

FEB8 Lett. 308, 7-13, 1992

A:Title: Molecular cloning and characterization of a novel calcium channel from rabbit

A:Reference number: S29236; MUID:92354772; PMID:1379552

A:Status: preliminary

A:Accession: S29236

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-2259 <NII>

A:Cross-references: UNIPROT-Q02343; EMBL:X67855; NID:g1472; PIDN:CAA48040.1; PID:g1473

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C:Keywords: transmembrane protein

[illegible]

RESULT 6

RECEIVED
C54972

voltage-dependent calcium channel $\alpha 1E$ - mouse
C; Species: Mus musculus (house mouse)

C;Date: 12-Apr-1995 #sequence revision 12-Apr-1995 #text change 09-Jul-2004

C;Accession: C54972
#sequence_revision 12-Apr-1995 #text_change 09-Jul-2004

R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.: phillips

J. Biol. Chem. 269, 22347-22357, 1994

A;Title: Structure and functional characterization of neuronal alpha-1E cal

A;Reference number: A54972; MUID:94350992; PMID:8071363

A;Accession: C54972

A; Status: preliminary; nucleic acid sequence not shown; not compared with c

A;Molecule type: mRNA

A;Residues: 1-2272 <WIL>

A; Cross-references: UNIPROT:Q61290; GB:L29346; NID:g522330; PIDN:AAA59206.1

A; Note: authors translated the codon AGG for residue 788 as Lys, and CCT for

C;superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match

Query Match	Score	DB 2;	Length
Best Local Similarity	13.7%	Score 1653.5;	DB 2; Length 2272;
Best Local Similarity	23.4%	pred No 1; 50	

Best local similarity 23.4%; pred. No. 1.5e-96;
Matches 596: Conservative 393. Mismatched 203.

Matches 396; Conservative 392; Mismatches 835; Indels 721; Gaps

Qy 73 PGSADSEA-----EGLPYPATAPVV-----

*J TGGADSCA-----EGLPIPALAPVV-----FFY
||| ||| :: | |
||| : |

Db 13 PGSGDSDOSRNRROGTVPASGPAAYKOSKAOBPTWALYNPTBIBONCEWMBCTDT

.. :0000000000QSKNRQGIFVFASGFAAHKQSKAQRARJMALYNBIPVRQNCFIVNRSLEI

QY 96 LSQDSRPRSWCLRTVCNPWFERVSMVLVLLNCVTLGMR--PCEDIACDSORCPRIQAE

[illegible]

Db 73 FGEDNIVRKYAKKLIDWPPFEYMI L A T I I A N C I V L A E O H L P E D D K T P M S R R --- I E K T F E

[illegible]

QY 154 DFIFAFVAVEMVKMVALG-IFGKKCYLGDTWNRDLFFIVIAGMLEYSLDLON--VSFSA

[illegible]

Db
130 PYFIGFCFEAGIKIVALGFIHFKGSLRNGWNVMDFIVLSGILATAGTHFNTHVDLRA 1

Q. 1. What is the name of the person who is the author of the book "The Great Gatsby"?

QY
211 VRTVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLCCFFVFFIFGIVGVQLWAGLLR 2

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db 190 LRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLFFAILMFAIIGLEFYSGKLH 2

Qv 371 NDCET DENIED BY CIVIC ENGINEERING

271 NRCFLPENFSLPLSVDLEPYQYQTENEDESPFICQPRENGMRSCRSVPTLRGEGGGPPC 3

250 PAGE NO. 11

250 RACFMNN-----SGILEGF-----DPPHPC-----GVQGC 2

Db 2130 LSYSSLMRHTGIGSPDPGSE-----GGSPIASQALSNASACLTESSNSLHPQOG 2179

QY 2228 QGSRPP---CSPGVCLRRRAPASD 2248

Db 2180 QHPSPQHYISEPYLALHEDHASD 2203

RESULT 7

T43262

calcium channel alpha-1 chain, L-type - Stylophora pistillata

C:Species: Stylophora pistillata

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T43262

R:Zoccola, D.; Tambutte, E.; Senegas-Balas, F.; Michiels, J.F.; Failla, J.P.; Jaubert, J.

Gene 227, 157-167, 1999

A:Title: Cloning of a calcium channel alpha subunit from the reef-building coral, Stylophora pistillata

A:Reference number: Z22375; MUID:99148007; PMID:10023047

A:Accession: T43262

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1891 <ZOC>

A:Cross-references: UNIPROT:O97017; EMBL:U64465; NID:G4204977; PID:G4204978; PIDN:AAD114

C:Genetics: CACHL

A:Gene: CACHL

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.7%; Score 1652.5; DB 2; Length 1891;

Best Local Similarity 24.8%; Pred. No. 1.4e-96;

Matches 523; Conservative 331; Mismatches 623; Indels 633; Gaps 60;

QY 115 PERVSMVLILNCVTLMGFRCEDIADCSQRILQAFDDFIF-AFFAVEMVVRKVALG- 172

Db 83 FDVMILITIFANCAALAAFEPLPE--KDSSEINDNLEVAEYVFLAVFTMEAVLXIAYGF 140

QY 173 IFGKKCYLGDWNRDLDFEVIAG---MLEYSLDLQNVSAVTVRLRLRAINRVP 228

Db 141 LFHPGALRNGWNLDFVIVVGUATILVATLSSGSPDKALRAFLRLVRLVSGVPS 200

QY 229 MRILVTLLDPLMLGNVLLCFVFFIFGIVGVLWAGLRLNRCFLPENFSLPLVDLE 288

Db 201 LQVNLNIIKALPLFHIALLVFVVIYAIIGVELFWGLHKTCT--DNVTGAESPE-E 257

QY 289 PYYQTNEDESFPICSPRENGMRSCSVPTLRGEGGPPCLSDYETYNSSNTTCCVN 348

Db 258 PH-----PCS-----SGSSGFQCDKA 273

QY 349 NQYTNCSAGEHNPFGAINFDNIGVAMIAIQQVITLGHVDMYFMDA-HSFYNIYF 407

Db 274 AGQV--CEGWKGNHGTNFDNIGLACMTVFOCITLEGWTDVLYWINDAVGNSWPVYF 331

QY 408 ILLIIVGSPFMNLCVLIATQFSETKQR-----ESQLMREQR-----VRELSNAS 453

Db 332 VTLLIIGSPFVLNLVLGSLGSEFAKEKARRQKSGEFQKREKQVEDAYNGYLDWITQAE 391

QY 454 TLASFEPSCVEELLKYLVIYLRKAARLIAQVRAIGVRAGLSSFPVARSQEPFSGS 513

Db 392 DIEGDESSSGDES-----KASK-----TSRQSKRT-----EDIEM 423

QY 514 CTRSHRLSLVHLLVHHHHHHHHHGLNGTLRVPRASPEIQDREANGSRRLMPPPTST 573

Db 424 IDRNERQDSI-----SQDTHY----- 441

QY 574 PSGGPPRGAESVHSFYHADCHLEPVRCAOPPRCPSEASGRTVSGKVPVTVHTSPPI 633

Db 442 ----- 441

QY 634 LKDKALVEAPSGPPTLTSFNIIPGPFSSMKHLLLETQSTGACHSSCKISSPCSKADSGA 693

Db 442 -----GNCHNEKKV----- 450

QY 694 CGPDCFCYARTGAGEBPESADHWPDSDEAVYETQDAQHSDDLDRDPHSRRRQRSLGPD 753

Db 451 -----LKKWHRRQTE----- 461

QY 754 EFSVULAFWRLICDTFRKIVDSKYFGRGMIAIALVNTLSMGIEYHQBELTNALISNI 813

Db 462 -----LRKAVTKQAFYVIVVVVFLNSLTALAHYDQDPLKFLDIANK 506

QY 814 VFTSLFALEMLLKLIVGPGYIKPYNIFDVIVV-----ISVWEIVQQGGGSLVLR 868

Db 507 LFLGIFTIEMIVVMYCYLGHFGYFASLFRFDCLVVWISSLELAI TEALKQPPIGISVLRC 566

QY 869 FLMRVLKLVRLPALQVQLVLMKTDNVATFCMLLMFIFIFISILGMHLPGCKFASER 928

Db 567 IRLLRIPKTVRWSSLSNLVASLNSMRSIAGLLLSLFLMLICLLGMQIFGGKP--NT 624

QY 929 DGDITLPRDRNFDLSLWAIIVVFQILTOEDWNKVLNGMAS-----TSSWAALFYALM 981

Db 625 DDDEIP-RSNFSEFWRALITVFQILTGEDWNAVMDGIRAWMGIGEGGSAITLIFYELV 683

QY 982 TFGNVLENLAVILVEGFGQAEAGDATKSESPDFSPVSDGDDRRKRLALVALGEHAE 1041

Db 684 VGVNILLNVFLAJAVNDLADENLTEMEE-----KKKK-----EKARE 724

QY 1042 RKSLPLPLIHTAATPMWHPKSSSTGVGEALGSGSRRTSSSGSAEPGAHAHEMKCP 1101

Db 725 KEAL-----KMKGSVDSQ-----RIDQGAIVN----- 749

QY 1102 SSPHSPWASAASWTSRRSSRNLSGRAPSLKRRSPSGERRSLLSGEGQESQDEESSBEDR 1161

Db 750 ---HS-----SASRSNVTLDKSTQELHSTG----- 771

QY 1162 ASPAGSDHRRHGSLEREAKSFDLPDITQVPLHRTASGRSSASEHQDCNCKSASGR 1221

Db 772 -----TLNGNGVARTAS-----HDDVEAQS----- 791

QY 1222 TLRTDDPQLDG-----DDNDENGLSKGERIQAWVRSELPAACCHERDSWSAYIFPPOS 1276

Db 792 ---TDISEIVGSKASVNNNESASASSDDID---RAPMP-----PESALFIFSP 839

QY 1277 RLICHRITTHKMDHVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAE 1336

Db 840 RVVCYKIATNTYFVNFILCLIIIVSSILLAAEDP-LNASAKENQVNLVDFYFFSVFTFEI 898

QY 1337 TVKVVALGWCFCGQAVLRSSWNVDGLLVLIIVSVIDILVMSVSDSGTKILGMRLVRL 1396

Db 899 LVFIFSYGLILHKGSCFRSAFNLLDLVWSVVISLR-----TSQFSWRLRLVLR 952

QY 1397 LRLPRVISRAQGLKLVVETLMSLSKPIGNITVWICCAFFIIFGILGVOLFKGKFEVCGED 1456

Db 953 LRLPLRAINRAKGLKHVVQSVFVAVKTIIGNIKLVTMLFQFLFAVIGVQLFGTFFSCNDE- 1011

QY 1457 TRNITKSDCAEASY-----RWVRHKYNFDNLGQALMSLFLVLASKDGV 1500

Db 1012 ---KILTAEEC-QGNYIDFKGPGLSNPWKERERWRHDFNFDVGNAMLTFTVMTFEGWP 1068

QY 1501 DIMYDGLDVGVDQOQPIMNHNPMMLLYFISFLIIVAFVNLVGVVNVNFKHCKROHBE 1560

Db 1069 GILENSIDSTEDVKGNNRNPWVAIYIYIIIAFEMVNI FVGFI VTF----- 1119

QY 1561 BEARRREERLRLRLEKRRSKQMAEACKPYSDYSERFLIVHHLCTSHVLDLFI 1620

Db 1120 -QSEGREEPKGCGLDKNQOCIEFALKAKPLKRYIPENLQPHIWPVVTVSQAFYLI 1178

QY 1621 IGLNVVTWAMEHYQQPQILDEALKICNYITVIFVFPESVFKLVAFARFFQDWMNOLD 1680

Db 1179 IVCNTVWLMVQYQBPPLYTRVLDGNIGTAVFLELCILKLIAPKPKNYFTDRNLPDP 1238

QY 1681 AVTLASIMGITLEETEVNLSLPINFTIIRIMRVLRVARVLKLLKMAVGRALLHTVM--- 1737

Db 1239 IIVGSIIDITMNEVSSEQMFAFG-----FFRLFRALRLVLLNQGSGIKTLTWTFIKSF 1293

QY 1738 QALPOVGNLGLLMLLFFIFALGVELFGDLECDETHCEGLGRHATFRNFGMAELTFLR 1797

Db 1294 QALFPV---ALLIVMFFIYAVIGMQEGRINSD---TAINRNNNFQTFPQSLMVLFR 1347

1798	YSTGNWNGIMK	-----DPSRCDQBSTCVNTVISPDIYFVSEVLTAQFVLVNVVVI	1847
QY		: :	
Db		: :	
1348	SATGENWQOIMLACTHRDDVKDONADQEPSEGLCGDFAYFYVSVYSFCSFLINLFV	1407	
QY		: :	
Db		: :	
1848	AVLMKHEESNKEAEAELEAELKMTLSPPHSPGLSGPFFLWPGVEGVNSTDSKPG	1907	
QY		: :	
Db		: :	
1408	AVIMONFDYLTRD	-----WSLIGPHHL--DEYVVMSEYDPD	1442
QY		: :	
Db		: :	
1908	APHTTAHGAAGSFSLEHPTM	-----VPHPE-----VPVPLGPDLLTVRKSGV	1951
QY		: :	
Db		: :	
1443	AHGCVKHVDIVTVLKRIAPPLGFKFCPHREACKRLVTMMNG	-----LTKDGMVDENATL	1497
QY		: :	
Db		: :	
1952	-----SRTHSLPNDSYMCNCRNSTAERSLGHRCWGLPKAQSGSILSVHSGPADTSCILQL	2005	
QY		: :	
Db		: :	
1498	FGLIRSLNKRPEGKSGIDKANEEVRNIIIRW	-----PKT-SWELLDKVVQSPGVRRDDTVV	1554
QY		: :	
Db		: :	
2006	PK-DVHYLLO	-----PHGAPTWGAIPKLPP-GRSPLAQRPLRRQAA	2045
QY		: :	
Db		: :	
1555	GKFIYAILQYEFRRFKARQKAQNAQNEPHGNSWALQAGLRTLHGLPQLRRRAISGOLG	1614	
QY		: :	
Db		: :	
2046	I-----RTDSLVDQGLSRRDLLSEVS-GPSCPLTRSSSF	-----WGSSSIQVQQ	2089
QY		: :	
Db		: :	
1615	SDDELFLKEDDSQAKHDKGFWSLSAVSVSPRHSFRSASFLSAGFLKXNGSGLETCK	1674	
QY		: :	
Db		: :	
2090	RSGIOQKVK	2099	
QY		: :	
Db		: :	
1675	KSSSMSNLSE	1684	
QY		: :	
Db		: :	
RESULT 8			
S29237			
Calcium channel protein BII-2, brain - rabbit			
C:Species: Oryctolagus cuniculus (domestic rabbit)			
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004			
C:Accession: S29237			
R:Niidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.			
FEBS Lett. 308, 7-13, 1992			
A:Title: Molecular cloning and characterization of a novel calcium channel from rabbit			
A:Reference number: S29236; MUID:92354772; PMID:1379552			
A:Accession: S29237			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-2178 <NII>			
A:Cross-references: UNIPROT.Q02343; EMBL.X67856; NID:g1474; PID:CAA48041.1; PID:g1475			
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain			
C:Keywords: transmembrane protein			
Query Match	13.7%;	Score 1652.5;	DB 2; Length 2178;
Best Local Similarity	23.8%;	Pred. No. 1.7e-96;	
Matches	601;	Conservative 376;	Mismatches 850;
Gaps	699;		
QY	62	GAAGAGTEKDPGGADS--EAEGLPYPALA	-----PV-----91
Db	5	GEAAGRPASEGSDQGNLPGTVFVPSAGSAAAYKQKQARTMALYNPIVPRQNCFT	64
QY	92	---VFFYLSQDSRPSRWCLRTVCMNPFVSMVLINLCVTLGMFR--PCEDIACDSQRC	146
Db	65	VNRSLFIQEDNIVKRYAKKLIDWPPFYMILATIIANCIVLALAEQHLPEDDTKTPMSRR	123
QY	147	RILOAFDFEIAFFAVEMVVMKVALG-LFGKCYLGDTWNRDLDFEIVIAGMLEYSLDLQN	205
Db	124	--LEKTEPYFIFGCFEAGIKIVAGLGFPHKGSYLRGNWVMDPIVVLGSLATAGTHFN	181
QY	206	--VSPSAVTRVRLPLRAINRVPGMRLIVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQ	263
Db	182	THVDLETLRAVRLPLKLVSGIPSLQIVLKSIMKAMVPLLIQILGLLFFAILMFAITGLE	241
QY	264	LMAGLLNRCLFIPENFSLPLVDLEPYQNTENEDSPFICSQPRENGMRSRCSVPTLRGE	323
Db	242	FYSGLKLRACFVNN-----SGVLEGF-----DPPHPC-----	268
QY	324	GGGGPCCSLDYETVNSSTNTTCVNNQVYVNCSEAGHNPFKGAINFONIGYATIAI PQVI	383

QY	1293	VIVIFLNCITIAMBRPKIDPHSABRIETLTLNSNYIFTAVFLAEMTVKVALGWCFGQAY	135
Db	1149	ILVIAAASGIALAEDPVLNTSERNRV-LRYFDYVFTGVFTFMWIKMIDGILLQDGSY	1207
QY	1353	LRSSWNVDGLLVLSVIDI-LVSMVSDSGTKILGMRLVRLRLTLRPLRVISRAOGLKL	1411
Db	1208	FRDLWNILDFVVVGALVAFALANALGTNGKRDIKTKSLRVLRLPLTKELPKLA	1267
QY	1412	VYETIMSSLKPIGNITWICCAFFIIFGLGVQLPKGKFFVC--QGEDTRN-----ITNK	1463
Db	1268	VFDVCVTSKVNFNILIVYKLFMFIAVAVQLPKGKFFYCTDSXSKTKECIGNYVDHE	1327
QY	1464	SDCAEASTR-WYRHKYNPDNLGOALMSLFLVLAASKDGWVIDMYDGLDAVGVDQOIPMHNHP	1522
Db	1328	KNKMEVKGREWKREHFEHYDNIIMALLTLFTYSTGEGWPQVLQHSVDVTEDERGPSRNRM	1387
QY	1523	WMLLYFISLLIIVAFVFNMGVVVENFHKCRHQHEEBEARRREKRLRLEKRRSKE	1582
Db	1388	EMSFYVYVYVVFVFFFNIFVALIITF-----QEQDGKMEE--CSLEKNERACI	1437
QY	1583	KQMAEAOCKPYYSYSR--FRLLVHHLCTSHYDLFITGVIGLVNVTMAEHYQQOQLD	1640
Db	1438	DFAISAKPLTYMPCNRHTFOYRWHFVSPSPFYTIMAIANTVVMKMYASACTYE	1497
QY	1641	BALKICNYIFTVIVFVSFKLVAFAPRRFQDRWNOLDIAIVLLSIMGITLEEIVNLS	1700
Db	1498	LALKYLNIAFTWPSLECVLKVIAFGFVNFVTRDTWNIFDITVIGSTEIVLTDKLVNT	1557
QY	1701	LPINPTIIRIMSVLRIARVLKLMVGMALLHTVMQALPQVGNIGLIFMLFFIFFAAL	1760
Db	1558	TGFNWSFLKUFRA--ARLKLRLQGYTIRILLMTFVQSFKALPYVCLLIAMLFFYAI	1614
QY	1761	GVLEFGDLECD-ETHPCGELGRATPRNCGWAFLLTFRVSTGDNWNGIMKO--PSRDCD-	1816
Db	1615	GMQVFGNIRUDESH---INRHNFRASFGSMLLFRSATGAWOJMLSLCGKGCPE	1670
QY	1817	-----QSTCYNTVISPIYVSVFLTAQFVLNVNVIAMKHLSESNKEAK-----	1862
Db	1671	DTTAPSGQCSERCGTDLAVYVVFSPFFGCSFLMLNLFAVIMDNFEYLTRUSSILGPH	1730
QY	1863	--BEAELEAELE-----LEWKTL-SQPHSPDG-----SPFLWPGEVGVNST	1901
Db	1731	LDFVRVWABYDRAACGRIHYTEMYEMLTMSF---PLGLKRCPSKVAYKRLVMN--	1784
QY	1902	DSPKPGAPHTTAH-----IGAASG-----FSLEHPTMV--PHEE-----	1934
Db	1785	---MPVAEDMTVHTSTLMALIRIATLDIKIAGGADROQLDELOKETIAMIWPLLSQML	1841
QY	1935	---VPVPLGDDLTVRKSGVSRTHSLPNDSYMCRNGSTAESRIGHRGWGLPKPAQSGSILS	1991
Db	1842	DLVLVMPKASD-LTVGKIVAA--MMIMDYKQSKVKKQRRQL-----EEQKNAMP	1889
QY	1992	VHSQPADTSCILQPKDVHYLLQPHCAPTGAIPKLPP-----PGRSPLAQRPLR	2042
Db	1890	QRMEPS-----SLPOEI--IANAKALP--CLPQGPAGLGGRCGCPAMSPLSQPIQL	1938
QY	2043	QAAIRTD-----SLDVQGLSGREDLLSVSGPSCPLTFSSSFW-----GSS	2084
Db	1939	TCMDPADDDQGOEQBSLVVTDPGSMRRSFSTIRD-----KXSSWLEEFMSERSDNT	1993
QY	2085	IQVQSGSGTQS-KVSKHRLPAPCGLEPSWAKOPPETRSSLELDELTSLSGDLPSQ	2143
Db	1994	YKSRRSYHSSLRLSAH-RL-----NSDSGHKSDTHRSG-GRGRGSK	2035
QY	2144	EEPLFPRDLKKCVSTQSCRRPFGWLDEQRHSIAVCLDSGQPLCPSPSSLOGQP	2203
Db	2036	REHLLSADVSRCSSEE---RGAQADWDSPERHPSPSGRQSPSPSGQTGSLSESSIP	2091
QY	2204	LGGPGSRPKKLSPPSISIDPPESQGSRPPC-----SPGVCLRRAPASDKDSVSSPL	2258
Db	2092	SVSDTSTPRQWQPQEEVLLHPHQCGWPCNDRKWMFG---RKGWSEKSHSLPHCGR	2148

QY	2259	DSTAAS	2264
			:
Db	2149	DSTGGA	2154

RESULT 9

S41080
 calcium channel alpha-1 chain - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 07-Oct-1994 #sequence revision
 C;Accession: S41080
 R;Coppola, T.; Waldmann, R.; Borzotto,
 FEBS Lett. 338, 1-5, 1994
 A;Title: Molecular cloning of a murine
 A;Reference number: S41080; MUID:94133
 A;Accession: S41080
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-2288 <COP>
 C;Superfamily: voltage-dependent calcium

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Query Match      13.7%; Score 1650.5; DB 2; Length 2288;
Best Local Similarity 23.8%; Pred No. 2.4e-96;
Matches 632; Conservative 367; Mismatches 783; Indels 875; Gaps 94;

Qy      60  GPGAGAGSTGTEKDPGSADSEAEGLP-----YPALAPV----- 91
      ||| ||| |||
Db      23  GGGAGGAGG-----PGGG-----GLPQGQVLYLKQSTAQARTMALYNFIPVKNCFVTN 72

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QY	60	GPGAGAGSTKDPG	SADSEAGHP	-----	YPALAPV	-----	91
Db	23	GGAGAGAG	-----	PGQG	-----	GLPGQGVLYKQSI	AQARATMALYNPI - PVKQNCFTVN 72
QY	92	-VFFYLSQDSRPS	WCLRTVCNPMFE	RVSMVLILLANCV	ILGMFPFCED	IACDSQRCRIIQ	150
Db	73	RSLFVSEDNVR	KYAKRITWPPF	EYMILATI	IANCIVLAL	-----	EOHLPDGDKTPMSE 128
QY	151	AFDD	-----	FIFAFFAVEMV	KVMVALG-IFGK	KCYLGD	TWNRDLDFEVIAGMLEVS - LDL 203
Db	129	RLDDTEPYG	IFCFEAGIKI	ALGFVFKGS	YLRNGWVMD	PVVLTGIL	TATGTDDEL 188
QY	204	QWVSFAVRV	VRURPAINR	VPSMRIL	VTLLD	TLPMLGNVLL	CFEVFFIFGIVGQV 263
Db	189	R	-----	TLRAVVRPLK	VSGIPSLQVVL	KSIKMAWPL	QIGILLFFAILMFGIIGLE 243
QY	264	LWAGLLNRCP	LPENFSLP	ISVDLEPY	QYOTENEDES	PFICSQPRE	NGMRSRCSVPTLRGE 323
Db	244	FYMGKFHKAC	-----	PNSTDEPY	-----		263
QY	324	GGGGPPCSLOYE	TYNSSNTTC	VNNQYV	TNCSAGEH	NPFKGIN	FDNIGYAWIAIFOVI 383
Db	264	--GDFPCGK	OPPARQCDG	TEC--REYWP	-----	GNFGIT	FDNLFILFAILTVFOCI 311
QY	384	TLQGVDMIFYMD	-AHSFYNFY	IFILLI	VGSGFFMIN	CLVIA	TQFSEYKORES - - - 438
Db	312	TMEGWTILY	NTDAAGT	WNWLYF	PLIIGSFF	MLNLVLG	VSZGFAKERVENRRA 371
QY	439	--QLMRQVR	VFLSNAST	IASFSEPG	SVBEILLKY	VILRKAA	RLLAQVSRAGVRAGL 496
Db	372	FLKURRQQOIE	-----	RELNGYLE	MIFFRAE	EVMLAEED	----- 404
QY	497	LSSPVASG	QEPGSGS	CTRSRHL	RSVHLVHHHH	HHHHHVL	GNLTURVPASPEIQDR 556
Db	405	-----KNAE	KSPDLVKRA	TKSRNDLIH	-----		AEGBDR 437
QY	557	DANGSRRL	MLPPBST	PTSPGPG	PRGAESVH	SFYHAD	CHLEPVRQCAPPCPSEASGRV 616
Db	438	-----					437
QY	617	GSKVPTVHT	SPPEILK	DKALVE	VPASPGP	PTLTSF	NIIPGPFSSMHKLETTQSTGAC 676
Db	438	-----					441
QY	677	HSSCKISS	PCSKAD	SGACG	DFSCP	CARTGAGE	PESADHVNPDSDSEAVYFTQDAQHS 736
Db	442	-----CA	VGSF	FAFAS	-----	LKSGKT	TESSYF - - - 464

QY 737 LRDPHSRRORSGLDPAEPPSVLAFWRLICDTFRKIYDVSKYFGRGIMAILVNTLSMGIE 796
 Db 465 -----RRKEK-----MREFF-----IRKMKAOQSYFVWVLCVVALNTLCVAMV 502
 QY 797 YHEQPEELTNALEISNIVFTSLFALEMLKLVVPGFYIKNPYINIFDGVIVVSVMEIV 856
 Db 503 HYNQFORLTALYFAEFVFLGLFTMSLKYGLGPRSYFRSSFCNCFDGVIVSIEFV 562
 QY 857 GQ-----QGGGLSVIRTEFLMRVLKLVFLPALQRLQVLVIMKTMDNVATFCMLMLFIFI 911
 Db 563 WAAIKPGTSGFGLSVLRLRLRIPKVTYKWSLRLNVVSLNSMKSIISLFLFLFLFVW 622
 QY 912 FSLIGMLHFGCKFASERDGLTLPDRKNFDSLMLWIVTFOILTQDWNKVLNGM----- 966
 Db 623 FALLGMQLFGQPNFQDETPT-----TIFDTFPAALITVFOILTQDWNKVLNGM----- 966
 QY 967 ASTSNAALYFIALMTFGNYVLFNLVAILVEGFOAEGDATKSESEPPFFSPSVDGDGR 1026
 Db 679 VSKGMFSSFYFVLTLFGNYTLNVLFLAIVNDLANAQLFKDBEEMEEAA----- 729
 QY 1027 KRRLALVALGEHAELKSLPLLIHTAATPMHPKSSSTGVGEALGSGSR----- 1077
 Db 730 NKLALQAKVAB-----VSPMSAANTISAAQONSAKARSVWEQASQLRLQNLRASCE 784
 QY 1078 -----RTSSSGAEPGAHH-----EMKCPPSARSSPHSPWSAASS 1113
 Db 785 ALYSEMDPEERLYASTHRVDRMDKTHMDRPLVWEPGRDGLGPGVGSKSPGCTEATESA 844
 QY 1114 WTSRSSRNSLGRAPSLKRRSPGERRSLSGEGQESQDEESSBEDRASP-----A 1165
 Db 845 DLPRHRRHR--DROKTSATAPAG-----GEQDETSTETGPREARPRRSHSKETP 895
 QY 1166 GSD-----HRRGSL-----LRTDDPOLQDDDDND----- 1237
 Db 896 GADTVRCRSRRHRRGSEPEATEREPRCHRAHRAQDSKEGTVPVLVPKGERRARHR 955
 QY 1177 -----REAKSFD-----LPDTLOVGLHETAS-----GRSSASEHDCNG 1212
 Db 956 GPTGPREANNEBETRRHRAHKVPPTLOPP-----EREAEKESNPVEGKETRNHQKPE 1013
 QY 1213 KSASGLRANT-----LRTDDPOLQDDDDND----- 1237
 Db 1014 HCDLEAIVDVGLPMLPSTCLQVDEQPEDADNQNVNTRMGSSQSPDPTTVHVPVLT 1073
 QY 1238 -----EGNL-----SKGR-----IQAWVRSLPACCREDSNAIIFPPQSR 1275
 Db 1074 GPPGETPVVPSGNNWLEQAGEKKEAEADVLRRGPRPIVPS-----SMCLSPNTL 1126
 QY 1276 FRLLCHRIITHKFDHVLVILFNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAR 1335
 Db 1127 FRFCHYIVTMYLEWVILVIALSSALAEADP-VRTDSFRNALIYMDYIIFGVFTCE 1185
 QY 1336 MTVKVWALGCFGEQAYLRSSWNVLDGLLVLSVIDILVSMV-SDSGTKILGMLRLVRL 1394
 Db 1186 MVTKMDLGLLHPGAFRDLNILD-----FIVSGALVAFAPSGSKGDKINTIKSLRLV 1241
 QY 1395 RTLRPLRVISRAQGLKLVWETLMSLKPIGNIVVICCAPIIFIGILQVLFKGFVFCQ 1454
 Db 1242 RVLRLPLTKIKRLKPKFVDSVNSLVNVLNVLVLMFVIFAVIAVQLFKGFVFCYTD 1301
 QY 1455 E-----DTN-----ITNKSDCAEASYR-WVRKYNFNDLGOALMSLFLVLASKDGVMDIMYD 1505
 Db 1302 ESKELEDRCGQYLDYEEKEVEAOPROWKDYFDHYNVNLWALLTLFVSTGEGPWLKH 1361
 QY 1506 GLDVGVDQOPIMNHNPMWMLYFISFLIIVAFFVLNPMVGVNENFKCRHQBEERARR 1565
 Db 1362 SVDATYEEQSPGFRMELSILYVYVFPVFPFVFNIFVALIITF-----QEGQDKVM 1415
 QY 1566 REEKRLRLLEKRRSKESKQMAEACKPYISYR--FELLVHLCTSHYLDLFTGVIGL 1623
 Db 1416 SE-----CSLEKNERACIDFAISAKPLTRYMPQNSQFQYKWTWVSPPPFIFAMIAL 1471
 QY 1624 NVVTWAMEHYQQPOLDEALKICNYIFTVIFVESVFKLVAFARFRFQDRWNQDLAIV 1683

Db 1472 NTVVAMKFDAPYEYELMKCLNIVFTSMFSECIILKIITAFGVNTRFRAWNVDFDTV 1531
 QY 1684 LLSTMGTLTBEIE-----VNLSLPIPNITIRIRVLRARVLRKLLKMAVGMALLHTVMQ 1738
 Db 1532 LGSITDILVTEIAETNNFINLS-----FLRLPRAALIKLRQGYTIRILLTFVQ 1582
 QY 1739 ALPOVGNLGLLMLLFFIFAALGVVELFDLECDTHPECEGLGRHATHFRNMGAEPLTFRV 1798
 Db 1583 SFKALPYVCLLIAMLFYIYAIQMGVFGNSALDDD--TSINRHNNEFTFQAIMLFLRS 1639
 QY 1799 STGNWNGIMKD--PSRDCD--QESCYNTIVISPIYFVSFVLTAQFVLVNVAVLAKH 1853
 Db 1640 ATGEAWHEIMSLCLDNACDPHANASEC-GSDFAFYFVFSFLCSFLMLMLFVAVIMDN 1698
 QY 1854 LEESNKAH-----EEAELEAELE-----LEM-KTSLPQHPSPVIG----- 1887
 Db 1699 FEYLTRDSIILPHILDEFIRWAEYDPAACGRISYNDMEMLKHMSP-----PLGLGKK 1754
 QY 1888 -SPFLPVGVEGVNSTDSPKPGAPHTTAHGAAGSFLSEHPTWVPEVPLGP-DLLT 1945
 Db 1755 PARVAYKELVRMNPISNEDMTVHTSTLMALITALE-----IKLADAWMT 1802
 QY 1946 V-----RKSGVSRTHSLNDSYMCENGSTABERSLGRGWGLPKAQSIL 1990
 Db 1803 VGKVAALMIFDYKQNKTRDQTHQAPG-----GL--SQMGVPS 1840
 QY 1991 SVHSQPADTSCILQPKDVHLLQPHGAPTGAIPKLPPLPPGSPPLAQR---PLRQAATR 2047
 Db 1841 LEHPKAT-----LEQTPAVLRCA-----RVFLRQKSATSLNGGAIQ 1879
 QY 2048 TDSLQVQGLGR-----EDLLSEVSGP-----SCPLTRSSFWGSSSIQVQR 2090
 Db 1880 T-----QESGSRSCPGRRGTQDALYEGRAPLERDHSKEIFVGOS-----GTLVDVQMQ 1930
 QY 2091 S-----GTQS--KVSKHILPA---PCGLEP-----SWA 2115
 Db 1931 NMTLRGPDGDPQGLSESGRAASMLRFLAAETOPAPNASPMKRSISTLAPRDPGTQLCSIV 1990
 QY 2116 KDP-----ETRSLELDT-----LSWISGDLPLSSQEEPLF 2148
 Db 1991 LDRPPSOASHHHHCHRRRDKQKRSLEKGFSLSDPEGAPSTAAAGPLGHEGSTAC 2050
 QY 2149 PRDLKCYSVETQSCRRRFGFWLDEORRHSIAVSC--LDGSGPLRCGPS----- 2197
 Db 2051 RRDKQERGSQB--RRQPSSSSEKQRF---YSCDLRGAGS--PQLMPSLSHSHTSPAAA 2104
 QY 2198 -----SLGGQPL-----GGPSRPPKKLISP-PSIS-----IDPPE 2226
 Db 2105 LEPAPHPQSGSVNGSPLMSTSGAITPGRRRQLPQTPLTFPSITYKTANSPPVFAE 2164
 QY 2227 SQGSRPPCPGP-----VCLRRRAPASD-----SKDPSVSPDLSTAAESPCK 2269
 Db 2165 GQGLFAFSPGLSRGLSEHNALLQKEPLSQPLAPGSRIGSDPYLGORLDEASHTLPE 2224
 QY 2270 DTLSL-----SGLSS 2279
 Db 2225 DTLTFFEAVATNSGRSS 2241

RESULT 10

A47447
 calcium channel protein alpha-1 chain (variant doe-1) - electric ray (Discopyge ommata)
 C:Species: Discopyge ommata
 C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A47447
 R:Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; Tsien, R.W.; Schwarz, T.L.
 Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993
 A:Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray Dis
 A:Reference number: A47447; MUID:93248175; PMID:7683405
 A:Accession: A47447
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA

Db	1714	-PLGLGKCPKSVKAYKLVLMNMPVTEKTVHFT-STLMLGLRTALQIKLARGA-----	1766	QY	283	LSVDLEPYQTENEDESPTCSQPRENMRSCRSVPTLRGEGGGPPCSLDYETYNSSN	342
QY	1928	MVPEPEVPLGPDLLTVKSGVSRTHSL--PNDSYMCNRNGSTAERSLGRGWGLPKAQ	1985	Db	256	NSTDAEPV-----GDFPCGEAPARLCEGD	280
Db	1767	---DKQQLDAELRKEIMTIWPHLSQKTLDLLVPMHTY-----SDLTVG-----	1809	QY	343	TTCVNNQYNTNCAGEHNPFGKAINFDNIGYAWIAIFQVITLLEGWVDIMVFVMD-AHSF	401
QY	1986	SGSILSVHSPADTSCILQLPKDVHYLLQPHGAPTGAIPKLPPEGSPLAQR---PLR	2041	Db	281	TEC-----REYMP-----GNFGITNFDNILFALTTFQCITMEGWTDILYNTDAAGNT	330
Db	1810	AAMIMDYKQSKNKYQKLQEE-----		QY	402	YNYEYFILLIIVGFFMINLCLVVIATQFSETKQES-----QIMREQRVRFUSNASTL	455
QY	2042	QQAIRTDSDLV--QGLSRREDLSEVSGPCLTRSSFWGSGSIQVQORSQISQSVSK	2099	Db	331	WNWLYFIPLIIGGFFMLNLVLGVSGEFAKERERVENRRAFLKLRRQOIE-----	382
Db	1849	PQIISSTKGLPYLQGTGPDVDSSEFT-PLVPLPPVMFOQRTSSQEEHKKQPKELK	1907	QY	456	ASFSEPGSCYBELLYLVILRKAARLAQVSRRAIGVFRAGLLSSPVARSGQPQPSGCT	515
QY	2100	HIRLPAP-----CPGLEPSWAKDPETRRSLEL-----DTLSMISGOLL	2139	Db	383	-----RELNGYLEWIEFKABEVMLEAED-----RNAEKSPLDVIK	417
Db	1908	KIKLEYPHYGHVLPENQGRAVSMRPLEIEGAEDTSPKRSLSLSTFAAHNSNSTWLNESYL	1967	QY	516	RSRRRLSVHHLVHHHHHHHHVHLNGTLRVRPRASPEIQDRDANGSRRLMLPPPSTPTPS	575
QY	2140	PSSOEPLFPRLKKCYVETOSRRRPGFWLDEORRHSIAVSLDQSGPRLCPSSSL	2199	Db	418	RAATKKSNDLIH-----AEGEDREAD-----	440
Db	1968	-----ERAGPELYKRWS-----RRP-----LRP-----PSRSSN	1992	QY	576	GGPPRGAESVHSFYHADCHLEPVRQAPPRCPSSEASGRTVSGSKVYPTVHTSPPEILK	635
QY	2200	GGQPLGGPGSRPKKLSPSISL-----DPESQG-----SRPPCSPGVCLRRRAPAS	2247	Db	441	-----	440
Db	1993	AGSRERG-RSRERKHLSPERSVCTGQCAHPSQHRGLDQRLSRSP-SFGYSHRPREQVN	2050	QY	636	DKALVEVAPSGPPTLTSTFNIPPGPFSSMHKLELTQSTGACHSSCKISPCSKADGACG	695
QY	2248	DKDPSPVSPDLSTAAASPFPKDDTSLSGLSDDP	2281	Db	441	-----	452
Db	2051	SSVS---ESPVSSTGSPKQGRQLPQTPSKP	2081	QY	696	PDSCPCYARTGAGEPESADHYMPDSDSEAVYEFTQDAQHSILDRDPSHRRRQSLGDAEP	755
RESULT 11				Db	453	-----LKSGETESSYF-----RREK-----	469
T45115				QY	756	SSVLAFLRLICDTRKIVDSKYFGRGIMIALVNTLSMGIYHEHOPELTNALEISNIVP	815
N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human				Db	470	-----MFRFF-----IRRMKQAQSYVWVLCVVALNTLCVAMVHQPRRLTTLTYFAEFV	521
C:Species: Homo sapiens (man)				QY	816	TSLEFALEMLKLLVYGPFGYIKNPYINFDGVIWVSVWEIVGQ-----QGGGSLVLTFR	870
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004				Db	522	LGLELTMSLKMVGLGPRSYFSSFCDFGVIVSGVFEVWAAIKPGSFGISVLRAIR	581
C:Accession: T45115				QY	871	LMRVLKVFLPALQQLVVLAKMTDNVATFCMLLMFIFIFISILGHLFGCKFASERDG	930
R:Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McC				Db	582	LLRIFKVTYKWSLRNLVSVLSNSMKSIIISLFLFLFVIVFALLGQWFGGQFNQDET	641
A:Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type				QY	931	DTLPDRKNFDSLIWAIIVTFQILTOEDWNKVLVNGM-----ASTSSWALYIFALMTFPGN	985
A:Reference number: A42566; MUID:92335886; PMID:1321501				Db	642	PT-----TNEDTTPAALTIVFQILTGDNVAMVHGIESQGVSKGMFSSFYFTVLTFGN	697
A:Status: preliminary; translated from GB/EMBL/DBJ				QY	986	YVLFNLLVAILVEGFOAEGDATKSESEPDFFPSVDGDRKKRLALVALGEHAELRKS	1045
A:Residues: 1-2237 <WIL>				Db	698	YTLNVLFLAIVADNLANAQELTKDEMEBEA-----NOKLALQKAEVAEV--SP	746
A:Molecule type: mRNA				QY	1046	LPLLIHTAATPMSPKSSSTGVGEA-----	1071
A:Cross-references: UNIPROT:Q00975; EMBL:M94173; NID:g179759; PIDN:AAA51898.1; PID:g1797				Db	747	MSAANISIAARQONSAKARSVWEORASQLQLNLASCEALYSEMDPEERLRFATTRLR	806
A:Experimental source: cell line IMR32; neuroblastoma				QY	1072	-----LQSGSRRTSSSGAEPGAA-----HH-----EMKCP-----	1097
C:Genetics:				Db	807	PDMKTHLDRLVAVELGRDARGPVGKARPEAAEPGDPVPRRHHHRDKDKTFAAGDQ	866
C:Function:				QY	1098	-----PSARSS-----PHSPMSAASWTSSRSRSLGRAPSLKRRSPSGERRSL	1142
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain				Db	867	DRAEAPKAESGEFGARBERPRPHKSHSKEAA--GPPEARSERGRGP-----GPGGGRHH	919
Query Match 13.68; Score 1640.5; DB 2; Length 2237;				QY	1143	LSGSGQPSQDEE-----ESSEEDRASPGASDRHRGSLF-----REAKSGFDLDTL	1189
Best Local Similarity 23.58; Pred. No. 1e-95;				Db	920	RGSGFEAAAREPRHRAHRHQDPSKCAKAGERRARHGGPRAGPREAESG-----	972
Matches 614; Conservative 350; Mismatches 815; Indels 839; Gaps 82;				QY	1190	QVPG-LHRTASGRSSASE--HQDCNGKASGRLLA-----RTLRTDDQLDQDDNDE	1238
59 PGCGAGAGSTKDPGSDASEAGLPPALAPV-----VFYLSQDSRPRSWCLRT				Db	973	BEPPARRRARRHKAQFAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPHEPCHDLETS	1032
32 PGFGLOPQGRVLYKQSIQARTMALYNPIPVKQNCFTVNRSLFVFSEDNVVRYAKRI							
110 VCNPFERVSMVILLNCVTLGMPFPCDIACQRCILQAFDD---FIFAFVAVMV							
92 TEWPFPEYMIATIANCIVIAL---EQHLPGDKTPTMSERLDDTFYFICICFPA							
167 KVALG-IFEGKCYLGTWNRDLDFIVLAGMLEYS---LDLQNVSFSAVRTVRLPLRA							
148 KIALGFVTHKGYSLRGNWVDFVVLGTILATAGTDFDLR-----TLRAVRVLRPLK							
223 INRVPSKRIIVLLDLTLPMLGNVLLCFVFFIFGIVGVQIWAGLLRNRCFLPENS							
203 VSGTIPSLQWLKSIKMAVPLIQIGLLFFAILPAITGLDFYMGKFKHACF-----							

QY	1239	GNLSKGERIQAWVRSLPACCR	-----DSW-----	1266
Db	1033	GTVTGVP-----MHTLPSTCLOKVEEQEDADNQNRVTRMGSPQDPNTIVHLPVMTG	1086	
QY	1266	-----	-----SAYIFPPQSRFFLLCHRI	1283
Db	1087	PLGEATVVPNGVNDVLESQAEGKEVEADVMRSGRPFIVPYSMFCSPNLRLRRFCHYI	1146	
QY	1284	ITHKMFDRHVLVIIFPLNCITTIAMBRPKIDPHSAERIFLTLSNYIIFTTAVELAEMTVKVAL	1343	
Db	1147	VTMRFEVVLVIAVIALSSIALAEDP-VRTDPSRNNALKYDIYFTGVFTFEMVIMIDL	1205	
QY	1344	GWCGEQAYLRSSNVNDGLLIVLSIVIDILYSMV-SDSGTKILGLMVLRLRLTLRPLRV	1402	
Db	1206	GLLLHPGAIFYRDLNILD-----FTWVSGALVAPAFSGSKGDINTIKSLRVLVRLPLKT	1261	
QY	1403	ISRAQGLKVVETLMSLSKPIGNIVITCCAFFIIFGILGVOLPKGPFVCOGE-----D	1456	
Db	1262	IKRLPKUKAVPDCVNSLKNVLNLIIVYMLFMFIFAVIAVQLFKGKFPFYCTDESKELERD	1322	
QY	1457	TRN--ITNKSDCABASYR-WVRHKYFNPDNLGOALMSLFLVASKDGWVDIMYDGLDAGVVD	1513	
Db	1322	CRGOVLDYEEVEEAQPRQMKYDFHDVNLWALLTLFTVSTGEGMPLVKHSVDATYEE	1381	
QY	1514	QOPTMHNPNMMLLYFISLLELIIVAFVLMFVNVVENPHKROHQEBEERREKRLR	1573	
Db	1382	QGPSGYRMELSIFVYVYFVVFVFFVFNIIVFALIIITF-----QBGDKMWSE-----CS	1431	
QY	1574	LEKKRKEKQMAPOACKPYYSYSR--PRLLVHHLCTSHYLDLFTGVIGLNVVTNAME	1631	
Db	1432	LEKNERACIDFASAKPLTYMPCNQOSFOYKTTWTFVSPPPFEYFIMAMIALNTVVLMMK	1491	
QY	1632	HYOQOQILDALKICNVITFVIFVFESVKLVAFARFRFODRWOLDIAVLLSTMGIT	1691	
Db	1492	FYDAPYEVELMKCLNIVFTSMESMECVLKLIAPGVNFRDAWNVDFVTVGLSGITDIL	1551	
QY	1692	LEETIE-----VNLSPINPTIIRIMVLRIRARVLKLLKMAVGMRALLHTVMQALPQVNL	1746	
Db	1552	VTEIATNPNILNS-----FLRLFAARLILKLROGYTIRILLTWTFVQSPKALPVV	1602	
QY	1747	GLLPMILFFIFAALGVLEGLCEDETHCEGLGRHATFRNFGMAFLTLFRVSTGDNNWG	1806	
Db	1603	CLLIAMLFFIYALIGQVGNIALDDD-----TSINRHNNFRTFLOALMLLFRSATGEAWHE	1659	
QY	1807	IMKD--PSRDCDOE--STCVNTVISPIYFVSFVLTAQFVLNVNVIATVLN-----	1851	
Db	1660	IMLSCLSNQACDQANATEGSDFAFYFVSFIFLCSFLMLNLFVAVIMDNPEYUTRDS	1719	
QY	1852	----KHLEE-----	1856	
Db	1720	ILGPHLHDEFIRYWAEDYPAAACRISYNDMFEMLKMSPPLGLGKKCPARVAYKELVRMN	1779	
QY	1857	-----SNKEAKEAELEABL-----ELEMKTLS--	1879	
Db	1780	MPISNEDMTVHTSTLUMALIRTALEIKIAPAGTKHQHCDALRKEISYVWANLFPQKTLIDL	1839	
QY	1880	-POPHSP--LGSPPF-----LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFLSEHPMTVP	1930	
Db	1840	LVPPHKPDWTVKGVYAALMIDFYKQNKTFDQWQAPGGLSQMGVPSLFP--HPLKAT	1896	
QY	1931	HPEEVPVPL-GBDLLTVRKSGVSRTHSI PNOSYMCNRNGSTABRSILGHRGWLGPKAQSGSI	1989	
Db	1897	LEQTQPAVLRGARVFLRQKSST-----SLNNGGAIQNESGIKESV--SWCTQRTQDA--	1947	
QY	1990	LSVHSPQADTSCILQPKDVHVLLOPHCAPTWGATPKLPPGRSEFLAQPLRROQAIRTD	2049	
Db	1948	-----PHEA-----RPPLERGHGSTEIPVGRSGALAVD	1974	
QY	2050	-----SLDVQGLGRBDLLSEVSGPSCPLTRSSSEFWGSSIQVQORSG	2092	
Db	1975	VQMOSITRRGPDGEPQGLSG--RAASMPRLAAETQPVTDASPMKRSISTLTAORPG	2031	
QY	2093	IOSKUSKHIRLPAPCPGLEPWSMAKDPETRS-----SLELOTELISWIS	2135	

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Db      2032 -----TLTCSSTP-----: ||||| | ||| |||
Qy      2136 GDLLPSSEEPFLFP-----RDLKKYSVETQSCRRRPGLWDBQRHHSIAVSCLDS 2186
Db      2077 MDGAPSSAVGGLPPGEGTGCRERRERQERGRSQEORQPSSSGEKQRF--YSCDRF 2133
Qy      2187 GSQ--PRLCPPSPSSLGGOPLGG--PGSRPK-----KKLSP-----PSTSIDPPESQ-- 2228
Db      2134 GGREFPKPSSLSSHFTPTAGQEGPHDAQSAGVFNPTPCCRETPSASPWLALALEA 2193
Qy      2229 -----GS-----RPPCSPGVCLRRRAPADSKDPSVSSP 2257
Db      2194 LTLTWGSVMTVRPLSTP--CLNTRSLRSRLWPPTRAAP 2229

RESULT 12
B54972 voltage-dependent calcium channel alpha 1E-1 - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
C:Accession: B54972
R:Williams, M.E.; Marubio, I.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, T.H.; Mill, J. Biol. Chem. 269, 22347-22357, 1994
A:Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A:Reference number: A54972; MUID:94350992; PMID:8071363
A:Accession: B54972
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-2251 <MW>
A:Cross-references: GB:I29384; NID:g495867; PIDN:AAA59204.1; PID:g495868
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match          13.6%; Score 1638; DB 2; Length 2251;
Best Local Similarity 23.7%; Pred. No. 1.5e-95;
Matches 600; Conservative 391; Mismatches 818; Indels 724; Gaps 86;
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Query Match 13.6%; Score 1638; DB 2; Length 2251;
Best Local Similarity 23.7%; Pred. NO. 1.5e-95;
Matches 600; Conservative 391; Mismatches 818; Indels 724; Gaps 86;

[illegible]

QY 569 PSTPTGGPPRGAEVSHFYHADCHLEPVRCQAPPCCPSEASGRVTGSGKVPTVHTS 628
 Db 429 ----- 428
 QY 629 PPPEILKXALVEVAPSPGPTLTSTFNIPPGPFSSMHKLEETQSTGACHSSCKISSPCSK 688
 Db 429 ----- 444
 QY 689 ADSGACPDSCFCYCARTGAGEPESADHVPDSDSEAVYFTQDACHDLRDPHRRORS 748
 Db 445 ASIKSAKVDGVSY-----FRHKE----- 462
 QY 749 LGPDABESSVLAFWELICDTRKIVDSKYFGGIMIALVNTLSMGIYHEOPBELTVAL 808
 Db 463 ----- 508
 QY 809 EISNIVFTSLALEMLKLLVGPYIKPNYINFDGVIVVISVMEIYQ-----QGGGL 863
 Db 509 YYABFLGLLEMSLWYMGPRLYFHSSNCFDFGVTVGSIFEVVAIFRPGTSFGI 568
 QY 864 SVLRTFRMLRVLKVRFPLALORQVLVLMKMDNVATFCMLLMILFIFSLGMLFGCK 923
 Db 569 SVLRALRLRTFKITKYWASRLNVLSLSSMKSIISLLFLFLFVIVFALLGMLFGGR 628
 QY 924 FASERDGTPLDRKNFDSLLWAIIVTFOILLTOEDANKVLYNGM-----ASTSSWAALYFI 978
 Db 629 F-NFNDG--TPSANFDTPFAAIMTVFQILLTGEDNVEVNYNGIRSGGVSSGMMWALYFI 684
 QY 979 ALMTFGNVLENLVAIVLVEGQABGDATKSE-SEPDFFS-----P 1018
 Db 685 VLTILFGNYLLNVFLAIVADNLANAQELTKDQEREEAFNQHALQKAKEVSPMSAPNMP 744
 QY 1019 SVDGDRKRLALNALGSHAEURKEL-----LPPILIHATPM-S 1059
 Db 745 STIERERRRHMS-VMEQRTSOLRKHQMOSOFALNREAPTWNPLNPLNLSLNLNA 803
 QY 1060 HP-----KSSSTGV-----GEALGSGSRTS-----SSGSAPGP 1088
 Db 804 HPSLYRRPRAIEGLALGALAKEFEERIISGGGLKGDGRSALDNQRTPLSLGQREPP 863
 QY 1089 --AAHEMKCPSPARSHPWSAASWTSRRSSRLSGRAPSGLKRRSPSGRRSLLSGE 1146
 Db 864 WLAPCHGNCPTQOEAA--GGGEAVVTFEDRARHRSQRRS--RHRRVRTEKSSAS 918
 QY 1147 GQESQDEESSEDRASPAGSDURHG-----SLIERAKSSFDLPDILQVPLHRTAS 1199
 Db 919 RRSASQERSLDEAMTEGEKDELGRNHGAKPTIOEERAQDLRTNSLMSVRSGLAG 978
 QY 1200 GRSSAS-----EHQDCMGKSASGRLAR-----T 1222
 Db 979 GLDEADTFLVLPHELEVGHVIVLTOEPGSGSEQALLGNVOLDMGRVISQSBDLSCIT 1038
 QY 1223 LRTD-----DPQIDG-----DODNDEGNLSK 1243
 Db 1039 ANTDKATTESTSVTVAIPDVPDVLDSVTWHISNKTGCEASPLKEAIREDEEEVEKKQK 1098
 QY 1244 GERIQAWRGLPACCRERDSWYIIPPQSRFLCHRIITHKMDHVLVILFNCIT 1303
 Db 1099 KEKRETC-KAMVPHS-----SMFIFSTNPIRRACHYIVNURYFEMCILLVIAASSIA 1150
 QY 1304 IAMEPKIDPHSAERIIFLISNYIFTAVFLAEMTVKVVVALGWCFGEQAYLRSSMNVLJGL 1363
 Db 1151 LAABDPVITNSERNKV-LRYFDYVFTGVFTFEMVIMQDGLIILQDGSYFRDLWNILDFV 1209
 QY 1364 LVILISVIDI-LVMSVSDSGTKILGMLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 1422
 Db 1210 VVUGALVAFALANALGNTKGRDITKISRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 1269
 QY 1423 IGNITWTCAPFIIGILGVOLFKGKPFVC--QGEDTN-----ITNKSCEASVYR-W 1473
 Db 1270 VFNILIVKLMFIFAVIAVQLFKGFYCYTDSKQTEKICIGNYVDHKKMVEKGEW 1329
 QY 1474 VRHKYFNELQALMSLFLVASKDGVDMYDGLDAVGVDQOQPMNHNPNWMLLYFISFL 1533

Db 1330 KRHEFHVDNIWALLTLTFTVSTGEGWPQVLOHSDVVTEDRGGRSRNMEMSIFYVYFV 1389
 QY 1534 IVAFVFLNMFVGVVFNHFKRQHQEERARRRERLEKRRKRRKRRKRRKRRKRRKRRKRR 1593
 Db 1390 VFPEFFVNFVALLIITF-----QEQGDMEE--CSLEKNERACIDPAISAKPLTR 1439
 QY 1594 YSDYSR--FRLLVHLCTSHYLDLFTITGVIGLVNVTWAMEHYQQOILDEALKICNYIFT 1651
 Db 1440 YMPQNRHTFOYRVWHFVVVSPSEYTIMAMIALNTVLMKYSAPCTYELALKYLNIAFT 1499
 QY 1652 VIFVESVFLKVAFAFRFFQDRNQDLALVILSIMGITILEEIVNLSLPINPTIIRIM 1711
 Db 1500 MVFSELCVKIATFAGFLNYFRDWNIEDFTVIGSITTEILITDSKLVNTSGNWSFKLF 1559
 QY 1712 RVLARIARVLKLLKMAVGRALLHTVMQALPOVGNLGLLMLFFIIFAALGVELFGDLECD 1771
 Db 1560 RA--ARLIKLRQGYTIRILLWTIVQSFKALPVYCLLIAMLFFIYAIIGVQFVGNIKLD 1616
 QY 1772 -ETHPCEGLGHATFRNFGMAFLITLFRVSTGDNWNGIMKD--PSRDCDOESTC----- 1821
 Db 1617 EESH-----INRHNFRSFFGSLMLLFRSATGEAMQEIIMSLCIGKGCPEPTIAPSGQEN 1672
 QY 1822 --YNTVISPIYFVSFLTAQFVLNVNVTAVIMKHLSESNKEAK-----EEAELEABL 1871
 Db 1673 ERCGTLAYVYVSPFFCFLMLMLFVAVIMDNFEYILTRDSSILGPHHLDFVURVWAEY 1732
 QY 1872 E-----LEMKTL-SPQPHSPLG-----SPFLMPGVEGVNSTDSKPOAPHTT 1912
 Db 1733 DBAACGRITHYTEMYLEMLTMSF---PLGLGKRCPSKVAYKRLVMN---MPVAEDMT 1783
 QY 1913 AH-----IGAAG-----PSLEHTMV--PHPEE-----VPVPLGPD 1942
 Db 1784 VHTSTLMALIRTALDIKIAKGADRQQLDSELOKETTALWPHLSQXMDLLVPMKASD 1843
 QY 1943 LITVKSQVSRTHSLPNOSYCMRCNGSTABRSILGHRGWGLPKAQSGSILSVHSQPADTSCI 2002
 Db 1844 -LTVGKIYAA--MMIMDYKOSKVKQKQOQ-----EEQKNAFMQMEPS----- 1886
 QY 2003 LQLPKDV-----HYLLQPHGAPTGAIPKLPPLPPGRSPLAQRPLRRQAAIRTDLSLDVQ 2055
 Db 1887 -SLPQELIANAKALPYLOD--PVSGLSGRSGYSPMSPLSPQDI FQLACM--DPADDDG 1940
 QY 2056 LGSREDLLSEVSGPCPL-----TRSSSWFGSSIOVQQRSGIQTQSKVSHIRLPAPC 2107
 Db 1941 FOERQSLV--VTDPSMRRSFSTIRDKRNSW-----DEEFSMERSS----- 1981
 QY 2108 PGLPESWAKDPPETRSLSLDT-ELSWIG--DILLPSQEEPLFPRDLKCYSVETQSC 2163
 Db 1982 ---ENTYKRRRSYHSLSLSAHLNSDSGHKSDTHPSGGRERRRRSKERKHLSPDVSR 2038
 QY 2164 ---RRRPGFWLDEQRHRSIAVSCLDGSGQPLRCPSPSSLGQPLGGPGRPKKLSPPS 2219
 Db 2039 NSEERTQADWESPERRQS-----RSPSEGRSOTPNRQGTGSLSESSIPS 2083
 QY 2220 IS--IDPPESQGRPPCSPG-----VCLARRA-----PASDKD--PSVSPLDSTAA 2263
 Db 2084 VSDTSTPRSRRLQPPVPKPRELLSYSLIRHAGSISPPADGSEGSPLTSQLAESNNA 2143
 QY 2264 -----SPSPKK 2269
 Db 2144 WLTESSNSPHPQQ 2156

RESULT 13

A54972
 voltage-dependent calcium channel alpha 1E-3 - human
 C:Species: Homo sapiens (man)
 C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
 C:Accession: A54972
 R:Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mi
 J. Biol. Chem. 269, 22347-22357, 1994
 A:Title: Structure and functional characterization of neuronal alpha-1E calcium channel

A:Reference number: A54972; MUID:94350992; PMID:8071363
A:Accession: A5972
A:Status: Preliminary
A:Molecule type:mRNA
A:Residues: 1-2270 <WIL>
A:Cross-references: UNIPROT:Q15878; GB:L29385; NID:9495
C:Superfamily: voltage-dependent calcium channel protein

Query Match 13.6%; Score 1637.5; DB 2; Length 2270;
Best Local Similarity 23.6%; Pred. NO. 1.6e-95;
Matches 601; Conservative 394; Mismatches 815; Indels 741; Gaps 87;

QY	73	PGAGDEA-----EGLPYPALA-----PV-----VFFY	95
Db	12	PGSGDSDQSRNRQGTVPASGQAAAYKQTKAQRARTMALYNPIPVQNCFTVNRSLFI	71
QY	96	LSQDSRPSRWCLRTVCNPNWERSMVLILNCVILGMFR--PCEDIAQDSQRCLQAPD	153
Db	72	FUEDNTRKAYAKKLIDWPPPEYMYLATIIANCIIVLALEQHLPEDDKTPMSRR--LEKTE	128
QY	154	DFIFAFVAVEMVVKWALG-IFGKKCVLGDWTNRLDFFIVIAAGMLEYSILDQ--VSFSA	210
Db	129	PYFIGIFCFEAGIKIVALGFPHKGSYLRNGWVMDFFIVLUSGIATAGTHTNHDVURT	188
QY	211	VTVRVLRBLRANRVPSMRLVTLTLDTPMLGNVLILCFVFFIFGIVGVQLMAGLRL	270
Db	189	LEAVRVLRPLKLVGSPSLQIVLKSIMKAMPVLIQIGLLAFFAILMFAILGLEFVSGKLH	248
QY	271	NRCFLPENSLPLSDVLEPYQOTENEDESPFIQSPRENGMRSCRSVPTLRGEGGGPPC	330
Db	249	RACFMNN-----SGLEGF-----DPHPC-----GVQC	273
QY	331	SLDYETYNSSNTTCVMNQYNTCSAGEHNPFGAINEDNIGYAWIAIFOVITLEGWVD	390
Db	274	PAGYE-----CKDW-----IGPDGITOQDNILFAVLTVFOCITMEGTT	313
QY	391	IMYFMDA-HSYNFIYFILLIIVGFFMINCLWVIATOFSETKORESOLMRQRVRL	449
Db	314	VLYTNDALGATWNLGYFLIIGFFVLNLVLGSLGSEFAKERRV---ENRRAF	368
QY	450	SNASTLAGSEPGSVEELLKVLVYTLRKAARPLAQVSRAI-GVRAGLLSPVARSQEP	508
Db	369	K-----LRQOQIERELNGYRAWIDKAEVMLAEN	399
QY	509	QPSGCTSRHRLSVHHLVHHHHHHHVLGNGTLRVPRASPEIQORDANGSRRLMPP	568
Db	400	KNAGTSALEVLRAT-----IKSRTEAMTRDSS-----	428
QY	569	PSTPTSGGPRGAESVHSFYHADCHLEPVRQAPPPRCPSEASGRTVSGSKVYPTVHTS	628
Db	429	-----	428
QY	629	PPPIIKDKALVEAPSPGPPTLTFSNIPPGPSSMHKLTQTSGACHSSCKISPCSK	688
Db	429	-----DEHCVDIS-----SVGTPLAR	444
QY	689	ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQR	748
Db	445	ASIKSAKVDGVSY-----FRHE-----	462
QY	749	LGPDAEPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVLTSMGIEYHEQPEELTNAL	808
Db	463	-----RLRISIRHMVKQSVFYVILSVLVALNACVAIVHHNQPLWJTHLL	508
QY	809	EISNIVTSLFALEMLKLVVGPFGYIKNPYNIEDGVTVIVSVMEIVCQ-----OGGGL	863
Db	509	YAEFLFLGLELLEMSLKNYGMGPRLYPFHSSNCFDFGVTGSIPEVWMAIFRPGTSFGI	568
QY	864	SVLRTFLMRVLKVRFLPALQQLVLMKTMNDNVATFCMLMLFIFISILGMHLFGCK	923
Db	569	SVLRALRLRIFKITYKAWASLRNLVLSMSSMKSIIISLLFLFLFVFPALGMQLFGGR	628
QY	924	FASEROGDTLPDRKNFSLMLWIVTVFOILLQEDMNKVLNGM-----ASTSSWALYFI	978

Db	1674	GEKCEPDTTAPSQNNERNRCGTLAVYFVSFIFFCSFLMLNFVAIVIMDNFEYLTRDS	1733	Db	283	LRQXCVLNPVPELGTNITHDEWNDVNNESHQXDFYDEWO--VC-----	325
Qy	1862	K-----EBAEAEAELE-----LEMKTL-SPQPHPLG-----SEFLWPG	1894	Qy	320	LRGGGGGPPCSLDYETVNSSNTTCV--NMQYTTNCSAGEHPFKGAINFDNIGYAMIA	378
Db	1734	SILGPHHLDFFVWVAEYDRAACGRIHYTEMVEMTLTMSPLG-----PLGKRCPSKVAYKR	1789	Db	326	--GNGTGAGKCG--NGTINGTAEWLCLPNICQ-----NPNHDTSFDFGMLLC	371
Qy	1895	VEGVNSTDSPKPGAPHTTAH-----IGAASG-----FSLEHPTMV--P	1930	Qy	379	IFQVITTEGWVDIMYFVMDAHSFYNIYFILLIIVGSFFMINLCLVVIATOFSETKORES	438
Db	1790	LVLMM-----MPVARDMTVHTSTLMLIRALTALDIKIAKGGADRQOLDSLELQKETAIW	1844	Db	372	AFRLMTQDFWESLHYLVLRAVSAHCLYFVLVILLGSFYLVNLLILAIIVANSYDET-QKQD	430
Qy	1931	HPEE-----VPVPLGPDLLTVRKGSVGRTHSLPNDYSYMCNRNGSTAERSLGHGWGLPKA	1984	Qy	439	QLMBEQRVRLSNASTLASFSPEPSCYPELLKYLVLRLKAAARLIA-QVSRGAIGVRAGLL	497
Db	1845	HLSQKMLDLVMPKASD-LTVGKIYAA--MMIMDYKQSKVKQKQOL-----EE	1892	Db	431	QADABEEA-----AERQE-----BEARKEALSIMTKSPSNGWNNDEAGVR----	472
Qy	1985	QSGSTLSVHESPADTSCILQLPKDV-----HYLLQPHGAPTGAIKLPPPGPSPLAQ	2037	Qy	498	SSPVARSQEPQSPSGCTSRHERLSVHHLVHHHHHHHHHHLNGTGLRVPFRASPIQORD	557
Db	1893	KQNAEMFORMEPS-----SLPQEIIANAKALPYLQD--PVSGLSGRSGYPSMSPLSP	1943	Db	473	---TAGDKAEKERLSLTSIDSHATSAHLKPSLNQKRH-----SLSLP-GSPYIHRN	521
Qy	2038	RPLRQAAIRTDLSLDVQGLGREDLLSEVGSFCL-----TRSSSFWGGSSIQVQO	2089	Qy	558	ANGSRRLMLPPPTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRV	617
Db	1944	QDIFOLACM--DPADDGQFQERQSLV--VTDFSSMRRSFSTRDRKNSNW-----LEE	1993	Db	522	SRGSQVSNRKPVPPTAKRS-----PCCPD-----PYCPDR-----	545
Qy	2090	RSQISQKSVKHRLPAPCGLESMAKDPETRSLSLEDT-ELSMISG-----DLLEPSQEE	2145	Qy	618	SGKVTPTVHTSPPPPEILKDKALVEVAPSPGPTLTSE--NIPPG--PFSMHKLLET	670
Db	1994	FSMERSS-----ENTYKSRRSYHSSLLLSAHLRNSDSGHKSDTHPSGGRE	2039	Db	546	QPLVHTHTLENLPLP-FADDSAAV--TPSSBDLCNFSFIRNPNGRRFSFASORPPDGT	600
Qy	2146	PLFPRLKKCYSVETQSC---RRRPGFWLDEQRHRSIAVCLDSGSPRLCPSPSLGG	2201	Qy	671	QSTGACHSSCKTSSPCSKADSGACGPDSCPYCARTGAGE-----PESA-D	714
Db	2040	RRSKERKHLSPDVGRCSNSEERGTQADWESPERRQS-----RSPSEGRS	2084	Db	601	GRSGRRRS--FASHNSRASRTSRG-----SQGDRTKTQTLNFKKGKVPDVLWD	649
Qy	2202	QPLGPGSPKKKLSPSPSIS--IDPPESQSRPPCSPG-----VCLRRRA-----PAS	2247	Qy	715	HVMPDSDSAVYFTQDAQHSDLRDPHSRRR---QRLGPDAPAESVLA-----	760
Db	2085	QTPNRQGTGSLSSSPSVDSTPRRSRQLPVPFKPRPLLSYSLIRHAGSISPPAD	2144	Db	650	KSLLDDQDSV--SSGSGHCPEKOKASESNPFLSHSPGPGPNVEMKDVMLDKILDQASG	707
Qy	2248	DSKD--PSVSSPLDSTAA-----SPSPKK 2269		Qy	761	-----FWRLIC-----DTRFKI-----VDSKYFGRGIMAILVN	789
Db	2145	GSEGSPLTSQALSNNAWLTSSNSPHFQQ 2175		Db	708	HRRSFVSMTSIHQRTWKDIMWKYFCTWCHDHPNFKQLRLVSLFIMDAFVDFITICILVN	767
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C;Species: Aplysia californica (California sea hare)							
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004							
C;Accession: T30902							
R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.							
DNA Cell Biol. 16, 347-356, 1997							
A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.							
A;Reference number: 220929; MUID:97238630; PMID:9115644							
A;Accession: T30902							
A;Status: preliminary; translated from GB/EMBL/DBJ							
A;Molecule type: mRNA							
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C;Superfamily: sodium channel protein							
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Best Local Similarity 25.8%; Pred. No. 1.7e-95;							
Matches 518; Conservative 348; Mismatches 702; Indels 442; Gaps 69;							
Qy	94	FYLSQDSRPRSWCLRTVCNPFVSRVSLVILNLCVTLLGM--FRPCDIAQDSQRCLIIQA	151	Qy	1005	AEAI-----DRFKRFGNWKVKKIIVCIKVLQKQKWRPP-----PTTQGS	1045
Db	119	FLLSFPNDIRIRAIYILVHPILFSLVMMTLVNCVFMAITSYTP-----PA	164	Qy	1070	EALGSGRRRTSSSGSAEPGAHHEMKCPGARSPPHSPWGAASWTSSRSRSLGRAPS	1129
Qy	152	FDDZTF-AFFAVEMVVKMVALGFGKK-CYLGDWTNRLDFTIV-IAGMLEYSLDLQNVSF	208	Db	1046	EVNG-----KDPVVVDGTVVSMKPTDPDFDPCPCFAQAIC-----	1082
Db	165	FVEHIFLGIYVEAVVLSRGFVLKPPTYLRDPNWLDFVVISIAYMTMTVKSGNL--	222	Qy	1130	LKRSPSGERRSLLSGEGSQDEESESDEDRASPGSDHHRHSLEAKSSFDLPTL	1199
Qy	209	SAVTVRVLRLPAINRVPMSRIITLLIDTLPMGLNVLCCFFVFIFGVGVGLWAGL	268	Db	1083	-----SAKKDLKSPSGS-HSNSGS-----	1100
Db	223	QALRTFVLRLAKTISVIPGLTIVGALLAEVRRURDVMILTVFVLSIFALIGMQLYGA	282	Qy	1190	QVPLHRTASGRSSASEHQCNGKASGRGLARTLTDLPOLDGDDDDNDEGNLSKGRIOA	1249
Qy	269	LNRCFTLPENFSLPLS-----VDLEPPYQTENEDESPFICSPQRENGMRSCRVP	319	Db	1101	-----SHCSSCSSESASQTKKID---LEADHEINEVEI-----V	1132

Db 1133 YKBPDDCFYMCYKRCPCWCKVSKIGRAWMA-----VRCFFYRLTENKYPDSFI 1184
QY 1294 LVIIFLNCITIAMERPKIDPHSAERIFLTLNVIFTAVFLAETWVKVVALGCFGEQAYL 1353
Db 1185 IAMILASSCALALEDAYLHEKILKEILYLDKVFATFIIEMLIKWLA---FGFKTYF 1240
QY 1354 RSNWNLGLLVLISVIDILVSM-VSDSGTKILGMLRVLRLRLTLRPLRVIAGRAQGLKL 1412
Db 1241 TDAMCWLDFIIVMLSVMLVADLTASEEGGSMWMSKSNRTLRALRPLRAVSRWEGMRV 1300
QY 1413 VETLMSLLKPIGNVIVICAPFIIGILGVLPKGFVCOGE-----DTRNITNKSDCA 1467
Db 1301 VNALFKALPISCNVLVLCLVFLWIFIGIMGVFLNGFKFHACRDEKGDYKPREVPNKTVCI 1360
QY 1468 EASYRVRHKNFNDNLGQALMSLFVLASDKDGVWDIMYDGLDVGVDQOPIMKHNPMWLLY 1527
Db 1361 DKGYNWTAQINFHDVLSAYLALFOVATYKGMIDIMNNAIDTEIGQQPSREENVIMYL 1420
QY 1528 FISFLIIVAFVFLNMFVGVVNFH--KROHQEBEEARRREKRLRLEKKRRSKQOM 1585
Db 1421 FVLFIVFGSFTNLNFIGVITENFNSQKKAGGSLEMFETDQKKYINAMKEMQSKSPQ- 1479
QY 1586 AEAQCKPYSDYSRFLIIVHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQOILDEALKI 1645
Db 1480 -KSIIPKX-----KLAGLIFDITDQKFDIAIMVILINMLTMMPEHHGMSAQMKNILGI 1534
QY 1646 CNYIFTVIFVPEFVKLVAFARFRFFODRWQOLDLAILVLLSTMGITLBEIEVNLSLPINP 1705
Db 1535 ENLIFITFAECVLKJGLRW-YFKIPWNVDFVWVVLVSLASSLSEFED--SFFISP 1591
QY 1706 TIIRIMVRLIARVLKLLKMAVGMRLALHTVMQALPOVGNLGLLPMLLFFIFAALGVLEF 1765
Db 1592 TLLRIVIRVRGRVRLVKSAGTITLFSMAVSLPALFNGLLGLIMFIYAIMGMNFF 1651
QY 1766 GDLCEDETHCEGLGRHATFRNCGMAFLTILFRVSTGDNWNGIMKDPDQDQSTCYNTV 1825
Db 1552 --MGAEQY---GLDDAFNFTFLRSFILLFQMCSTAGMSDVLNGLIARCAPEGTCKDYN 1706
QY 1826 ISPIYFVSFVLTAQFVLVNVVIAVLKMLHLESNEKEAEAELEAELEMLTSPQHPSP 1895
Db 1707 VATIYLATYLVSVLVVNVVIAVILENFQSDTE--EQQLTTPD-DFDMYIEKWEKYDP 1763
QY 1886 LGSFLLMPGVEGNSTDSKPGAPHTTAHIGAASGF--SLEHPTWVHPHE-----EVPVP 1938
Db 1764 KASKYI-----PLDQLSDFDVLYLEELRPLKPNHFIIVKLDIP 1801
QY 1939 LGP-----DLTVRKSGVSRTHSLP 1958
Db 1802 ICENDRCYCRDILDALTKNFLGTGETSDIP 1831

RESULT 15
A37490
voltage-dependent calcium channel alpha 1E - rat
C;Species: Rattus norvegicus (Norway rat)
C;date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A37490
R;Soong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P.
Science 260, 1133-1136, 1993
A;Title: Structure and functional expression of a member of the low voltage-activated ca
A;Reference number: A37490; MUID:93262464; PMID:8388125
A;Accession: A37490
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-2222 <SOO>
A;Cross-references: UNIPROT:Q07652; GB:L15453; NID:g310082; PIDN:AAA40855.1; PID:g310083
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBI:P:132101)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.6%; Score 1632.5; DB 2; Length 2222;
Best Local Similarity 23.6%; Pred. No. 3.3e-95;
Matches 587; Conservative 389; Mismatches 819; Indels 697; Gaps 81;

QY 94 FYLSQDSRPSRNCRLRTVCNPMFERVSMVLVILLNCVTLMFR--PCBDIACDSORCIILOA 151
Db 21 FIFGEDNIVRKYAKKLDWPPPEYMLATI IANCIIVALEQHLPEDDKTPMSR---LEK 77
QY 152 FDDFIFAFVEMVVMKVALG-IFGKKCYLGTWRDLFFVIAGMLEYSLDLQN--VSF 208
Db 78 TEPYFIGIFCFAGIKI VALGFI FHKSYLRNGMNMDFIVVLSGILATAGTFHFNTHVDL 137
QY 209 SAVTRVRLRPLRAINRPSMEILVTLTLDLTPMLGNVLLLCFFVFFFGIVGVQVLAQGL 268
Db 138 RTLRAVRVRLPLKLVSGIPSLQVLKSMKAMVPLQLGLLFFAILFAIIGLFYSK 197
QY 269 LNRCPLENFSLPLSVLEPYQYOTENDESPFICSPRENGMRSCRSVPTILRGEGGGP 328
Db 198 LHRACFMNN-----SGILEGF-----DPHPG-----GVQ 222
QY 329 PCSLDYETYNSSNTTCVNMNQYITNC SAGEHNPKGAINFDNIGYAMIAI FQVITLWGM 388
Db 223 GCPAGYE-----CKDW-----IGPNDGITQFDNILFAVLTVPQCITMEGW 262
QY 389 VDIMYFVMDA-HSFYNRIYFILLIIVGSPFMNLCVVIATQFSETKQRESQLMREQVR 447
Db 263 TTVLYNTNDALGATWNLIFYPLIIIGSFVNLVGLVSGEFAKERBRY-----ENRA 317
QY 448 FLSNASTLASPSFSCSYEBELLKYLVIILKAAARLAQVSRAT-GVRAGLLSSPVARSGQ 506
Db 318 FMK-----LRRQQIERELNGYRAWIDKAEVWMLAE 348
QY 507 BPOPSGSCTRSHRSLSVHLVHHHHHHHHHVLNGTLRVPRASPEIQDRDANGSRRLML 566
Db 349 ENKSGTSALEVLRRAT-----IKRSRTTEAMTRDSS----- 379
QY 567 PPPSTPTSPGSGPRGABSVHSFYHADCHLEPVRQCAPPRPCPSASGRVTSGKVYPTVH 626
Db 380 ----- 379
QY 627 TSPPEILKALVEVAPSGPPTLTLSFNIPPGPSSMHKLTQTSTCACHSSCKISPPC 686
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QY 687 SKADSGACGPDSPCYCARTGAGEPESADHWVPSDSSEAVYEFTODAOHSDLRDPHSRRRQ 746
Db 394 ARASIKTKVDGASY-----FRHKE----- 413
QY 747 RSLGPDABSPSVLAFWRLLICDTERKIVDSKYFGRGIMAILVNTLSMGIEVHEQPELTN 806
Db 414 -----RLLRISIRHMVKVQVFWIVLSVVALNTACVAIVHHNQPOWLTH 457
QY 807 ALBISNIVFTSLFALEMLLKLIVGPPGYIKNPYNIFDGVIVVISVWEIYVQ-----QGG 861
Db 458 LLYYAEFFFLGLGLELLEMSLKMVGMPRLYPHSSFCNCFDGVTVGSIPEVVAIIPRPGTSF 517
QY 862 GLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDNVATFCMLLMPIFTFSILGMHLFG 921
Db 518 GISVLRAALRLRIKTKYKVASLRNLVWSLSMKSIIISLLFLFLFVIVFALLGMQLFG 577
QY 922 CKFASERDGTLPDRKNFOSLLWAIIVTFQILTQEDWNKVLYNGM-----ASTSSWAALY 976
Db 578 GRF-NENDG---TPSANFTDTPAINTVQILTGEDWNEVNGIRSQGGVSGMWSAIY 633
QY 977 FIAMTFTGNVPLNLIIVAILVEGFOAGDATKSE-SEPDFFS----- 1017
Db 634 FIVLTLFGNYTLNVLFLAIVDNLANAQLTKDEQEEAEAFNQKHALOKAKEVSPMSAPN 693
QY 1018 -PSVDGDDGRKKELAI-----VALGEAEHLRSLKLL 1046
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QY 1047 PPLIIHTAATPMS-----HP---KSSSTGVGEALGSG-----SERTSSSGSAE----- 1086
Db 754 PPMNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLN 813

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1087 QY -----PGAAHEMKCPSPARSPPSPW-----SAASSWTSRRS 1119
814 Db LTVSLDNQSRPLSLGKRPPMLPRSCHG--NCDPTQQTGGGTWVTEDRARHQSORR 871
1120 QY SRNSLGRAPSLKRRSPGSRRLSLGSGOESDEEESDEORASPAGSDHRRHGRSLEREA 1179
872 Db SRHRRVTEGKESASASRSR-----SASQERSLDEGVSDIDGKEHEFPQSSHRSKPTIHEE 927
1180 QY KSSFDL--PDTIQVP---GL-----HRTASGRSSASBHQDCNGKASGRLL 1219
928 Db ERTQDLRTNSLMVPRGSLVGLALDEAETPLVQPOPELEVGDAAALTEQAEAGSSEQALL 987
1220 QY A-----RTURDDPOL-----DQ- 1232
988 Db ADVQLDVGRIQSQEPDLSCMTTNDKATTESTSVTVLAIPOVDPLVDSTVMSNKTDE 1047
1233 QY -----DDNDEGNLSGERIOAMVRRLPACCRERDSWASAIFFPQSRFLLCH 1281
1048 Db ASPLKEAETKEEEEEVEKKQKKEKRETG-KAMVPHS-----SMFIFSTTNPIRKACH 1099
1282 QY RIITHKMFHVVLVIIFLNCITIAMERPKIDHSAERIFLTLSNYIFTAVFLAEMTVKV 1341
1100 Db YIVNLRYPFWCILLVIAASIALAABDPVLTNSERNKV-LRYFDYVFTGVTFFEMVIKMI 1158
1342 QY ALWCFCGEQAYLRSSWNVLGDLVLSVIDI-LVSMVSDSGTKILGMLRLVRLRLRL 1400
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1401 QY RVISRAQGLKLVVETIMSSLPKIGNTWICCAPFIIFGILGVLQFKGKFFVC--QGEDTR 1458
1219 Db KTKRLPKLKAVIDCVVTSKNVFNILIVYKLPWFIFAVIAVQLFKGKFFYCTDSSKOTE 1278
1459 QY N-----ITNKSCAEASYR-WVRHXYFNQNLQALMSLFLVASKOGWVDIMYDGLDANG 1511
1279 Db KECIGNVVDHEKMKMEVKGEWKREHREPHYDNIITWALLTLFTVSTGEGWQVLOHSDVYTE 1338
1512 QY VDOQPIMNHPWMLLYFISLLIVAFVLMVFNMGVVVFNHFKCRQOEDEEAREERKRL 1571
1339 Db EDGRPSRNMEMSIFVYVYVFPFPPFVFNIFVALLIITF-----QEGDKMEEB--- 1388
1572 QY RRLKRRSRKEKQMAEACKPYSDYSR--FRLVHHLCTSHYLDLFTIGVILNVVTVMA 1629
1389 Db CSLEKNERACIDFAISAKPLTRYMPQNEHTFOYRVWFHVVSPSFEYTIMAMIALNTVWLM 1448
1630 QY MEHYQQPQIILDEALKICNYIFTVFVESVFKLVAFAPRRFPQDRNQQLDLAIVLSIMG 1689
1449 Db MKYYSAPWTVELALKYLNIAFTMVFSLECVLKVIAGFLNFRDYNIFDITVIGSITE 1508
1690 QY ITLEEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMRALLHTVMQALPOVGNLGLL 1749
1509 Db IILTDSKLVNTSGNMGFLKLFRA--ARLKLROGYTIRILLWTTFVQSFKALPYVCLL 1565
1750 QY FMLIFFTIFAALGVELFGLECD-ETHPCEGLGRHATPFGMAFLTILFRVSTGDNWNGIM 1808
1566 Db IAMLFFIYAIIGMVQVGNKILDESH---INRHNFRSPFGSLMILLFRSATGEAWQOIM 1621
1809 QY KD--PSRDCQESTC-----YNTVISPIYFVSFLTAQFVLVNVVIAVLMKHEES 1857
1622 Db LSCLGKGECDPTAPSGQNESERCGLDAYVYFVSFFCPSFLMLNLFVAVIMDNFEYL 1681
1858 QY NKEAK-----EEAELEALE-----LEMKTL-SPQPHSPLG-----SPF 1890
1682 Db TRDSSILGPHLDHFVRVWAEYDRAACORIHYTEMYMLTLMSP---PLGLGKRCPKSV 1737
1891 QY LMPGVEGVNSTDSPKGPAPHTTAH-----IGAASG-----FSLHEPTM 1928
1738 Db AYKRLVLMN-----MFAEDMTVHTFTLMAIRLTALDIKIAKGADQQLDSELOKETL 1792
1929 QY V--PHPEE-----VPVPLGPDLLTVKSGVSRTHSLPNDSYMCHNGSTAEBSLHRCGWG 1980
1793 Db AIWPHLSQKMLDLLVPMNPKASD-LTVGKIYAA---MMDIYKQSKVKQKQQL----- 1842
1981 QY LPKAGSGSILSVHSQPAD-TSCILQPKDVHYLLOPHGAGTGAIPKLPFPFGRSPLAORP 2039

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Search completed: November 18, 2004, 13:34:36
 Job time : 94.7329 secs

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1843 Db --EEQKNAPMFQRMPEPSPSLPQEIISNAKALPYLOD---PVSGLSGRGYFSMGPLSPQE 1897
2040 QY LRRQAAITDLSLDYQGLGSRREDLLSEVSGPSCPL-----TRSSSFW----- 2080
1898 Db IFQLACM--DPADGQFOEQSLV--VTDPMSMRSPSTIRDKRNSSSWLEEFSSMERSSSE 1953
2081 QY -----GSSSIQVQ-----ORSG-----IOSKYSKHIRLP--APC----- 2107
1954 Db NYKSRRSYHSSLELSAHLNLSDSGHKSDTHRSGRGRGRSKERKHLSPDVSRCNSEE 2013
2108 QY PGLPSW-----AKOPPETRSSLELDELTELWSIGDILLPSQOEELFPDRDLKKCVSVET 2160
2014 Db RGTQADWESPERRQSRSPSEGRSQTNRQGTGSLSESSIPSISDSTPRRQRQLPPPP 2073
2161 QY QSCRPRPGFWLDEQRHHSIAVSCLDGSGQPLCPSPSLGQPLGQPLGPGSRPKK--LSPPS 2219
2074 Db ---KRPRLLSYSSLMRHTGGISPPPDGSE-----GGSPLASQALESNACLTESS 2120
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2121 Db NSLHPQOGQHPSPQHVISEPYLALHEDSHASD 2152

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2004, 13:06:30 ; Search time 254.167 Seconds
(without alignments)
5177.235 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

Sequence: 1 MLPHRVPRCVRTPPLNGSAR.....KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	11657	96.9	2254	1	CCAG_RAT	O54898 rattus norv
2	11657	96.9	2254	1	AAG35186	Aag35186 rattus no
3	11532	95.9	2288	2	O9WUB8	O9WUB8 rattus norv
4	11372.5	94.6	2295	2	O9WUT2	O9WUT2 mus musculu
5	11263	93.6	2248	2	O6PRV8	O6PRV8 mus musculu
6	11263	93.6	2248	2	AAH57399	AAH57399 mus muscu
7	10732.5	89.2	2377	1	CCAG_HUMAN	O43497 homo sapien
8	6809.5	56.6	1389	2	O6ZPX4	O6ZPX4 mus musculu
9	6809.5	56.6	1389	2	BAC98104	Bac98104 mus muscu
10	6226	51.8	2359	1	CCAH_RAT	O9EQ60 rattus norv
11	6222	51.7	2353	1	CCAH_HUMAN	O95180 homo sapien
12	6190	51.5	2365	1	CCAH_MOUSE	O88427 mus musculu
13	5418	45.0	2223	1	CCAI_HUMAN	O920X4 homo sapien
14	5354	44.5	1835	1	CCAI_RAT	O920Y8 rattus norv
15	4750.5	39.5	1994	2	O7Z6S8	O7Z6S8 homo sapien
16	4188.5	34.8	1762	2	O7PQV4	O7PQV4 anopheles g
17	4137.5	34.4	2893	2	O9W433	O9W433 drosophila
18	3856.5	32.1	1837	2	O96TR4	O96TR4 caenorhabdi
19	3849	32.0	1852	2	O7Z002	O7Z002 caenorhabdi
20	3849	32.0	1852	2	AAAR25651	Aar25651 caenorhab
21	3830	31.8	1844	2	O7Y2R6	O7Y2R6 caenorhabdi
22	3830	31.8	1844	2	AAAR25653	Aar25653 caenorhab
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24	3824.5	31.8	1885	2	AAAR25652	Aar25652 caenorhab
25	3665	30.5	1460	2	O80TJ2	O80TJ2 mus musculu
26	2941.5	24.5	1418	2	O7JPB4	O7JPB4 caenorhabdi
27	2941.5	24.5	1418	2	AAAR30210	Aar30210 caenorhab
28	2813.5	23.4	1942	2	O86SH0	O86SH0 lymnaea sta
29	2098.5	17.4	1211	2	O8MQ95	O8MQ95 caenorhabdi
30	1727	14.4	541	2	O6P892	O6P892 mus musculu
31	1727	14.4	541	2	AAH58206	Aah58206 mus muscu

32	1720.5	14.3	1810	2	O44930	O44930 aiptasia pa
33	1678	14.0	2327	1	CCAB_MOUSE	O55017 mus musculu
34	1674	13.9	2339	1	CCAB_HUMAN	Q00975 mus sapien
35	1673	13.9	2331	2	O9TTA4	Q9TTA4 bos taurus
36	1666.5	13.9	1599	2	O7PNK9	O7PNK9 anopheles g
37	1665.5	13.8	2259	1	CCAE_RABIT	O02343 oryctolagus
38	1661	13.8	2333	2	O89089	O89089 rattus norv
39	1660	13.8	2295	2	O923K6	O923K6 rattus norv
40	1656	13.8	2304	2	O9BMQ4	O9BMQ4 blattella g
41	1653.5	13.7	2272	1	CCAE_MOUSE	Q61290 mus musculu
42	1652.5	13.7	1891	2	O97017	O97017 stylophora
43	1650	13.7	2312	1	CCAE_HUMAN	O15878 homo sapien
44	1649.5	13.7	1984	2	O28644	O28644 oryctolagus
45	1646.5	13.7	1847	2	Q6RKB0	Q6RKB0 brachydanio

ALIGNMENTS

RESULT 1
CCAG_RAT
ID CCAG_RAT STANDARD; PRT; 2254 AA.
AC O54898;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-gated calcium channel alpha subunit Cav3.1).
GN Name=Cacna1g;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=98154730; PubMed=9495342;
RA Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J.,
RT Williamson M.P., Fox M., Rees M., Lee J.-H.;
RT "Molecular characterization of a neuronal low-voltage-activated T-type calcium channel.";
RL Nature 391:896-900(1998).

CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1G gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Moderate expression in heart; low expression in placenta, kidney and lung.

CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.

CC -!- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.

CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

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EMBL; AF027984; AAC67372.1; --

PIR; T09053; T09053.

RGD; 68942; Cactna1g.

InterPro; IPR001682; Ca/Na_pore.

InterPro; IPR002111; Cat channel_TrpL.

InterPro; IPR005821; Ion trans.

InterPro; IPR005820; Mchannel_nlg.

InterPro; IPR005445; TVDCCALPHAL.

Pfam; PF00520; Ion trans; 4.

PRINTS; PR01629; TVDCCALPHAL.

Calciun channel; Calcium-binding; Glycoprotein; Ion transport;

Ionic channel; Multigene family; Phosphorylation; Repeat;

Transmembrane; Voltage-gated channel.

REPEAT 68 398 I.

REPEAT 730 968 II.

REPEAT 1242 1519 III.

REPEAT 1564 1822 IV.

DOMAIN 1 80

TRANSMEM 81 101

DOMAIN 102 119

TRANSMEM 120 141

DOMAIN 142 150

TRANSMEM 151 170

DOMAIN 171 175

TRANSMEM 176 193

DOMAIN 194 213

TRANSMEM 214 234

DOMAIN 235 370

TRANSMEM 371 395

DOMAIN 396 744

TRANSMEM 745 765

DOMAIN 766 778

TRANSMEM 779 800

DOMAIN 801 806

TRANSMEM 807 825

DOMAIN 826 833

TRANSMEM 834 857

DOMAIN 858 868

TRANSMEM 869 889

DOMAIN 890 940

TRANSMEM 941 965

DOMAIN 966 1251

TRANSMEM 1252 1274

DOMAIN 1275 1292

TRANSMEM 1293 1313

DOMAIN 1314 1323

TRANSMEM 1324 1343

DOMAIN 1344 1357

TRANSMEM 1358 1379

DOMAIN 1380 1389

TRANSMEM 1390 1413

DOMAIN 1414 1491

TRANSMEM 1491 1516

DOMAIN 1517 1578

TRANSMEM 1579 1599

DOMAIN 1600 1613

TRANSMEM 1614 1635

DOMAIN 1636 1642

TRANSMEM 1643 1661

DOMAIN 1662 1675

TRANSMEM 1676 1699

DOMAIN 1700 1713

TRANSMEM 1714 1734

DOMAIN 1735 1794

TRANSMEM 1795 1822

DOMAIN 1823 2254

TRANSMEM 290 295

DOMAIN 496 506

FT	DOMAIN	1527	1530	Poly-Glu.
FT	SITE	354	354	Calcium ion selectivity and permeability
FT	SITE	924	924	(By similarity).
FT	SITE	1465	1465	Calcium ion selectivity and permeability
FT	SITE	1770	1770	(By similarity).
FT	CARBOHYD	173	173	Calcium ion selectivity and permeability
FT	CARBOHYD	246	246	(By similarity).
FT	CARBOHYD	306	306	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	310	310	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	322	322	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1427	1427	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1430	1430	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1666	1666	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	2254	2254	AA; 697BBE06360CF0F6 CRC64;
Query Match				
Best Local Similarity				
Matches 2219; Conservative				
Score 11657; DB 1; Length 2254;				
Pred. No. 0;				
Mismatches 6; Indels 0; Gaps 0;				
QY	62	GAAGAGSTEKOPG	SADSEAGL	PYPALAPVVFYLSQSRPSWCLRTVCNPFERSVML 121
DB	30	GRQPGSTEKOPG	SADSEAGL	PYPALAPVVFYLSQSRPSWCLRTVCNPFERSVML 89
QY	122	VILLNCVTLGWER	PCEDIACDSORCE	IIQAOPDFIFAPFAVEMVVMVAIGIFGKKCYLG 181
DB	90	VILLNCVTLGWER	PCEDIACDSORCE	IIQAOPDFIFAPFAVEMVVMVAIGIFGKKCYLG 149
QY	182	DTWNEIDFFVIAG	MLEYSLDLQNV	SFSAVRTVRVLRPLRANRVPMSRILVTLTDLTP 241
DB	150	DTWNEIDFFVIAG	MLEYSLDLQNV	SFSAVRTVRVLRPLRANRVPMSRILVTLTDLTP 209
QY	242	MLGNVLLLCFFV	FFIFGIVGVQ	LMAGLLNRCFLPENSLPLVDLEPYQYQENEDESFP 301
DB	210	MLGNVLLLCFFV	FFIFGIVGVQ	LMAGLLNRCFLPENSLPLVDLEPYQYQENEDESFP 269
QY	302	ICSQPRENMRSCR	SVPTLRGGG	PGCSDLYETVNSSNTTCVNNWNYNCSSAGEHN 361
DB	270	ICSQPRENMRSCR	SVPTLRGGG	PGCSDLYETVNSSNTTCVNNWNYNCSSAGEHN 329
QY	362	PFKGAINFDNIG	YAMIAIFQVIT	LRGWVDIMYFVMDAHSFYNFYIFILLIIVGSPFMINL 421
DB	330	PFKGAINFDNIG	YAMIAIFQVIT	LRGWVDIMYFVMDAHSFYNFYIFILLIIVGSPFMINL 389
QY	422	CLWVIATQFSE	TKQRESQMLR	EQRVFLSNASTLASFPFGSCYELLKYLVLKKAAR 481
DB	390	CLWVIATQFSE	TKQRESQMLR	EQRVFLSNASTLASFPFGSCYELLKYLVLKKAAR 449
QY	482	RLAQVSRALGV	RAGLLSSPV	ARGSQPQSGSCSTRSHRLSVHHLVHHHHHHHHYHLGN 541
DB	450	RLAQVSRALGV	RAGLLSSPV	ARGSQPQSGSCSTRSHRLSVHHLVHHHHHHHHYHLGN 509
QY	542	GTILRVPRASPE	IQDRDANGSR	RLMLPPSTPTPSGGPPRGAESVHGFYHADCHLEPVRCQ 601
DB	510	GTILRVPRASPE	IQDRDANGSR	RLMLPPSTPTPSGGPPRGAESVHGFYHADCHLEPVRCQ 569
QY	602	APPPRCPSASG	RTVGSGKVY	PTVHTSPPEILKDKALVEAPSPGPTTTSFNIPPGPF 661
DB	570	APPPRCPSASG	RTVGSGKVY	PTVHTSPPEILKDKALVEAPSPGPTTTSFNIPPGPF 629
QY	662	SSMKHLELTOST	CACHSSCKI	SSPCSKADSGAGCPDSCPCYARTGAGEPESADHVMFDS 721
DB	630	SSMKHLELTOST	CACHSSCKI	SSPCSKADSGAGCPDSCPCYARTGAGEPESADHVMFDS 699
QY	722	SEAVYEFTQDA	QHSDLRDP	HSRRQRSLGPDAPSSVLAPWRILCTFRKIVDSKYFGRG 781
DB	690	SEAVYEFTQDA	QHSDLRDP	HSRRQRSLGPDAPSSVLAPWRILCTFRKIVDSKYFGRG 749
QY	782	IMTALLVNTLS	MGIEVHEQPE	LTNALISNIYFTSLFALEMLLKILIVGPGFYKPNYN 841


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Db 750 IMIALVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPYKPNYN 809
Qy 842 IFDGVIVVISWEIVGOOGGLSVLRTPLMRVLKLVREFLPALORQLVLMKTDWNVATF 901
Db 810 IFDGVIVVISWEIVGOOGGLSVLRTPLMRVLKLVREFLPALORQLVLMKTDWNVATF 869
Qy 902 CMLMLFIFIPSIIGMLFGCKFASERDGLTLPDRKNFDSLWAIWIVTFQILTOEDWNKV 961
Db 870 CMLMLFIFIPSIIGMLFGCKFASERDGLTLPDRKNFDSLWAIWIVTFQILTOEDWNKV 929
Qy 962 LYNCAWSTSSWAALFYFALTMTFGNYVFNLLVAILVEGQAEQATKSESPDFPSVD 1021
Db 930 LYNCAWSTSSWAALFYFALTMTFGNYVFNLLVAILVEGQAEQATKSESPDFPSVD 989
Qy 1022 GDGRKKRLALVALGEHAELRKSLLPLLIHTAATPMHSHPKSSSTGCEALGSGSRRTSS 1081
Db 990 GDGRKKRLALVALGEHAELRKSLLPLLIHTAATPMHSHPKSSSTGCEALGSGSRRTSS 1049
Qy 1082 SGSAEPGAHHMKCPSARSPPHSPWSAASSWTSRRSSRNSLGRAPSLKERSPSGERRS 1141
Db 1050 SGSAEPGAHHMKCPSARSPPHSPWSAASSWTSRRSSRNSLGRAPSLKERSPSGERRS 1109
Qy 1142 LLSGEGODEEBSSEEDRASPAGSDHRRGSLERAKSFDLPDLTQVPLGHLRTASGR 1201
Db 1110 LLSGEGODEEBSSEEDRASPAGSDHRRGSLERAKSFDLPDLTQVPLGHLRTASGR 1169
Qy 1202 SSASEHQDCNGKSGASGRLATRTDDPOLQDGDNDDEGNLSKGERIOAWRSRLPACRE 1261
Db 1170 SSASEHQDCNGKSGASGRLATRTDDPOLQDGDNDDEGNLSKGERIOAWRSRLPACRE 1229
Qy 1262 RDSWSAIFPPQGRFLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFL 1321
Db 1230 RDSWSAIFPPQGRFLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFL 1289
Qy 1322 TLSNYLFTAVFLAEMTVKVALGWCFCGEQAYLSSWNVLGLLVLISVIDILVSMVSDSG 1381
Db 1290 TLSNYLFTAVFLAEMTVKVALGWCFCGEQAYLSSWNVLGLLVLISVIDILVSMVSDSG 1349
Qy 1382 TKILGMLRVLLRLTLRLPLRVISRAQGLKLWETLMSLAKPIGNIVVICAFPIIFILG 1441
Db 1350 TKILGMLRVLLRLTLRLPLRVISRAQGLKLWETLMSLAKPIGNIVVICAFPIIFILG 1409
Qy 1442 VQLFKGKFFVQCGEDTRNITNKSDEASVYRVRHKYNFNLGQALMSLFLVASKOGWVD 1501
Db 1410 VQLFKGKFFVQCGEDTRNITNKSDEASVYRVRHKYNFNLGQALMSLFLVASKOGWVD 1469
Qy 1502 IMYDGLDAVGVDQOPIMNHNPNMLLYFISLLIVAFVLMNFVGVVVENPHKCRQHQEEE 1561
Db 1470 IMYDGLDAVGVDQOPIMNHNPNMLLYFISLLIVAFVLMNFVGVVVENPHKCRQHQEEE 1529
Qy 1562 EARRREKRLRLLEKRRSKEKQMAEAOCKPYYSYDSRFRLLVHLLCTSHYLDLFTIGVI 1621
Db 1530 EARRREKRLRLLEKRRSKEKQMAEAOCKPYYSYDSRFRLLVHLLCTSHYLDLFTIGVI 1589
Qy 1622 GLNVVTAMEHYQOQILDEALKICNYIFTVIFVESVFKLVAFARFRFQDRWNQLDLA 1681
Db 1590 GLNVVTAMEHYQOQILDEALKICNYIFTVIFVESVFKLVAFARFRFQDRWNQLDLA 1649
Qy 1682 IVLLSITMGITLSEIENVLSLPINPFTIIRIMRVRIARVLKLLKQAVGMRALHTVMOALP 1741
Db 1650 IVLLSITMGITLSEIENVLSLPINPFTIIRIMRVRIARVLKLLKQAVGMRALHTVMOALP 1709
Qy 1742 QVGNLGLLFMLLFFIFAALGVELPGDLECDETHPCSLGHEATFRNFGMAFLTLFRVSTG 1801
Db 1710 QVGNLGLLFMLLFFIFAALGVELPGDLECDETHPCSLGHEATFRNFGMAFLTLFRVSTG 1769
Qy 1802 DNWNGIMKOPSRDCQDQESTCNTYIVISPIYFVSFVLTAQFVLVNVWLVAILMKHLEENKEA 1861
Db 1770 DNWNGIMKOPSRDCQDQESTCNTYIVISPIYFVSFVLTAQFVLVNVWLVAILMKHLEENKEA 1829
Qy 1862 KEAELEAELEBMKTLSPQPHSPLSGPFLWPGVEGVNSTDSPKGPAPHTTAHGAASGF 1921
Db 1830 KEAELEAELEBMKTLSPQPHSPLSGPFLWPGVEGVNSTDSPKGPAPHTTAHGAASGF 1889
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Qy 1922 SLEHPTWVPHPEEVPVLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTABERSLGHGWGL 1981
Db 1890 SLEHPTWVPHPEEVPVLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTABERSLGHGWGL 1949
Qy 1982 PKAQSGSILSVHSPADTSCILQPKDVHYLLQPHGAPTWCAGAI PKLPPGSPPLAQRPLR 2041
Db 1950 PKAQSGSILSVHSPADTSCILQPKDVHYLLQPHGAPTWCAGAI PKLPPGSPPLAQRPLR 2009
Qy 2042 RQAAIRTDSLVDQGLGSRDRELLSEVSGPSCPLTRSSSFWSGSSI:QVQORSGIQSKVSKHI 2101
Db 2010 RQAAIRTDSLVDQGLGSRDRELLSEVSGPSCPLTRSSSFWSGSSI:QVQORSGIQSKVSKHI 2069
Qy 2102 RLPAPCGLPEPSWAKDPETRSLSLELDTLSWISGDLPLPSSQEBPLPRDLKICYSVETO 2161
Db 2070 RLPAPCGLPEPSWAKDPETRSLSLELDTLSWISGDLPLPSSQEBPLPRDLKICYSVETO 2129
Qy 2162 SCRRRPFWLDEQRHRSIAVSCLDGSGQPRLCPSPSILGGQPLGPGSRPKKLSPPSIS 2221
Db 2130 SCRRRPFWLDEQRHRSIAVSCLDGSGQPRLCPSPSILGGQPLGPGSRPKKLSPPSIS 2189
Qy 2222 IDPPESGGRPPCPGVCRLRRRAPASDKDPSVSSPLDSTAASPPKDTLSLSGLSDP 2281
Db 2190 IDPPESGGRPPCPGVCRLRRRAPASDKDPSVSSPLDSTAASPPKDTLSLSGLSDP 2249
Qy 2282 TDMDP 2286
Db 2250 TDMDP 2254
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RESULT 2

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AAG35186
ID AAG35186 PRELIMINARY; PRT; 2254 AA.
AC AAG35186;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE Calcium channel alpha-1-G subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=brain;
RX PubMed=11073957;
RA McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,
RA Baillie D.L., Stea A., Snutch T.P.;
RT "Molecular and functional characterization of a family of rat brain T-
RT type calcium channels."
RL J. Biol. Chem. 276:3999-4011(2001).
DR EMBL; AF290212; AAG35186.2; -.
SQ SEQUENCE 2254 AA; 250405 MW; 697BBE06360CF0F6 CRC64;
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Query Match 96.9%; Score 11657; DB 2; Length 2254;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2219; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 62 GAAGAGSTEKDPGSADSEAGLPYPALAPVVFYLSQDSRPSRSCVLTVCNPFWRVSM 121
Db 30 GROGPOSTEKDPGSADSEAGLPYPALAPVVFYLSQDSRPSRSCVLTVCNPFWRVSM 89
Qy 122 VILLNCVTIGMFRPCEDIIACDSQRCRILQAFDDIFAFFAVEMVVMVVALGIFGKKCYLG 181
Db 90 VILLNCVTIGMFRPCEDIIACDSQRCRILQAFDDIFAFFAVEMVVMVVALGIFGKKCYLG 149
Qy 182 DTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRVRLPLRAINRVSMRILVTLTDLTP 241
Db 150 DTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRVRLPLRAINRVSMRILVTLTDLTP 209
Qy 242 MLGNVLLLCFFVFFVFFIGVGVQLWAGLLNRCLFNPENFSLPLSVDLPEYVQYOTENEDESP 301
Db 210 MLGNVLLLCFFVFFVFFIGVGVQLWAGLLNRCLFNPENFSLPLSVDLPEYVQYOTENEDESP 269
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QY 302 ICSQPRENGMRSRCSVPTLRGEGGGPPCSLDYETYNSSNTTCCVNNQYNTCSAGBN 361
DB 270 ICSQPRENGMRSRCSVPTLRGEGGGPPCSLDYETYNSSNTTCCVNNQYNTCSAGBN 329
QY 362 PFKAINDNTGYAWIALFOVITILEGWDIMYFVMDAHSFYNFYIFILLIIVGFFMINL 421
DB 330 PFKAINDNTGYAWIALFOVITILEGWDIMYFVMDAHSFYNFYIFILLIIVGFFMINL 389
QY 422 CLVVIATQFSEKQRESQMBEQRVFLSNASTLASFSEPGSCYBELLKYLVIYLKKAAR 481
DB 390 CLVVIATQFSEKQRESQMBEQRVFLSNASTLASFSEPGSCYBELLKYLVIYLKKAAR 449
QY 482 RLAQVSRRAIGVRAIGLLSPVARSQGPQSPGSCSTRSHRRLSVHLLVHHHHHHHHYHLGN 541
DB 450 RLAQVSRRAIGVRAIGLLSPVARSQGPQSPGSCSTRSHRRLSVHLLVHHHHHHHHYHLGN 509
QY 542 GTLRVRPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAEVHSFYHADCHLEFVRQC 601
DB 510 GTLRVRPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAEVHSFYHADCHLEFVRQC 569
QY 602 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTLSFNIPPGPF 661
DB 570 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTLSFNIPPGPF 629
QY 662 SSMHKLLETQSTGACHSSCKISSPCSADSGACGPDSCPCYARTGAGEPESADHVMPPDS 721
DB 630 SSMHKLLETQSTGACHSSCKISSPCSADSGACGPDSCPCYARTGAGEPESADHVMPPDS 689
QY 722 SEAVYEFTQDAQSHDLRDPHSRRRORSLGPDAPSPSVLAFWRLI CDTFRKIVDSYFGRG 781
DB 690 SEAVYEFTQDAQSHDLRDPHSRRRORSLGPDAPSPSVLAFWRLI CDTFRKIVDSYFGRG 749
QY 782 IMAILVNTLSMGIEVHEQEPELTNALEISNIVFTSLFALEMLKLLVYGPFGYKPNYN 841
DB 750 IMAILVNTLSMGIEVHEQEPELTNALEISNIVFTSLFALEMLKLLVYGPFGYKPNYN 809
QY 842 IPDGIVIVISWEIVGQGGGLSVLRTFRLMVLKLVRELPAQOLVVLKMTMNVATF 901
DB 810 IPDGIVIVISWEIVGQGGGLSVLRTFRLMVLKLVRELPAQOLVVLKMTMNVATF 869
QY 902 CMLMLFIFISILGMLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTOEDWNKV 961
DB 870 CMLMLFIFISILGMLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTOEDWNKV 929
QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLVAILVEGFOAGDQATKSESEDDFFSPSYD 1021
DB 930 LYNGMASTSSWAALYFIALMTFGNYVLFNLVAILVEGFOAGDQATKSESEDDFFSPSYD 989
QY 1022 GGDGRKRLALVALGHAELRKSLLPPLIHTAATPMWHPKSSSTGVGALGSGSRRTSS 1081
DB 990 GGDGRKRLALVALGHAELRKSLLPPLIHTAATPMWHPKSSSTGVGALGSGSRRTSS 1049
QY 1082 SGSAEPGAHHMKCPSPARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1141
DB 1050 SGSAEPGAHHMKCPSPARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1109
QY 1142 LLSGEGQESQDEESESSEDRASPAGSDHHRGSLEREAKSFDLPDLQVGLHRTASGR 1201
DB 1110 LLSGEGQESQDEESESSEDRASPAGSDHHRGSLEREAKSFDLPDLQVGLHRTASGR 1169
QY 1202 SSASEHODCNKGASGRLATLTDDPOLDDDDNDGNLSKGERIQAWVRSLPACCRE 1261
DB 1170 SSASEHODCNKGASGRLATLTDDPOLDDDDNDGNLSKGERIQAWVRSLPACCRE 1229
QY 1262 RDSWSAYIFPPQSRFLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSABRIFL 1321
DB 1230 RDSWSAYIFPPQSRFLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSABRIFL 1289
QY 1322 TLSNYIFTAFLAEMTVKVALGWCFOEQAYLRSSMNVLGHLVLSVIDILVSMVSDSG 1381
DB 1290 TLSNYIFTAFLAEMTVKVALGWCFOEQAYLRSSMNVLGHLVLSVIDILVSMVSDSG 1349

QY 1382 TKILGMLRVLRLLRTRPLRVISRAQGLKLVVETLMSLKPIGNIVIVICCAFFIIFGLG 1441
DB 1350 TKILGMLRVLRLLRTRPLRVISRAQGLKLVVETLMSLKPIGNIVIVICCAFFIIFGLG 1409
QY 1442 VOLPKGPFVFCQGGEDTRNITNKSDCAEASYWVPHKYNFNDLGOALMSLFLVASKDGWD 1501
DB 1410 VOLPKGPFVFCQGGEDTRNITNKSDCAEASYWVPHKYNFNDLGOALMSLFLVASKDGWD 1469
QY 1502 IMYDGLDAVGVDQOPIMNHNPMMLLYFTSFLLIIVAFFVLNMFVGVVVENFHKRQHOBEE 1561
DB 1470 IMYDGLDAVGVDQOPIMNHNPMMLLYFTSFLLIIVAFFVLNMFVGVVVENFHKRQHOBEE 1529
QY 1562 EARREERKRLRLEKRRSEKQMAEAQCKPYYSRFRLLVHLLCTSHYLDLPIITGVI 1621
DB 1530 EARREERKRLRLEKRRSEKQMAEAQCKPYYSRFRLLVHLLCTSHYLDLPIITGVI 1589
QY 1622 GLNVVTWAMEHYQOQOILDEALKICNYITFTVIFVESVFKLVAFAFRFFQDRNNOLDLA 1681
DB 1590 GLNVVTWAMEHYQOQOILDEALKICNYITFTVIFVESVFKLVAFAFRFFQDRNNOLDLA 1649
QY 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALIHTVMQALP 1741
DB 1650 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALIHTVMQALP 1709
QY 1742 QVGNLGLLFFMLFFIFAALGVLEFGDLECDETHPCGELGRHATFRNFGMAFUTLFRVSTG 1801
DB 1710 QVGNLGLLFFMLFFIFAALGVLEFGDLECDETHPCGELGRHATFRNFGMAFUTLFRVSTG 1769
QY 1802 DNWNGIMKDPBRDCQESTCYNTVISPIYFSFVLTAQFVLNVNVIIVLMKHLESNKEA 1861
DB 1770 DNWNGIMKDTLRDCQESTCYNTVISPIYFSFVLTAQFVLNVNVIIVLMKHLESNKEA 1829
QY 1862 KEEAELEAELEEMKTLSPQHPSPGSPFLMPGVEGVNSTDSKPCGAPHTTAHI GAASGF 1921
DB 1830 KEEAELEAELEEMKTLSPQHPSPGSPFLMPGVEGVNSTDSKPCGAPHTTAHI GAASGF 1889
QY 1922 SLEHPTMVPHEEVPVPLGPDLLTVRKSGVSTHSLPNDSYMCRNGSTAERSLGHRGWL 1981
DB 1890 SLEHPTMVPHEEVPVPLGPDLLTVRKSGVSTHSLPNDSYMCRNGSTAERSLGHRGWL 1949
QY 1982 PKAQSGSILSVHSQADTSCILQPKDVHYLLQPHGAPTWGAI PKLPGRSPLAQRPLR 2041
DB 1950 PKAQSGSILSVHSQADTSCILQPKDVHYLLQPHGAPTWGAI PKLPGRSPLAQRPLR 2009
QY 2042 ROAAIRTDSDLVQGLSGREDLLSEVSGSPCLTRSSSEFWGSSIQVQQRSGIQSKVSKHI 2101
DB 2010 ROAAIRTDSDLVQGLSGREDLLSEVSGSPCLTRSSSEFWGSSIQVQQRSGIQSKVSKHI 2069
QY 2102 RLPAPCPGLEPSWAKDPPETRSSELDLTELSTWISGDLPLSSQBEPLFPADLKKCYSVETQ 2161
DB 2070 RLPAPCPGLEPSWAKDPPETRSSELDLTELSTWISGDLPLSSQBEPLFPADLKKCYSVETQ 2129
QY 2162 SCRRPFGWLDRORHSTAVSCLDGSGOPRLCPSPSSILGQPLGGPSPKPKLSPSPSIS 2221
DB 2130 SCRRPFGWLDRORHSTAVSCLDGSGOPRLCPSPSSILGQPLGGPSPKPKLSPSPSIS 2189
QY 2222 IDPPPSQGRSPCPSCVCLRRRAPASDSKDPVSVSPDLSTAAASPSPKDTLSLGSJSSDP 2281
DB 2190 IDPPPSQGRSPCPSCVCLRRRAPASDSKDPVSVSPDLSTAAASPSPKDTLSLGSJSSDP 2249
QY 2282 TMDMP 2286
DB 2250 TMDMP 2254

RESULT 3

Q9WUB8
ID Q9WUB8 PRELIMINARY; PRT; 2288 AA.
AC Q9WUB8;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE T-type calcium channel isoform.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=20081696; PubMed=10615950;
 RA Zhuang H., Bhattacharjee A., Hu F., Zhang M., Goswami T., Wang L.,
 RA Wu S., Berggren P.O., Li M.;
 RT "Cloning of a T-type Ca2+ channel isoform in insulin-secreting
 RT cells.";
 RL Diabetes 49:59-64(2000).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
 CC family.
 DR EMBL; AF125161; AAD26858.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.
 DR GO; GO:0005261; F:voltage-gated activity; IEA.
 DR GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR002077; Ca_channel_alpha.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M_channel_nlg.
 DR InterPro; IPR005445; TVDCCalpha.
 DR Pfam; PF00520; Ion_trans; 4.
 DR PRINTS; PR00167; CACHANNEL.
 DR PROSITE; PS01629; TVDCCALPHA.
 DR Calcium channel; Calcium-binding; Ion transport; Ionic channel;
 KW Transmembrane. Transport; Voltage-gated channel.
 KW SEQUENCE 2288 AA; 253476 MW; B99DB5A1D81757F CRC64;
 SQ
 Query Match 95.9%; Score 11532; DB 2; Length 2288;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 2206; Conservative 1; Mismatches 18; Indels 34; Gaps 2;
 QY 62 GAAGASTGKDPGSADEAGLPPALAPVVFYLSQDSRPSWCLRTVCNPFERSVSM 121
 DB 30 GRQPGSTGKDPGSADEAGLPPALAPVVFYLSQDSRPSWCLRTVCNPFERSVSM 89
 QY 122 VILLNCVTGLMPRPCEDIACDSORCILOAFDFIFAFFAVEMVVMVALGIFGKKCYLG 191
 DB 90 VILLNCVTGLMPRPCEDIACDSORCILOAFDFIFAFFAVEMVVMVALGIFGKKCYLG 149
 QY 182 DTWNRLDFFIVTAGMLSEYSLDLQNVSFSAVRTVRLRLPRLAINEVPMSRILVTLTLLDTP 241
 DB 150 DTWNRLDFFIVTAGMLSEYSLDLQNVSFSAVRTVRLRLPRLAINEVPMSRILVTLTLLDTP 209
 QY 242 MLGNVLLLCFFVFFIFGIVGVQVWAGLLNRCPLPENFSLPLSDLEPYQTNEDESPF 301
 DB 210 MLGNVLLLCFFVFFIFGIVGVQVWAGLLNRCPLPENFSLPLSDLEPYQTNEDESPF 269
 QY 302 ICSQPRENGMRCRSVPTLRGEGGPPCPCLSDYETVNSSNTTCVANNQYVNCSSAGEHN 361
 DB 270 ICSQPRENGMRCRSVPTLRGEGGPPCPCLSDYETVNSSNTTCVANNQYVNCSSAGEHN 329
 QY 362 PFKGAINFNIGNYAWIAIFQVITLEGWVDIMYFVMDAHSFYFNFIYFILLIIVGSFFMINL 421
 DB 330 PFKGAINFNIGNYAWIAIFQVITLEGWVDIMYFVMDAHSFYFNFIYFILLIIVGSFFMINL 389
 QY 422 CLVVIATQSETKQRESQMLREORVRLFNASTLASFPSPGSCYEBLLKYLVLKKAAR 481
 DB 390 CLVVIATQSETKQRESQMLREORVRLFNASTLASFPSPGSCYEBLLKYLVLKKAAR 449
 QY 482 RLAQVSRALGVRAGLLSSPVARSQBPQSGSCSTRSHRLSVHHLVHHHHHHHHVHLGN 541
 DB 450 RLAQVSRALGVRAGLLSSPVARSQBPQSGSCSTRSHRLSVHHLVHHHHHHHHVHLGN 509
 QY 542 GTLRVPSPASPEIQDRDANGSRRLMLPPPTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 601

DB 510 GTLRVPSPASPEIQDRDANGSRRLMLPPPTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 569
 QY 602 APPRCPSEASGRVTGSGKVPYVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPGPF 661
 DB 570 APPRCPSEASGRVTGSGKVPYVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPGPF 629
 QY 662 SSMHKLLETOSTGACHSSCKISSPCSKADSGAGCPDSCPCYARTGAGEPESADHVMDS 721
 DB 630 SSMHKLLETOSTGACHSSCKISSPCSKADSGAGCPDSCPCYARTGAGEPESADHVMDS 689
 QY 722 SEAVYEFTQDAHQSDRLDRPHSRRRQSLGPDAPSSVLAFWRLICDTRFKIVDSKYFGRG 781
 DB 690 SEAVYEFTQDAHQSDRLDRPHSRRRQSLGPDAPSSVLAFWRLICDTRFKIVDSKYFGRG 749
 QY 782 IMTALLVNTLSMGIEYHQPEELTNALISNIVFTSLFALEMLLKLIVYGPFGYKPNYN 841
 DB 750 IMTALLVNTLSMGIEYHQPEELTNALISNIVFTSLFALEMLLKLIVYGPFGYKPNYN 809
 QY 842 IFDGVTVVISWEIVGQGGGLSVLATERLMRVLKVRFLPALORQIVLMKTMNDVATF 901
 DB 810 IFDGVTVVISWEIVGQGGGLSVLATERLMRVLKVRFLPALORQIVLMKTMNDVATF 869
 QY 902 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIYTVFOILTQEDWNKV 961
 DB 870 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIYTVFOILTQEDWNKV 929
 QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAE----- 1003
 DB 930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEIGKREDASGQSLCIQLP 989
 QY 1004 -----GDATKSESEPDFFSPVDGDKRKLALVALGHAELRKSLLPLLIHTAATPM 1058
 DB 990 VNSQGGDATKSESEPDFFSPVDGDKRKLALVALGHAELRKSLLPLLIHTAATPM 1049
 QY 1059 SHPKSSTGVEALGSGSRRTSSGSAEPGAHHEMKPPSARSSPHSPWSAASSWTSRR 1118
 DB 1050 SLPKSSTGVEALGSGSRRTSSGSAEPGAHHEMKPPSARSSPHSPWSAASSWTSRR 1109
 QY 1119 SSNSILGRAPSLKRRSPSGERRSLLSGEQESQDEEESSEEDRASPGSDHRRHGLERE 1178
 DB 1110 SSNSILGRAPSLKRRSPSGERRSLLSGEQESQDEEESSEEDRASPGSDHRRHGLERE 1169
 QY 1179 AKSSFDPDLTQVPGHLRTASGSSASEHQDCKGKASGRRLARTLTDDPOLDGDDNDE 1238
 DB 1170 AKSSFDPDLTQVPGHLRTASGSSASEHQDCKGKASGRRLARTLTDDPOLDGDDNDE 1229
 QY 1239 GNLKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFHVLVIIF 1298
 DB 1230 GNLKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFHVLVIIF 1289
 QY 1299 LNCITIAMRPKIDPHSAERIIFLTLSNYIFTAVFLAEMTVKVVVALGCFGEQAYLRSSWN 1358
 DB 1290 LNCITIAMRPKIDPHSAERIIFLTLSNYIFTAVFLAEMTVKVVVALGCFGEQAYLRSSWN 1349
 QY 1359 VLDGLLVLSVIDILVSVYSDGSKILGMLVRLRLTLPRLVISAQGLKLVWETLMS 1418
 DB 1350 VLDGLLVLSVIDILVSVYSDGSKILGMLVRLRLTLPRLVISAQGLKLVWETLMS 1409
 QY 1419 SLKPIGNIIVVICAPFIIFGILGVQLFGKFFVCOGEDTRNITNKSDCAEASVYRVRHKY 1478
 DB 1410 SLKPIGNIIVVICAPFIIFGILGVQLFGKFFVCOGEDTRNITNKSDCAEASVYRVRHKY 1469
 QY 1479 NFDNLGQALMSLFLVASKDGWVDIMYDGLDAVGVDQQPIIMNHNPMWLLYFISFLLIIVAFP 1538
 DB 1470 NFDNLGQALMSLFLVASKDGWVDIMYDGLDAVGVDQQPIIMNHNPMWLLYFISFLLIIVAFP 1529
 QY 1539 VLNMFVGVVVENFHKCRHQHEEERREKRLRLEKRR-----SKEQMAE 1587
 DB 1530 VLNMFVGVVVENFHKCRHQHEEERREKRLRLEKRRNMLDLDVIASGSSASAASE 1589
 QY 1588 AOCKPYSDYSRFRLLVHHLCTSHYLDLFTICVIGLVVTVMAHEHYQQPILDEALKICN 1647

Db 1590 AOCKPYSDYSRPFLVHLLCTSHVLDLFTVGVLGNVVTWMBHYQQPQLDEALKICN 1649
Qy 1648 YIFTVIFVFBSVFKLVAFRRPFRQDRWNQDLDAIVLLSIMGITLBEIEVNLSPINPTI 1707
Db 1650 YIFTVIFVFBSVFKLVAFRRPFRQDRWNQDLDAIVLLSIMGITLBEIEVNASUPINPTI 1709
Qy 1708 IRIMRVLRIRARVLLKMAVGMRLHTVMQALPOVGNLGLLFLMFLPFIIPAALGVLEFGD 1767
Db 1710 IRIMRVLRIRARVLLKMAVGMRLHTVMQALPOVGNLGLLFLMFLPFIIPAALGVLEFGD 1769
Qy 1768 LECDETHCEGLGRHATFRNFCMAFLTLFRVSTGDNWNGIMKDPDRDCDQESTCYNTVIS 1827
Db 1770 LECDETHCEGLGRHATFRNFCMAFLTLFRVSTGDNWNGIMKDLTRDCDQESTCYNTVIS 1829
Qy 1828 PIYFVSFVLTAQFVLVNVVIAVLMKHEESNKEAKEAELEAELEMKTLSPQPHSLG 1887
Db 1830 PIYFVSFVLTAQFVLVNVVIAVLMKHEESNKEAKEAELEAELEMKTLSPQPHSLG 1889
Qy 1888 SPFLWPGEVGNSTDSPKPGAPHTTAHIGAASGFSLEHPTWVPHPEEVVPLGPDLLTVR 1947
Db 1890 SPFLWPGEVGNSTDSPKPGAPHTTAHIGAASGFSLEHPTWVPHPEEVVPLGPDLLTVR 1949
Qy 1948 KSGVSRTHSLPNDSTCMCRNGSTAESLGRHGMGLPKAOSGSLSVHSQPADTSCILQPK 2007
Db 1950 KSGVSRTHSLPNDSTCMCRNGSTAESLGRHGMGLPKAOSGSLSVHSQPADTSCILQPK 2009
Qy 2008 DVHYLLQPHGAPTGAIPKLPPLPGSRPLAQRPLRQAARTDSLQVGLGSGREDLLSEVS 2067
Db 2010 DVHYLLQPHGAPTGAIPKLPPLPGSRPLAQRPLRQAARTDSLQVGLGSGREDLLSEVS 2069
Qy 2068 GPSCLTRSSSPFWGSSIQVQSRGSIQSKVSHIRLPAPCPGLEPSWAKDPETRSLEL 2127
Db 2070 GPSCLTRSSSPFWGSSIQVQSRGSIQSKVSHIRLPAPCPGLEPSWAKDPETRSLEL 2129
Qy 2128 DTELWISGDLPLSSQEEPLPRDLKCYSVETQSCRRRPGFWLDEQRHSHIAVCLDSG 2187
Db 2130 DTELWISGDLPLSSQEEPLSPDLKCYSVETQSCRRRPGFWLDEQRHSHIAVCLDSG 2189
Qy 2188 SOPRLCPSPSSIGGQPLGGGSRPKKLSPPSISIDPPESQSGRPSPGVCCLRRAPAS 2247
Db 2190 SOPRLCPSPSSIGGQPLGGGSRPKKLSPPSISIDPPESQSGRPSPGVCCLRRAPAS 2249
Qy 2248 DSKDPFVSSFLDSTAASPKKDTLSLGLSDPDMDP 2286
Db 2250 DSKDPFVSSFLDSTAASPKKDTLSLGLSDPDMDP 2288
RESULT 4
Q9WUT2
ID Q9WUT2 PRELIMINARY; PRT; 2295 AA.
AC Q9WUT2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Voltage-gated calcium channel, alpha-1-G subunit.
GN Name=Cacna1g;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99189326; PubMed=10087148;
RA Klugbauer N., Marais E., Lacinova L., Hofmann F.;
RT "A T-type calcium channel from mouse brain."
RL Pflugers Arch. 437:710-715 (1999).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.
CC EMBL; AJ012569; CAB40793.1; -.
DR MGD; MGI:1201678; Cacna1g.
DR GO; GO:0005886; C:plasma membrane; IDA.

DR GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat channel_Txpl.
DR InterPro; IPR002077; Ca_Channel_alpha.
DR InterPro; IPR005821; Ion_channel_nlg.
DR InterPro; IPR005820; M_channel_nlg.
DR InterPro; IPR005445; TVDCCAlphal.
DR Pfam; PF00520; Ion trans; 4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR01429; TVDCCALPHAL.
KW Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW Transmembrane; transport; Voltage-gated channel.
SQ SEQUENCE 2295 AA; 253957 MW; FE817D054ED26984 CRC64;
Query Match 94.6%; Score 11372.5; DB 2; Length 2295;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 2178; Conservative 12; Mismatches 34; Indels 43; Gaps 4;
Qy 62 GAAGAGSTKDPGGSADSEAGLPYAPALAPVVFYLSQDSRPSWCLRTVCNPFWRVSM 121
Db 30 GRQPGSTKDPGGSADSEAGLPYAPALAPVVFYLSQDSRPSWCLRTVCNPFWRVSM 89
Qy 122 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDRTFAFAVMMVMVALGIFGKKCYLG 181
Db 90 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDRTFAFAVMMVMVMVALGIFGKKCYLG 149
Qy 182 DTWNRDLDFVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRINRVFVSMRILVTLTLLDTP 241
Db 150 DTWNRDLDFVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRINRVFVSMRILVTLTLLDTP 209
Qy 242 MGNVLLLCFFVFTFEGIVGVOLMAGLLRNRCFTLPENFSLPLSVLEPYQTEDESPF 301
Db 210 MGNVLLLCFFVFTFEGIVGVOLMAGLLRNRCFTLPENFSLPLSVLEPYQTEDESPF 269
Qy 302 ICSPRENGMSCRVPTLRGEGGPGPCSJDYETVNSSTTTCVNNQYVNCISAGEHN 361
Db 270 ICSPRENGMSCRVPTLRGEGGPGPCSJDYETVNSSTTTCVNNQYVNCISAGEHN 329
Qy 362 PFKGAINFDNIGYAMIAIFQVITLLEGWVDIMYFVMDAHSFYNFYFILLIIVGSFMINL 421
Db 330 PFKGAINFDNIGYAMIAIFQVITLLEGWVDIMYFVMDAHSFYNFYFILLIIVGSFMINL 389
Qy 422 CLVVIATQFSETKQRESQIMREQRVRFSLNASTLASFSPEGSCYEELLYVILKKAAR 481
Db 390 CLVVIATQFSETKQRESQIMREQRVRFSLNASTLASFSPEGSCYEELLYVILKKAAR 449
Qy 482 RLAAQVSRAGVRAGLLSPPVARSQPOPSGSCSTRSHRRLSVHLLVHHHHHHHHYHLCN 541
Db 450 RLAAQVSRAGVRAGLLSPPVARSQPOPSGSCSTRSHRRLSVHLLVHHHHHHHHYHLCN 509
Qy 542 GTLRVPRASPEIQDRDANGSRMLMPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 601
Db 510 GTLRVPRASPEIQDRDANGSRMLMPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 569
Qy 602 APPPCPBESAGRTVSGKVPTVTSPPPELTKKALVEVAPSQCPPTLTFSNIPPGPF 661
Db 570 APPPCPBESAGRTVSGKVPTVTSPPPELTKKALVEVAPSQCPPTLTFSNIPPGPF 629
Qy 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESADHWMPDSD 721
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESADHWMPDSD 689
Qy 722 SEAVYEFTQDAQHSDLRDPHRRRRORSRGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 781
Db 690 SEAVYEFTQDAQHSDLRDPHRRRRORSRGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 748
Qy 782 IMAILVNTLSMGIEYHEQPELTNALEISNIVFSLFALEMLKLLVVGPGYIKNPYN 841
Db 749 IMAILVNTLSMGIEYHEQPELTNALEISNIVFSLFALEMLKLLVVGPGYIKNPYN 808
Qy 842 IPDGVTVIVSWVEIVGQQGGGSLVLRFTFRMLRVLKLVRFALQRLVLMKTMQNVATF 901
Db 809 IPDGVTVIVSWVEIVGQQGGGSLVLRFTFRMLRVLKLVRFALQRLVLMKTMQNVATF 868

QY 902 CMLLMFIFIFSIILGMLFGCKFASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
 Db 869 CMLLMFIFIFSIILGMLFGCKFASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 928
 QY 962 LYNMGASTSSWAALFYFIALMTFGNVVLPNLVAILVEGFAE-----1003
 Db 929 LYNMGASTSSWAALFYFIALMTFGNVVLPNLVAILVEGFAE-----1003
 QY 1004 -----GATKSESDPDPFSPVSDGDKRKLALVALGEHAEELKSLPLLIHTAATPM 1058
 Db 989 VNSGGDATKSESDPDPFSPVSDGDKRKLALVALGEHAEELKSLPLLIHTAATPM 1048
 QY 1059 SHPKSSSTGVEALGSGSRRTSSGSAEPGAAHEMKCPPGARSPPHSPWASAASWTSSR 1118
 Db 1049 SLPKSSSTGVEALGSGSRRTSSGSAEPGTAHEMKSPPARSPHSPWASAASWTSSR 1108
 QY 1119 SSRNLSGRAPSLKRRSPSGRRSLLSGEGQBSQDEESSEEDRASPAGSDHRRHGSLE 1178
 Db 1109 SSRNLSGRAPSLKRRSPSGRRSLLSGEGQBSQDEESSEEDRASPAGSDHRRHGSLE 1168
 QY 1179 AKSFDLPDLOVPLHRTASGRSSASEHODCNKGSAGRLARTLRDTPOLDGDDNDE 1238
 Db 1169 AKSFDLPDLOVPLHRTASGRSSASEHODCNKGSAGRLARTLRDTPOLDGDDNDE 1228
 QY 1239 GNLKSGERIQAWRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMPDHWVLVIF 1298
 Db 1229 GNLKSGERLAWVRARLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMPDHWVLVIF 1288
 QY 1299 LNCITIAMERPKDIPHAERIFLTLSNYIFTAVFLAEMTVKVALGFCGEGQAYLRSSN 1358
 Db 1289 LNCITIAMERPKDIPHAERIFLTLSNYIFTAVFLAEMTVKVALGFCGEGQAYLRSSN 1348
 QY 1359 VLGLLVLISVIDILVMSVDSGTGKIIGMLRVLRLEPLRVLISPAQGLKLVETLMS 1418
 Db 1349 VLGLLVLISVIDILVMSVDSGTGKIIGMLRVLRLEPLRVLISPAQGLKLVETLMS 1408
 QY 1419 SLKPIGNIVVICCAFFIFIGILGVQLFKGFFVCGQEDTRNITNKSCEASVYRWVRHKY 1478
 Db 1409 SLKPIGNIVVICCAFFIFIGILGVQLFKGFFVCGQEDTRNITNKSCEASVYRWVRHKY 1468
 QY 1479 NFNILQALMSLFLVASKDQWIMDYGDLDAVGVDQOQPIMNHPNMLLYFISFLLIVAFF 1538
 Db 1469 NFNILQALMSLFLVASKDQWIMDYGDLDAVGVDQOQPIMNHPNMLLYFISFLLIVAFF 1528
 QY 1539 VLNMFGVVVVENFHKCRHQHEEAREERREKRLRLEKRSKEKQMA-----1586
 Db 1529 VLNMFGVVVVENFHKCRHQHEEAREERREKRLRLEKRSKEKQMA-----1586
 QY 1587 -----EAQCKPYSDYSRFRLLVHLLCTSHYLDLFTITVIGLVNVTMAEHYQQOQILD 1640
 Db 1589 SASAASEAQCKPYSDYSRFRLLVHLLCTSHYLDLFTITVIGLVNVTMAEHYQQOQILD 1648
 QY 1641 EALKICNYIFTVIFVESVFKLVAFAFRFPQDRWNQDLIAIVLLSIMGITLIEEIVNLS 1700
 Db 1649 EALKICNYIFTVIFVESVFKLVAFAFRFPQDRWNQDLIAIVLLSIMGITLIEEIVNLS 1708
 QY 1701 LPNPTIIRIMRVLRIRVILKLLKMAVGRALLHTVMQALPOVGNIGLLPMLFFIFAAL 1760
 Db 1709 LPNPTIIRIMRVLRIRVILKLLKMAVGRALLHTVMQALPOVGNIGLLPMLFFIFAAL 1768
 QY 1761 GVLEFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPDRDCQEST 1820
 Db 1769 GVLEFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCQEST 1828
 QY 1821 CYNVTISPIFYFVFLTAQFVLNVVIAVLMKHLEESNKEAEAELEAELEEMKTLSP 1880
 Db 1829 CYNVTISPIFYFVFLTAQFVLNVVIAVLMKHLEESNKEAEAELEAELEEMKTLSP 1888
 QY 1881 QPHSPGLSGFLMPGVGVNSTSDPKGAPHTTAHIGAA-SGFSLEPHTVPHPPEVVPVL 1939
 Db 1889 QPHSPGLSGFLMPGVGVNSTSDPKGAPHTTAHIGAA-SGFSLEPHTVPHPPEVVPVL 1948

RESULT 5

Q6PFV8
 ID Q6PFV8 PRELIMINARY; PRT; 2248 AA.
 AC Q6PFV8;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Ccna1g protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057399; AAH57399.1;
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
 DR InterPro; IPR001682; Ca/Na pore.
 DR InterPro; IPR002111; Cat channel_TrpL.
 DR InterPro; IPR005821; Ion-trans.
 DR InterPro; IPR005820; M+channel_nlg.

QY 2090 RSGIQSKVSKHRLPAPCPGLEPWSAKDPPETRSLSLELDTLSWISGDLPLSSQEEPLFP 2149
 DB 2052 RSGSQSKVSKHRLPAPCPGLEPWSAKDPPETRSLSLELDTLSWISGDLPLSSQEEPLSP 2111
 QY 2150 RDLKKCYSVETQSCRRRRGFWMDEORRHSIAVCLDGSQPRLCPSLSSGQPIGGPGS 2209
 DB 2112 RDLKKCYSVETQSCRRRRGFWMDEORRHSIAVCLDGSQPRLCPSLSSGQPIGGPGS 2171
 QY 2210 RPKKKLSPPSISIDPPESQGRPPCPGVCLLRRRAPASDKDPSVSLDSTAASPSPKK 2269
 DB 2172 RPKKKLSPPSISIDPPESQGRPPCPGVCLLRRRAPASDKDPSVSLDSTAASPSPKK 2231
 QY 2270 DTLSSGLSSDPTMDP 2286
 DB 2232 DALSSGLSSDPTMDP 2248
 RESULT 6
 AAH57399 PRELIMINARY; PRT; 2248 AA.
 AC AAH57399;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Caenag protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Viallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalka J., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC057399; AAH57399.1; -;
 SQ SEQUENCE 2248 AA; 248888 MW; 332C5A8D9115A64F CRC64;
 Query Match 93.6%; Score 11263; DB 2; Length 2248;
 Best Local Similarity 96.3%; Pred. No. 0;
 Matches 2155; Conservative 12; Mismatches 40; Indels 30; Gaps 4;
 QY 62 GAAGAGSTKDPGASABEGLYPALAPVVFYLSQDSRPSWCLRTVCNPFERSVML 121
 DB 30 GROGPGSTKDPGASABEGLYPALAPVVFYLSQDSRPSWCLRTVCNPFERSVML 89
 QY 122 VILLNCVTLMGPRCEDIACDSQRILQAFDDFIFAFAVEMVVKVVALGIFGKKCYLG 181
 DB 90 VILLNCVTLMGPRCEDIACDSQRILQAFDDFIFAFAVEMVVKVVALGIFGKKCYLG 149

182 DTWNLDEFIIVAGMLEYSLDLQNVFSFSAVTRVRLPRAINRVPSMRILVTLLDLP 241
 DB 150 DTWNLDEFIIVAGMLEYSLDLQNVFSFSAVTRVRLPRAINRVPSMRILVTLLDLP 209
 QY 242 MLGNVLLLCFFVFFIFGIVGVLWAGLNRNCFLENFSLPLSDVLEPYQTENEDSPF 301
 DB 210 MLGNVLLLCFFVFFIFGIVGVLWAGLNRNCFLENFSLPLSDVLEPYQTENEDSPF 269
 QY 302 ICSPRENGMRSRCSVPTLRGEGGGPPCSDLYETYNSSNTTCVNMQYTNCSAGBN 361
 DB 270 ICSPRENGMRSRCSVPTLRGEGGGPPCGLDYAYNSSNTTCVNMQYTNCSAGBN 329
 QY 362 PFKGAINFDNIGYAWIAFQVITILEGWDIMYFMDAHSFNFIYFILLIIVGSFFML 421
 DB 330 PFKGAINFDNIGYAWIAFQVITILEGWDIMYFMDAHSFNFIYFILLIIVGSFFML 380
 QY 422 CLVVIATQFSETKQESQLMREQVRFLSNASTLASFSEPGSCYEELLKYVYLIRKAAR 481
 DB 381 -----FSETKQESQLMREQVRFLSNASTLASFSEPGSCYEELLKYVYLIRKAAR 432
 QY 482 RLAQVSRAGVRAGLLSPVARSQEPQPGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 541
 DB 433 RLAQVSRAGVRAGLLSPVVRGQEPQPGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 492
 QY 542 GTLRVPRASPEIODRDANGSRRLMLPPSTPTPSGGPRGASVHSFVHADCHLEPVRQ 601
 DB 493 GTLRVPRASPEIODRDANGSRRLMLPPSTPTPSGGPRGASVHSFVHADCHLEPVRQ 552
 QY 602 APPPRCPSEASGRVTVSGKVPVHTSPPEILKDKALVEVAPSGPPTLTSENPBGPF 661
 DB 553 APPPRCPSEASGRVTVSGKVPVHTSPPEMLKDKALVEVAPSGPPTLTSENPBGPF 612
 QY 662 SSMHKLLETOSTGACHSSCKISSPCSKADGACGPDSCPCYARTGAGEPESADHMPDS 721
 DB 613 SSMHKLLETOSTGACHSSCKISSPCSKADGACGPDSCPCYARTGAGEPESADHMPDS 672
 QY 722 SEAVYFTQDAQSDLRDPSRRQRSLGDPABSSVLAFWRLICDTFRKIVDSKYFGRG 781
 DB 673 SEAVYFTQDAQSDLRDPSRRQRSLGDPABSSVLAFWRLICDTFRKIVDSKYFGRG 731
 QY 782 IMTALLVNTLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLKLLVYGFVKPNYN 841
 DB 732 IMTALLVNTLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLKLLVYGFVKPNYN 791
 QY 842 IFDGVIVISVBEIVGQGGGLSVLRTRFLMRVLKIVRFLPALQRLVLMKTMNDVATF 901
 DB 792 IFDGVIVISVBEIVGQGGGLSVLRTRFLMRVLKIVRFLPALQRLVLMKTMNDVATF 851
 QY 902 CMLLMFLIFITSLGMHLFGCKEASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNV 961
 DB 852 CMLLMFLIFITSLGMHLFGCKEASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNV 911
 QY 962 LYNGMASTSSWAALYFIATLMTFGNYVLNLLVAILVEGFOAGDATKSESEDPFSPSVD 1021
 DB 912 LYNGMASTSSWAALYFIATLMTFGNYVLNLLVAILVEGFOAGDATKSESEDPFSPSVD 971
 QY 1022 GGDGRKKRLALVALGEAHLKSLPLIHTAATPMSPKSSSTGVGEALGSGSRTSS 1081
 DB 972 GGDGRKKRLALVALGEAHLKSLPLIHTAATPMSPKSSSTGVGEALGSGSRTSS 1031
 QY 1082 SGSAEPGAHHEMKCPSPARSPPHSPWASSTWTSRRSRNSLGRAPSLKRRSPSGERS 1141
 DB 1032 SGSAEPGAHHEMKCPSPARSPPHSPWASSTWTSRRSRNSLGRAPSLKRRSPSGERS 1091
 QY 1142 LLSGEGQESQDEESEEDRASPGSDHHRHRSLEAKSSFDLPDLTQVPGHLRTASGR 1201
 DB 1092 LLSGEGQESQDEESEEDRASPGSDHHRHRSLEAKSSFDLPDLTQVPGHLRTASGR 1151
 QY 1202 SSASEHQDCNGKSASGRRLARTLRTDDPQDGDGDDNDEGNLSKGERIQAWVRSLPACCRE 1261
 DB 1152 SSASEHQDCNGKSASGRRLARTLRTDDPQDGDGDDNDEGNLSKGERIQAWVRSLPACCRE 1211
 QY 1262 RDSWSAYIFPPQSRFELLCHRIITHKMFHDHVVVILFNCITIAMERPKIDPHSAERIFL 1321

Db 1212 RDSAVIFPQSRRLCHRIITHKFDHVVVIFLNCITIAMERPKIDPHSAERFL 1271
Qy 1322 TLSNYIFAVFAEATVAVKVALGWCFCGQAYLRSSNNVLDGLLVLIISVIDILVSNVSDSG 1381
Db 1272 TLSNYIFAVFAEATVAVKVALGWCFCGQAYLRSSNNVLDGLLVLIISVIDILVSNVSDSG 1331
Qy 1382 TKILGMLRVLRLLRLPLRVISRAQGLKLVVETILMSSIKPIGNIVLCVCCAFFIIFGLTG 1441
Db 1332 TKILGMLRVLRLLRLPLRVISRAQGLKLVVETILMSSIKPIGNIVLCVCCAFFIIFGLTG 1391
Qy 1442 VOLPKGFVFCQGEDTRNITKSDCAEASYSWRHKYFNDFNLGOALMSLFLVLSKDGWVD 1501
Db 1392 VOLPKGFVFCQGEDTRNITKSDCAEASYSWRHKYFNDFNLGOALMSLFLVLSKDGWVD 1451
Qy 1502 IMYDGLDVGVDQOPIMNHNPMMLLYFISFLIVAFFVNLMPGVVVVFHFKROHQEE 1561
Db 1452 IMYDGLDVGVDQOPIMNHNPMMLLYFISFLIVAFFVNLMPGVVVVFHFKROHQEE 1511
Qy 1562 EARRREKRLRLLEKRR-----SKEQMAEACQKPYYSYDSRFRLLVHLLCTS 1610
Db 1512 EARRREKRLRLLEKRR-----SKEQMAEACQKPYYSYDSRFRLLVHLLCTS 1571
Qy 1611 HYLDLFTVIGLVNVTWAMEHYQOPILDEALKICNVITFVFPESVKLVAFAPRRF 1670
Db 1572 HYLDLFTVIGLVNVTWAMEHYQOPILDEALKICNVITFVFPESVKLVAFAPRRF 1631
Qy 1671 FQDRWNQDLAIVLISIMGITLEEIVNLSLPINPTIIRIMVLRIRARVLRKLLKXAVGMR 1730
Db 1632 FQDRWNQDLAIVLISIMGITLEEIVNLSLPINPTIIRIMVLRIRARVLRKLLKXAVGMR 1691
Qy 1731 ALLHTVMQALPOVGNLGLIFMLIFRFAALGVELFGLDECDTHPCGEGLRHATFRNFGM 1790
Db 1692 ALLHTVMQALPOVGNLGLIFMLIFRFAALGVELFGLDECDTHPCGEGLRHATFRNFGM 1751
Qy 1791 AFLTLFRVSTGDNWNGIMKDPDRDCQESTCYNTVISPFIYFVSFVLTAQFVLVNVVIAVL 1850
Db 1752 AFLTLFRVSTGDNWNGIMKDLRDCQESTCYNTVISPFIYFVSFVLTAQFVLVNVVIAVL 1811
Qy 1851 MKHLEESNKAEEAELEAELEMLKTLSPQHSPLGSPFLMPGVGVNSTSPKPGAPH 1910
Db 1812 MKHLEESNKAEEAELEAELEMLKTLSPQHSPLGSPFLMPGVGVNSTSPKPGAPH 1871
Qy 1911 TTAHTGAA-SGRSLEHTWVPHPEEVPVLPDPLLTVRKSGVSRTHSLNDSTMCBNGST 1969
Db 1872 TTAHTGAASGFSLEHTWVPHPEEVPVLPDPLLTVRKSGVSRTHSLNDSTMCBNGST 1931
Qy 1970 AERSLGHRCWGLPKAQSGSTLSVHSPADTSCILQLPKDVHLYLLOPHGAPTWGAIPKLP 2029
Db 1932 AERSLGHRCWGLPKAQSGSTLSVHSPADTSCILQLPKDVHLYLLOPHGAPTWGAIPKLP 1991
Qy 2030 PGRSPLAQRLRQAIRTDLSVQGLSREDLLSEVSGPSCPLTRSSFWGSSSTOVQ 2089
Db 1992 PGRSPLAQRLRQAIRTDLSVQGLSREDLLSEVSGPSCPLTRSSFWGSSSTOVQ 2051
Qy 2090 RSGIQSKVSKHILPAPCGLEPSWAKDPETRSSLELDTLSWISGDLPLPSSQEBPLFP 2149
Db 2052 RSGIQSKVSKHILPAPCGLEPSWAKDPETRSSLELDTLSWISGDLPLPSSQEBPLFP 2111
Qy 2150 RDLKCYSVETQSCRRPFGWLDQRRHSIAVCLDSGQPRICPSPSSLGGLPGLGPGS 2209
Db 2112 RDLKCYSVETQSCRRPFGWLDQRRHSIAVCLDSGQPRICPSPSSLGGLPGLGPGS 2171
Qy 2210 RPKKLSPPSISIDPPESQSRPPCSGVCLRRAPASDKDPSVSPDLSTAAASPKK 2269
Db 2172 RPKKLSPPSISIDPPESQSRPPCSGVCLRRAPASDKDPSVSPDLSTAAASPKK 2231
Qy 2270 DTLSLSGLSDPTMDP 2286
Db 2232 DALSLGLSDPTDLDP 2248

CCAG HUMAN
ID CCAG HUMAN STANDARD; PRT; 2377 AA.
AC Q4397; Q4397; Q9NYU4; Q9NYU5; Q9NYU6; Q9NYU7; Q9NYU8;
AC Q9NYU9; Q9NYU0; Q9NYV1; Q9UHN9; Q9UHP0; Q9ULU6; Q9UNG7; Q9Y5T2;
AC Q9Y5T3;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-gated calcium channel alpha subunit Cav3.1) (Cav3.1c) (NBR13).
GN Name=CACNA1G; Synonyms=KIAA1123;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 4 AND 5).
RP TISSUE=Brain;
RX MEDLINE=200114446; PubMed=10548410;
RA Mittman S., Guo J., Agnew W.S.;
RT "Structure and alternative splicing of the gene encoding alpha1G, a human brain T calcium channel alpha subunit.";
RL Neurosci. Lett. 274:143-146(1999).
RN [2] SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Brain;
RX MEDLINE=20115462; PubMed=10648811;
RA Cribbs L.L., Gomora J.C., Daud A.N., Lee J.-H., Perez-Reyes E.;
RT "Molecular cloning and functional expression of ca(v)3.1c, a T-type calcium channel from human brain.";
RL FEBS Lett. 466:54-58(2000).
RN [3] SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 1-2 AND 6-13).
RP TISSUE=Brain;
RX MEDLINE=20158909; PubMed=10692398;
RA Monteil A., Chemin J., Bourinet E., Mennessier G., Lory P., Nargeot J.;
RT "Molecular and functional properties of the human alpha1G subunit that forms T-type calcium channels.";
RL J. Biol. Chem. 275:6090-6100(2000).
RN [4] SEQUENCE FROM N.A. (ISOFORM 14).
RP Kishi F.;
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [5] SEQUENCE OF 550-2377 FROM N.A. (ISOFORM 13).
RP TISSUE=Brain;
RX MEDLINE=22158633; PubMed=12168954;
RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
RT "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones.";
RL DNA Res. 9:99-106(2002).
RN [6] SEQUENCE OF 750-2377 FROM N.A. (ISOFORM 13).
RP TISSUE=Brain;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirose M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
RN [7] SEQUENCE FROM N.A. (ISOFORM 3), AND GENE STRUCTURE.
RP TISSUE=Prostatic carcinoma;
RX MEDLINE=99421245; PubMed=10493502;
RA Toyota M., Ho C., Ohe-Toyota M., Bayliss S.B., Issa J.-P.J.;
RT "Inactivation of CACNA1G, a T-type calcium channel gene, by aberrant methylation of its 5' CpG island in human tumors.";
RL Cancer Res. 59:4535-4541(1999).
RN [8] SEQUENCE OF 1126-1444; 1778-1927 AND 2021-2312 FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=98154730; PubMed=9495342;


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RESULT 8
Q6ZPX4
ID Q6ZPX4 PRELIMINARY; PRT; 1389 AA.
AC Q6ZPX4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE MKTAA1123 protein (Fragment).
GN Name=mKIAA1123;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
DR EMBL; AK129294; BAC98104.1; -.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat channel TrpL.
DR InterPro; IPR02077; Ca channel_alpha.
DR InterPro; IPR005821; Ion trans_nlg.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion trans; 2.
DR PRINTS; PR00167; CACHANNEL.
DR KEGG; Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW Transmembrane; Transport; Voltage-gated channel.
FT NON_TER 1 1
SQ SEQUENCE 1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;

Query Match
Best Local Similarity 94.8%; Pred. No. 0;
Matches 1317; Conservative 8; Mismatches 29; Indels 35; Gaps 3;

QY 933 LPDRKPFDSLLWAIVTVFQILTQEDMNKVLNGMASTSSWAALFYIALMTFGNYVLFNLL 992
Db 1 LPDRKPFDSLLWAIVTVFQILTQEDMNKVLNGMASTSSWAALFYIALMTFGNYVLFNLL 60
QY 993 VALLVGEFQAE-----GDAKSESEPDPPSPVDGGRKKR 1029
Db 61 VALLVGEFQAEETGKREDTSGQLPVSQGGDAKSESEPDPPSPVDGGRKKR 120
QY 1030 LALVALGEHAELRSLPLPIIHTAATPMSPKSSSTGVCEALGSGSRRTSSSSSAEPGA 1089
Db 121 LALVALGEHSELKSLPLPIIHTAATPMSLPKSSSTGVCEALGSGSRRTSSSSSAEPGT 180
QY 1090 AHHEMKCPSPARSPPHSPWASASWTSSRRSNLSGRAPSLKRSPSGRRSLLSGEGOE 1149
Db 181 AHHEMKSPSPARSPPHSPWASASWTSSRRSNLSGRAPSLKRSPSGRRSLLSGEGOE 240
QY 1150 SQDEESSREDRASPAGSDHRRHGSIEREAKSFDLPDTPVGLHRTASGRSSASEHQD 1209
Db 241 SQDEESSREDRASPAGSDHRRHGSIEREAKSFDLPDTPVGLHRTASGRSSASEHQD 300
QY 1210 CNKKSASGRILARTLRDTPDGLDGDNDNDEGNLSKGERIOAWVSRIPACCRERDSWYI 1269
Db 301 CNKKSASGRILARTLRDADPDLGDGDNDNDEGNLSKGERLRWVRARLPACCRERDSWYI 360
QY 1270 FPPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPDKIDPHSAERIFLTLSNYIFT 1329

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RESULT 9

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Db 361 FPPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPDKIDPHSAERIFLTLSNYIFT 420
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Db 421 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLDDLGLVLISVIDILVSMVSDSGTKILGMUR 480
QY 1390 VLRLRLTLPRLVISAQGLKLWETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGRF 1449
Db 481 VLRLRLTLPRLVISAQGLKLWETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGRF 540
QY 1450 FVQCQEDRNITNKSDCAEASVWRVHKYNFNLQALMSLFLVASKQGWDMYDGLDA 1509
Db 541 FVQCQEDRNITNKSDCAEASVWRVHKYNFNLQALMSLFLVASKQGWDMYDGLDA 600
QY 1510 VGVDQQPIMNHNPMWLLYFISFLIVAFVFLNMFGVVVFHFKCRQHQEERARRREK 1569
Db 601 VGVDQQPIMNHNPMWLLYFISFLIVAFVFLNMFGVVVFHFKCRQHQEERARRREK 660
QY 1570 RLRLLEKRR-----SKEQMAEACPKPYSDYSRFRLLVHHLCTSHYLDLFT 1618
Db 661 RLRLLEKRRMLDDVVIASGSSASAAEACPKPYSDYSRFRLLVHHLCTSHYLDLFT 720
QY 1619 GVIGLVVTVMAEHYQOQIILDEALKICNYITVIFVESVFKLVAFAPRFFQDRWNQL 1678
Db 721 GVIGLVVTVMAEHYQOQIILDEALKICNYITVIFVESVFKLVAFAPRFFQDRWNQL 780
QY 1679 DLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIRVLRVLRVLRVLRVLRVLRVLRV 1738
Db 781 DLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIRVLRVLRVLRVLRVLRVLRVLRV 840
QY 1739 ALPOVGNLGLLFWLLFFIIPALGVLELFGDLECDTHPCCEGLRHRATFRNFGMAFLTFRV 1798
Db 841 ALPOVGNLGLLFWLLFFIIPALGVLELFGDLECDTHPCCEGLRHRATFRNFGMAFLTFRV 900
QY 1799 STGDNWNGIMKDPSCDCQSTCVNTVISPIYFVSFVLTQAQFVLNVVIVIAVMKHLSESN 1858
Db 901 STGDNWNGIMKDTLRDCDCQSTCVNTVISPIYFVSFVLTQAQFVLNVVIVIAVMKHLSESN 960
QY 1859 KEAKEAEAELEAELEMKTLSPQHPSPGLSPFPLWPGVEGVNSTDSPKPGAPHTTAHGA 1918
Db 961 KEAKEAEAELEAELEMKTLSPQHPSPGLSPFPLWPGVEGVNSTDSPKPGAPHTTAHGA 1020
QY 1919 -SGFSLEHPTMVPHEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGH 1977
Db 1021 -SGFSLEHPTMVPHEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGH 1080
QY 1978 GWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTGAIPKLPDPPGRSPLAQ 2037
Db 1081 GWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTGAIPKLPDPPGRSPLAQ 1140
QY 2038 RPLRQAAIRTDLDVQGLGSRREDLLSEVSGPCPLTRSSSFWGSSSIQVQSGSGTSKV 2097
Db 1141 RPLRQAAIRTDLDVQGLGSRREDLLSEVSGPCPLTRSSSFWGSSSIQVQSGSGTSKV 1200
QY 2098 SKHIRLPACPGLEPSWAKDPPETRSLELDTLSWISGDLPLSPSSQEEPLFPDRDLKKCY 2157
Db 1201 SKHIRLPACPGLEPSWAKDPPETRSLELDTLSWISGDLPLSPSSQEEPLFPDRDLKKCY 1260
QY 2158 VETQSCRRRPPGFWLDRQHRHSIAVSCLDGSPQLCPSPSSILGGQPLGPGSPRPPKLLSP 2217
Db 1261 VEAQSCRRRPPGFWLDRQHRHSIAVSCLDGSPQLCPSPSSILGGQPLGPGSPRPPKLLSP 1320
QY 2218 PSISIDPPESQSRPPCSPGVCLRRRAPASDSKDPSSVSPPLDSTAASPSPKDTLSLSGL 2277
Db 1321 PSISIDPPESQSRPPCSPGVCLRRRAPASDSKDPSSVSPPLDSTAASPSPKDTLSLSGL 2277
QY 2278 SSDPTMDP 2286
Db 1381 SSDPTDLDP 1389

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BA Baillie D.L., Stea A., Snutch T.P.;
 RT "Molecular and functional characterization of a family of rat brain T-
 type calcium channels.";
 RL J. Biol. Chem. 276:3999-4011(2001).
 CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
 entry of calcium ions into excitable cells and are also involved
 in a variety of calcium-dependent processes, including muscle
 contraction, hormone or neurotransmitter release, gene expression,
 cell motility, cell division and cell death. The isoform alpha-1H
 gives rise to T-type calcium currents. T-type calcium channels
 belong to the "low-voltage activated (LVA)" group and are strongly
 blocked by nickel and mibefradil. A particularity of this type of
 channels is an opening at quite negative potentials, and a
 voltage-dependent inactivation. T-type channels serve pacemaking
 functions in both central neurons and cardiac nodal cells and
 support calcium signaling in secretory cells and vascular smooth
 muscle. They may also be involved in the modulation of firing
 patterns of neurons which is important for information processing
 as well as in cell growth processes.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in brain.
 CC -!- DOMAIN: Each of the four internal repeats contains five
 hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
 positively charged transmembrane segment (S4). S4 segments
 probably represent the voltage-sensor and are characterized by a
 series of positively charged amino acids at every third position.
 CC -!- PM: In response to raising of intracellular calcium, the T-type
 channels are activated by CaM-kinase II.
 CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
 family.
 CC
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL: AF290213; AAC35187.1; -.
 CC RGD: 68943; Cnacnal.
 CC InterPro: IPR001682; Ca/Na pore.
 CC InterPro: IPR002111; Cat_channel_TrpL.
 CC InterPro: IPR005821; Ion_trans.
 CC InterPro: IPR005820; M-channel_nlg.
 CC InterPro: IPR005445; TVDCCalpal.
 CC Pfam: PF00520; Ion_trans; 4.
 CC PRINTS: PR01629; TVDCCALPAL.
 CC Calcium channel; Glycoprotein; Ion transport; Ionic channel;
 KW Multigene family; Phosphorylation; Repeat; Transmembrane;
 KW Voltage-gated channel.
 FT REPEAT 87 422 I.
 FT REPEAT 776 1015 II.
 FT REPEAT 1292 1569 III.
 FT REPEAT 1607 1868 IV.
 FT DOMAIN 1 100
 FT TRANSMEM 101 119 Cytoplasmic (Potential).
 FT DOMAIN 120 139 S1 of repeat I (Potential).
 FT TRANSMEM 140 160 Extracellular (Potential).
 FT DOMAIN 161 169 S2 of repeat I (Potential).
 FT TRANSMEM 170 184 Cytoplasmic (Potential).
 FT DOMAIN 185 193 S3 of repeat I (Potential).
 FT TRANSMEM 194 212 Extracellular (Potential).
 FT DOMAIN 213 232 S4 of repeat I (Potential).
 FT TRANSMEM 233 252 Cytoplasmic (Potential).
 FT DOMAIN 254 394 S5 of repeat I (Potential).
 FT TRANSMEM 395 419 Extracellular (Potential).
 FT DOMAIN 420 790 S6 of repeat I (Potential).
 FT TRANSMEM 791 811 S1 of repeat II (Potential).
 FT DOMAIN 812 824 S2 of repeat II (Potential).
 FT TRANSMEM 825 846 Extracellular (Potential).
 FT DOMAIN 847 852 S2 of repeat II (Potential).
 FT TRANSMEM 853 871 Cytoplasmic (Potential).
 FT TRANSMEM 871 891 S3 of repeat II (Potential).

FT DOMAIN 872 879 Extracellular (Potential).
 FT TRANSMEM 880 903 S4 of repeat II (Potential).
 FT DOMAIN 904 914 Cytoplasmic (Potential).
 FT TRANSMEM 915 935 S5 of repeat II (Potential).
 FT DOMAIN 936 987 Extracellular (Potential).
 FT TRANSMEM 988 1012 S6 of repeat II (Potential).
 FT DOMAIN 1013 1301 Cytoplasmic (Potential).
 FT TRANSMEM 1302 1324 S1 of repeat III (Potential).
 FT DOMAIN 1325 1342 Extracellular (Potential).
 FT TRANSMEM 1343 1363 S2 of repeat III (Potential).
 FT DOMAIN 1364 1373 Cytoplasmic (Potential).
 FT TRANSMEM 1374 1393 S3 of repeat III (Potential).
 FT DOMAIN 1394 1407 Extracellular (Potential).
 FT TRANSMEM 1408 1429 S4 of repeat III (Potential).
 FT DOMAIN 1430 1439 Cytoplasmic (Potential).
 FT TRANSMEM 1440 1463 S5 of repeat III (Potential).
 FT DOMAIN 1464 1540 Extracellular (Potential).
 FT TRANSMEM 1541 1566 S6 of repeat III (Potential).
 FT DOMAIN 1567 1621 Cytoplasmic (Potential).
 FT TRANSMEM 1622 1642 S1 of repeat IV (Potential).
 FT DOMAIN 1643 1656 Extracellular (Potential).
 FT TRANSMEM 1657 1678 S2 of repeat IV (Potential).
 FT DOMAIN 1679 1685 Cytoplasmic (Potential).
 FT TRANSMEM 1686 1704 S3 of repeat IV (Potential).
 FT DOMAIN 1705 1718 Extracellular (Potential).
 FT TRANSMEM 1719 1742 S4 of repeat IV (Potential).
 FT DOMAIN 1743 1756 Cytoplasmic (Potential).
 FT TRANSMEM 1757 1777 S5 of repeat IV (Potential).
 FT DOMAIN 1778 1840 Extracellular (Potential).
 FT TRANSMEM 1841 1868 S6 of repeat IV (Potential).
 FT DOMAIN 1869 2359 Cytoplasmic (Potential).
 FT TRANSMEM 521 531 Poly-His.
 FT DOMAIN 1594 1597 Calcium ion selectivity and permeability
 FT SITE 378 (By similarity).
 FT SITE 971 Calcium ion selectivity and permeability
 FT SITE 1515 Calcium ion selectivity and permeability
 FT SITE 1813 Calcium ion selectivity and permeability
 FT CARBOHYD 192 192 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 271 271 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 1477 1477 N-linked (GLCNAC...) (Potential).
 SQ SEQUENCE 2359 AA; 261138 MW; F738083E94180081 CRC64;
 Query Match 51.8%; Score 6226; DB 1; Length 2359;
 Best Local Similarity 56.3%; Pred. No. 4.5e-303;
 Matches 1356; Conservative 248; Mismatches 518; Indels 286; Gaps 58;
 QY 30 LARGWTRRMERAPRSRDSFV-ASRSSTTCPG---PGAAGAG-STEKDPGS---AD---S 78
 DB 6 LAADDEVPLGASPPAPAPVRASPGAPGREGSGSGVLAPESGTGCGALGAD 65
 QY 79 EAEGLPYPALPVVFFYLSQDSRPSWCLRTVCNPFVRSVLMVLLNCLVTGLMPRCD 138
 DB 66 EEPQVPYPALAATVFFCLGQTTRPSWCLRLVCNPFVRSVLMVLLNCLVTGLMPRCD 125
 QY 139 IACDSORCILQAFDDFIFAFFAVEMVVMKVALGIFGKCYLGDTWNRIDFFIVIAMLE 198
 DB 126 VECRERCISILEAFDDFIFAFFAVEMVVMKVALGIFGKCYLGDTWNRIDFFIVIAMLE 185
 QY 199 YSLDQNVSFSAVRTVRVLRPLRINRVPSMRILVTLTLDLTPMLGNVLLLCFFVFFIFG 258
 DB 186 YSLDGHNVSLSAIRTVRVLRLPLRINRVPSMRILVTLTLDLTPMLGNVLLLCFFVFFIFG 245
 QY 259 IVGVOLWAGLLNRCFLPNFSLPLSVD-LEPYQTENEDESFFICSPRENGMRSCRV 317
 DB 246 IVGVOLWAGLLNRCFLDLSAFVRNNNLTLFLRPPYQTEEGEENPFICSSPRDNGMKCSHI 305
 QY 318 PT---LRGEGGGPPCSLDIYETY-----NSSSNITTCVNNQYNTNCASAGHNPFKGA 367
 DB 306 PSRRLRVQ-----CTLGWEAYGQPAEDGAGRNACINWNNQYNNVCRSGEENPHNGAI 359

QY	1392	RLRLTLPLRVLISRAQGLKLVWETLMSLSLPIGNIWIVICCAFFIIFGILGVQLFKGKFFV	1451
Db	1410	RLRLTLPLRVLISRAQGLKLVWETLMSLSLPIGNIWIVICCAFFIIFGILGVQLFKGKFFV	1469
QY	1452	QOEDTNIITNKSCAASRYRWHKYNFDMGALMSLFLVASKDQWIMYDGLDVG	1511
Db	1470	CEGTDRTNITTKAACHAARVWRKYNFDMGALMSLFLVSKDQWIMYDGLDVG	1529
QY	1512	VDQOPIMNHNPMWLLYITISFLIIVAFVNNFVGVVNFHFKCRHQHQBEEBARREERKL	1571
Db	1530	IDQOPVQNNHNPMWLLYIFISFLIIVFVFLNMFVGVVNFHFKCRHQHQBEEBARREERKL	1589
QY	1572	RLLEKRSRSEKQMAEACQKDYSDYFRLLVHLCTSHYLDLITGVIGLVNVTMAME	1631
Db	1590	RLLEKRSRSEKQMAEACQKDYSDYFRLLVHLCTSHYLDLITGVIGLVNVTMAME	1642
QY	1632	HYQOQILDEALKICNYITFTVIVFESVFKLVAFAPRFFODRMNQLDLAIVLLSIMGIT	1691
Db	1643	HYQOQILDEALKICNYITFTVIVFESVFKLVAFAPRFFODRMNQLDLAIVLLSIMGIT	1702
QY	1692	LEEIEVNLSPINPTIIRIMRVLRARVLKLMVAVGMRALLHTVMQALPQVGNLGLPM	1751
Db	1703	LEEIEVNLSPINPTIIRIMRVLRARVLKLMVAVGMRALLHTVMQALPQVGNLGLPM	1762
QY	1752	LLFFIPAALGVLEFGLDECEDETHPCGELGRHATFNFQMAFLTLFRVSTGDMNWMGIMKDP	1811
Db	1763	LLFFIPAALGVLEFGLDECEDETHPCGELGRHATFNFQMAFLTLFRVSTGDMNWMGIMKDP	1822
QY	1812	SRDC--DOESICYNVTSPIVFVFLTAQVFLVNVVIAVLMKHLSEKAEAELE	1868
Db	1823	LRECTREDKHCUSYLPALSPVYFVTFMLVAQVFLVNVVIAVLMKHLSEKAEAELE	1882
QY	1869	ASLEIEVNLSPINPTIIRIMRVLRARVLKLMVAVGMRALLHTVMQALPQVGNLGLPM	1928
Db	1883	ASLEIEVNLSPINPTIIRIMRVLRARVLKLMVAVGMRALLHTVMQALPQVGNLGLPM	1904
QY	1929	VHPPEVVPVLPDPLLTVRKSGVSRHSLPNDSYMCNGSTAESLGHGWLPL	1982
Db	1905	-----QGTQDPTNLLVVRKSVSRMLSLPNDSYMCNGSTAESLGHGWLPL	1954
QY	1983	KAQSGSILSVHSPADTSCILQLP-----KDVHLLQPHGAPTGAIPKLPFGGRS	2033
Db	1955	ETVTGPTVTAHSPPLPRASFQVPSAASSPARVSDPLCALSPRGTP-----RS	2002
QY	2034	PLAQRPLRQAARTDLDL--VOGLSREDLSEVSGPCLTRSSSFWG-----	2082
Db	2003	LSLSRLILCRQEAHSESELEGKVDVVG--DSIPDYTEPAENMSTQASTGAPSPPCSPR	2060
QY	2083	SSIQVOQRSGIOSKVSXKIRLPAPCPGLEPFSWAKOPPETRSSLELDTLSWISGDLPS	2141
Db	2061	PASVTRKHTFGORCISR-----PPTLGGDEAABD-----ADEEVSHITSSAHPW	2108
QY	2142	SQEEPLPP-----RDLKCYSVETQSCRRRPGFVLDQRRHSIAV-----	2181
Db	2109	PATEPHSPASPTASPVKGTWGSGRDPRRCSDVAQSFCLKPG-RPDAQWSSVELDNGE	2167
QY	2182	SLDLSGS-----QPRLCPSSESLGGQPLGGSPRKKLSPPSISIDPP--ESQSR	2231
Db	2168	SHLESGEVRKASELEPAL-----GSRKKKMSPPCISIBPTTKDESSR	2212
QY	2232	PPCSFG--VCLRRAPASDS--KDPVSVSPDLSTAAAP-----SPKDDTLISUG	2276
Db	2213	PPAEEGNTLRRTPSCAALHRDCPEPTGCTGGDPVAKGERWQASCRASHLITVPN	2272
QY	2277	LSSDPTDM 2284	
Db	2273	FAPEPLDM 2280	

RESULT 11
CCAH HUMAN
ID CCAH HUMAN STANDARD; PRT: 2353 AA.
AC Q95180; Q95802; Q8W16; Q96Q16; Q96R29; Q9NY4; Q9NY5;

QY	368	NFONIGYAWIAFOVITLEGWVDIMYFMDAHSPYNTIYFILLIIVSGFFMINCLVIVIA	427
Db	360	NFDNIGYAWIAFOVITLEGWVDIMYFMDAHSPYNTIYFILLIIVSGFFMINCLVIVIA	419
QY	428	TOFSETKOREQOLMREORVFLSNASTIASSEPGSCYEEELKVLVILTKAARLAQVS	487
Db	420	TOFSETKOREQOLMREORVFLSNASTIASSEPGSCYEEELKVLVILTKAARLAQVS	479
QY	488	RAIGVRAGLLSSPYAR-----SGOEPQSPGCTSRSHRLSVHLLV-HHHHHHHHHYHLGN	541
Db	480	ARMOSRMKKVDPSTVGVQGGPRPRAG-----RTASVHLLVYHHHHHHHHYHFSH	534
QY	542	GTLRVPRASPEIQDRDANGSRRLM--LEPPPTPTSPGGPRGAESVHSHADCHLEPVR	599
Db	535	GGPR--RPSPE-----PGAGDNELVRACAPPPSPGHGPP-DSESVHSHADCHVEGPQ	587
QY	600	COAPPRCPSEASGRVSGS--KVYPTV-----HTSPPEILKDKALVEVAPSP	646
Db	588	ERARVAHSIATAASLKLASGLGTMYPTILPSGTVNSKGGTSRSPKGLRG-----AGAP	641
QY	647	GPPTLTISFNI--PPGPFSSMHKLLETQSTGACHSSCK--ISSPC-----SKADSGACGDSCP	700
Db	642	GAUVSPISLGSGRPYEYKIQDVVGQGLGRASSHLSGLSVPCPLPSPOAGTLTCLKSCP	701
QY	701	YCARTGAGEP--ESADHVPDSDSEAVYFTQDAQHSDLRDP-----HSERROR	747
Db	702	YCA-SALEDEPEFSGESGSDAHGVYFTQDVHGDGRDPEVQVQPHVEYGTGCHSNERR	760
QY	748	S-LGPDABESSVLAFWRLLICDTRFKIVDSKYGRGIMAILNVLNLSMGIEYHEQPELTN	806
Db	761	TPLRASQPGGGLHWASFGKLRIVDSKYFNRGIMAILNVLNLSMGIEYHEQPELTN	820
QY	807	ALEISNIVTSLFALBMLKLVYGPFGYIKXPYINFDGVIIVVISVWEIVGQGGGLSVL	866
Db	821	ALEISNIVTSLFALBMLKLVYGPFGYIKXPYINFDGVIIVVISVWEIVGQGGGLSVL	880
QY	867	RTFLMRVLKLVFLPALQOLVLMKMDNVATFCMLMLFIFISILGMHLFGCKEAS	926
Db	881	RTFLMRVLKLVFLPALQOLVLMKMDNVATFCMLMLFIFISILGMHLFGCKFSL	940
QY	927	ERD-GDTLPDRKDFSLIWAIVTFQILLTQEDMNVLNMGASTSSWAAIFYFVALMTFGN	985
Db	941	KTDSGTVPDRKDFSLIWAIVTFQILLTQEDMNVLNMGASTSSWAAIFYFVALMTFGN	1000
QY	986	YVFLNLLVALIVGVFOAEGDATKSEPPDFPSVDGDRKXRL-----ALVALG	1036
Db	1001	YVFLNLLVALIVGVFOAEGDATKSEPPDFPSVDGDRKXRL-----ALVALG	1060
QY	1037	EHAELRSLPLPILIIHTAATPMGHPKSS-STGVGEALGSGSRRTSSSGSAEPGAHHEM	1095
Db	1061	GHLEGRSLPPLPILIIHTAATPMGHPKSS-STGVGEALGSGSRRTSSSGSAEPGAHHEM	1116
QY	1096	CPFSARSPPHSPSAASSTSRSSRNSLGRAPSLKRRSPSGERRSLLSGEGESQDEE-	1154
Db	1117	SLASLRSPCTPMGPNAGSRRSSWNSLGRAPSLKRRSPSGERRSLLSGEGESQDEE-	1176
QY	1155	ESSEEDRASPAQSHRHRGSLERAKSSFDLPDTLQVPLHRTASGRSSA--SEHODCN	1211
Db	1177	EDSRPSTGTHPGSPGPRATPLRAE-SLDHRSLDL-----CPFRPAALLPTKFHDCN	1229
QY	1212	GKSASGLARTLRTDQLDGDNDNDEGLSKGERIQAWVRSRLPACCRERDSVAYIFP	1271
Db	1230	QGMVALPSEFFLRIDSHKDAEEDDDIEDCCFRHLKVLPEYAPQWCRSRESWALYIFP	1289
QY	1272	QPSRFLRCHRIITHKMDHVVVLIIFLNCITIAMERKIDPHSAERIFLTLSNYIFAV	1331
Db	1290	PONRLRVSCQVIAHKMDHVVVLIIFLNCITIALERPDIDPGSTERAFLSVSNYIFAI	1349
QY	1332	FLAEMTVKVALGWCFCQVQVIRSNVNLGDLVLIVSVIDILVSNVSGTKILGMLRVL	1391
Db	1350	FVVENMVKVALGGLLWGEHVIQSSWNLGDLVLIVSVIDILVSNVSGTKILGMLRVL	1409

DT 15-JUL-1999 (Rel. 38, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-
 DE gated calcium channel T-type calcium channel alpha-1H subunit (Voltage-
 DE gated calcium channel alpha subunit Cav3.2) (Low-voltage-activated
 DE calcium channel alpha 3.2 subunit).
 GN Name=CACNA1H;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Heart;
 RX MEDLINE=98333998; PubMed=9670923;
 RA Cribbs L.L., Lee J.-H., Yang J., Satin J., Zhang Y., Daud A.N.,
 RA Barclay J., Williamson M.P., Fox M., Rees M., Perez-Reyes E.,
 RT "Cloning and characterization of alpha1H from human heart, a member of
 RT the T-type Ca²⁺ channel gene family.";
 RL Circ. Res. 83:103-109(1998).
 RN [2]
 RP REVISIONS.
 RA Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thyroid carcinoma;
 RX MEDLINE=99127945; PubMed=9930755;
 RA Williams M.E., Washburn M.S., Hans M., Urrutia A., Brust P.F.,
 RA Prodanovich P., Harpold M.M., Staufferman K.A.;
 RT "Structure and functional characterization of a novel human low-
 RT voltage activated calcium channel.";
 RL J. Neurochem. 72:791-799(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=21096910; PubMed=11157797;
 RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
 RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Higgs D.R.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2
 RT Mb of the short arm of human chromosome 16.";
 RL Hum. Mol. Genet. 10:339-352(2001).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Testis;
 RX MEDLINE=21864207; PubMed=11751928; DOI=10.1074/jbc.M105345200;
 RA Jagannathan S., Punt E.L., Gu Y., Arnould C., Sakas D., Barrett C.L.,
 RA Publicover S.J.;
 RT "Identification and localization of T-type voltage-operated calcium
 RT channel subunits in human male germ cells. Expression of multiple
 RT isoforms.";
 RL J. Biol. Chem. 277:8449-8456(2002).
 RN [6]
 RP SEQUENCE OF 86-817 FROM N.A.
 RA Cobley V.E.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 424-661 AND 838-2373 FROM N.A. (ISOFORM 1).
 RA Mittman S., Agnew W.S.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
 CC entry of calcium ions into excitable cells and are also involved
 CC in a variety of calcium-dependent processes, including muscle
 CC contraction, hormone or neurotransmitter release, gene expression,
 CC cell motility, cell division and cell death. The isoform alpha-1H
 CC gives rise to T-type calcium currents. T-type calcium channels
 CC belong to the "low-voltage activated (LVA)" group and are strongly
 CC blocked by nickel and mibefradil. A particularity of this type of
 CC channels is an opening at quite negative potentials, and a
 CC voltage-dependent inactivation. T-type channels serve pacemaking
 CC functions in both central neurons and cardiac nodal cells and
 CC support calcium signaling in secretory cells and vascular smooth

CC muscle. They may also be involved in the modulation of firing
 CC patterns of neurons which is important for information processing
 CC as well as in cell growth processes.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Alh-a;
 CC IsoId=O95180-1; Sequence=Displayed;
 CC Name=2; Synonyms=Alh-b;
 CC IsoId=O95180-2; Sequence=VSP_000949;
 CC -!- TISSUE SPECIFICITY: Expressed in kidney, liver, heart, brain.
 CC Isoform 2 seems to be testis-specific.
 CC -!- DOMAIN: Each of the four internal repeats contains five
 CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
 CC positively charged transmembrane segment (S4). S4 segments
 CC probably represent the voltage-sensor and are characterized by a
 CC series of positively charged amino acids at every third position.
 CC -!- PTM: In response to raising of intracellular calcium, the T-type
 CC channels are activated by CaM-kinase II.
 CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
 CC family.
 CC -!- CAUTION: AT-AC pre mRNA splicing gives rise to the isoform 1 shown
 CC in this entry. The additional 20 amino acids found in the Ref.4
 CC and Ref.6 sequences are due to a misunderstanding of the real type
 CC of splicing mechanism involved.
 CC -----
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 CC or send an email to license@sib-sb.ch).
 CC -----
 CC EMBL; AF051946; AAC67239.3; -
 CC EMBL; AF073931; AAD17668.1; -
 CC EMBL; AE006466; AAK61268.1; ALT_SEQ.
 CC EMBL; AJ420779; CAD12846.1; -
 CC EMBL; AL031703; CAC42094.1; ALT_SEQ.
 CC EMBL; AF223562; AAF60162.1; -
 CC EMBL; AF223563; AAF60163.1; -
 CC Genew; HGNC:1395; CACNA1H.
 CC MIM; 607904; -
 CC GO; GO:0005891; C-voltage-gated calcium channel complex; TAS.
 CC GO; GO:0008332; F:low voltage-gated calcium channel activity; TAS.
 CC GO; GO:0006936; P:muscle contraction; TAS.
 CC GO; GO:0007520; P:myoblast fusion; TAS.
 CC GO; GO:0008016; P:regulation of heart rate; TAS.
 CC GO; GO:0006810; P:transport; TAS.
 CC InterPro; IPR001682; Ca/Na_pore.
 CC InterPro; IPR002111; Cat_channel_TripL.
 CC InterPro; IPR005821; Ion_trans.
 CC InterPro; IPR005820; M-channel_nlg.
 CC Pfam; PF00520; Ion_trans_4.
 CC PRINTS; PR01629; TVDCCALPHA1.
 CC Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;
 CC Ion transport; Ionic channel; Multigene family; Phosphorylation;
 CC Repeat; Transmembrane; Voltage-gated channel.
 CC REPEAT 87 422
 CC REPEAT 779 1018 I.
 CC REPEAT 1281 1558 II.
 CC REPEAT 1602 1863 III.
 CC REPEAT 1602 1863 IV.
 CC DOMAIN 1 100 Cytoplasmic (Potential).
 CC TRANSMEM 101 119 S1 of repeat I (Potential).
 CC DOMAIN 120 139 Extracellular (Potential).
 CC TRANSMEM 140 160 S2 of repeat I (Potential).
 CC DOMAIN 161 169 Cytoplasmic (Potential).
 CC TRANSMEM 170 184 S3 of repeat I (Potential).
 CC DOMAIN 185 193 Extracellular (Potential).
 CC TRANSMEM 194 212 S4 of repeat I (Potential).
 CC DOMAIN 213 232 Cytoplasmic (Potential).
 CC TRANSMEM 233 253 S5 of repeat I (Potential).

Mon Nov 22 06:47:53 2004

FT	DOMAIN	254	394	Extracellular (Potential).	QY	263	QLWAGLLRNRCFLPENFSLPLSVD-LEPYQTENEDESPICQPRENGMRSCRSVPTLR	321
FT	TRANSMEM	395	419	S6 of repeat I (Potential).	Db	250	QLWAGLLRNRCFLDSAFRNNTLFLRPYQTEEGEENPFICSSRRDNGMKCHSHIP---	306
FT	DOMAIN	420	793	Cytoplasmic (Potential).	QY	322	GEAGGPPCSLDVETYN-----SSNTTCVNNOYVYTNCSAGEHNPFGKAINFDNIGY	374
FT	TRANSMEM	794	814	S1 of repeat II (Potential).	Db	307	GRRELMPCTLGWEAYTQPAEGVGAARNACINNOYVYVNCSDGSPHNGAINFDNIGY	366
FT	DOMAIN	815	827	Extracellular (Potential).	QY	375	AWIAIFOVITLEGWVDIMYFVMDAHSFYNYFILLIIVGFFMINCLVVIATQFSETK	434
FT	TRANSMEM	828	849	S2 of repeat II (Potential).	Db	367	AWIAIFOVITLEGWVDIMYFVMDAHSFYNYFILLIIVGFFMINCLVVIATQFSETK	426
FT	DOMAIN	850	855	Cytoplasmic (Potential).	QY	435	QRESQLMREQRVFLSNASTLASPEGSCYEELLYVILYILRKAARLAQVRAIGVRA	494
FT	TRANSMEM	856	874	S3 of repeat II (Potential).	Db	427	QRESQLMREQRARHLNSDSTLASPEGSCYEELLYVILYILRKAARLAQVRAIGVRA	486
FT	DOMAIN	875	882	Extracellular (Potential).	QY	495	GLLSVPARSQOEPPQSGSCSTRHR-----LSVHLV-HHHHHHHHHHVLNGTLRV	546
FT	TRANSMEM	883	906	S4 of repeat II (Potential).	Db	487	RKKVDPSAVQGGP-----GHRORAGHTASVHLVYVHHHHHHHHVHSHGSPRR	538
FT	DOMAIN	907	917	Cytoplasmic (Potential).	QY	547	PRASPEIQDRDANGSRRLML--PPSTPTPGGPPRGAESVHSFYHADCHLE--PVRQQA	602
FT	TRANSMEM	918	938	S5 of repeat II (Potential).	Db	539	POPEPGACD-----TLVRAGAPSPSPGRGPP--DAESVHSIYHADCHIEGPPQERARV	591
FT	DOMAIN	939	990	Extracellular (Potential).	QY	603	PPRCPSEASGR-TVGSKV-YPTV-----HTSPPEILKDKALVEVAPSP----	646
FT	TRANSMEM	991	1015	S6 of repeat II (Potential).	Db	592	AHAATAAASLRATGLTGMYPITLPGVSGSGKSTSPGPK-----GKWAGPPGTG	644
FT	DOMAIN	1016	1290	Cytoplasmic (Potential).	QY	647	--GPPTLTSFNIPPGPFSSMHKLLETQSTGAC--HSS-----CKISSPCKADSGACGPD	697
FT	TRANSMEM	1291	1313	S1 of repeat III (Potential).	Db	645	GHGPIUSLNS-----PDYKIPHVVEHGLGQAPGHLGSLVCPCLPSP--PAGTLTCELK	698
FT	DOMAIN	1314	1331	Extracellular (Potential).	QY	698	SCPYCART--GAGEPESADHVPDSDSEAYVEFTQAOHSDLRDP-----	740
FT	TRANSMEM	1332	1352	S2 of repeat III (Potential).	Db	699	SCPYCTRALEDPEGELSGSESGSDGSGVYFTQDVRHGRDWDTPFPTRATDTPGPGPS	758
FT	DOMAIN	1353	1362	Cytoplasmic (Potential).	QY	741	HSRRQRSIGDPAEPSSVLAFWRLICDTRKKAIVDSYFCGRGMIALVNTLSMGIEYHQ	800
FT	TRANSMEM	1363	1382	S3 of repeat III (Potential).	Db	759	PORRAQOQRAAP--GEGCMGRLWVTFSGKLURRIVDSYFSGRGMIALVNTLSMGIEYHQ	817
FT	DOMAIN	1383	1396	Extracellular (Potential).	QY	801	PEELTNALRISNIVFTSLFALEMLKLVGPGYGIKPNYPNIPDGVIIVISVMEIVGQOG	860
FT	TRANSMEM	1397	1418	S4 of repeat III (Potential).	Db	818	PEELTNALRISNIVFTSLFALEMLKLVGPGYGIKPNYPNIPDGVIIVISVMEIVGQAD	877
FT	DOMAIN	1419	1428	Cytoplasmic (Potential).	QY	861	GGLSVLRTFLRMLVRLPALORQOLVLMKTMNVATFCMLMLFIFISILGHLF	920
FT	TRANSMEM	1429	1452	S5 of repeat III (Potential).	Db	878	GGLSVLRTFLRMLVRLPALORQOLVLMKTMNVATFCMLMLFIFISILGHLF	937
FT	DOMAIN	1453	1529	Extracellular (Potential).	QY	921	GCKFASERD-GDTLPDRKNFDSLLWAIVTVFQILTOEDMKNKLYNGWASTSSWAALYFIA	979
FT	TRANSMEM	1530	1555	S6 of repeat III (Potential).	Db	938	GCKFSLKTDGTVPRDKNFDSLLWAIVTVFQILTOEDMKNKLYNGWASTSSWAALYFVA	997
FT	DOMAIN	1556	1616	Cytoplasmic (Potential).	QY	980	LMTFGNVLPNLVAILVEGFOAEGDATKSESPDFSPSDVDGDKRKLALVAL----	1035
FT	TRANSMEM	1617	1637	S1 of repeat IV (Potential).	Db	998	LMTFGNVLPNLVAILVEGFOAEGDATKSESPDFSPSDVDGDKRKLALVAL----	1057
FT	DOMAIN	1638	1651	Extracellular (Potential).	QY	1036	-----GSHABRLKSLPLLIHTAATPMHSHPKSS--TGVEGALGSGRRPSSSSGABPCA	1089
FT	TRANSMEM	1652	1673	S2 of repeat IV (Potential).	Db	1058	LAVTPNGHLEGRGSLSPPLINCTAATPMTPKSPFLDAAPSLPDSRSGSSGSDPPLIG-	1116
FT	DOMAIN	1674	1680	Cytoplasmic (Potential).	QY	1090	AHEMKCPPARSPHSPWASAASWTSSRRSRLGRAPSLKRRSPSGERSRLLSGEGQE	1149
FT	TRANSMEM	1681	1699	S3 of repeat IV (Potential).	Db	1117	---DQKPPASLRSPCAPGSGAWSSRRSRLGRAPSLKRRSPSGERSRLLSGEGKG	1173
FT	DOMAIN	1700	1713	Extracellular (Potential).	QY	1150	SQDEESESDEDRASPA--GSDHRRGSLEREAKSSFDLPDTL-----QVPLGH-----R	1196
FT	TRANSMEM	1714	1737	S4 of repeat IV (Potential).	Db	1174	STDDE--AEDGRAAPGPRATPLREASLDLPRLPAALPTKCRDRDQGVVALPSPFLR	1231
FT	DOMAIN	1738	1751	Cytoplasmic (Potential).	QY	1197	TAGRSASASHQDCKGKSASGRLARTLRTDDPOLDDGDDNDGSLNGERIQAWVRSLP	1256
FT	TRANSMEM	1752	1772	S5 of repeat IV (Potential).	Db	1232	IDSHREDAAEIADDSEDSCLRLHKVLEPYKQ-----W-----	1265
FT	DOMAIN	1773	1836	Extracellular (Potential).	QY	1257	ACCRERDSWSAIFPPQSRPRLCHRIITHKQVHDVWLVIIFLNCITIAMERPKIDPHSA	1316
FT	TRANSMEM	1837	1863	S6 of repeat IV (Potential).	QY			
FT	DOMAIN	1864	2353	Cytoplasmic (Potential).	QY			
FT	TRANSMEM	2354	2378	Poly-His.	QY			
FT	DOMAIN	2379	2380	Poly-Ser.	QY			
FT	TRANSMEM	2381	2382	Poly-Arg.	QY			
FT	DOMAIN	2383	2384	Calcium ion selectivity and permeability	QY			
FT	TRANSMEM	2385	2386	(By similarity).	QY			
FT	DOMAIN	2387	2388	Calcium ion selectivity and permeability	QY			
FT	TRANSMEM	2389	2390	(By similarity).	QY			
FT	DOMAIN	2391	2392	Calcium ion selectivity and permeability	QY			
FT	TRANSMEM	2393	2394	(By similarity).	QY			
FT	DOMAIN	2395	2396	Calcium ion selectivity and permeability	QY			
FT	TRANSMEM	2397	2398	(By similarity).	QY			
FT	DOMAIN	2399	2400	Calcium ion selectivity and permeability	QY			
FT	TRANSMEM	2401	2402	(By similarity).	QY			
FT	DOMAIN	2403	2404	N-linked (GlcNAc. . .) (Potential).	QY			
FT	TRANSMEM	2405	2406	N-linked (GlcNAc. . .) (Potential).	QY			
FT	DOMAIN	2407	2408	Query Match	QY			
FT	TRANSMEM	2409	2410	Best Local Similarity	QY			
FT	DOMAIN	2411	2412	Matches 1370; Conservative 208; Mismatches 529; Indels 310; Gaps 62;	QY			
FT	TRANSMEM	2413	2414	25 PPGFRLARGWTRRRMERAPRSRSP--VASRSSTTCGPGAGAGSTKDPGSDSABEG	QY			
FT	DOMAIN	2415	2416	19 PPGPALVG-----ASPESGAPGREAERGSELGVSPGESPAERGAELGA--DEEQR	QY			
FT	TRANSMEM	2417	2418	83 LPALAPVVFYLSQDSRRSCRLTVCPNPFERVSMLVLLNCVILGMPFPCEDIACD	QY			
FT	DOMAIN	2419	2420	70 VPYALAAVFFCLGQOTRPRSCRLVCPNPFERVSMLVLLNCVILGMPFPCEDIACD	QY			
FT	TRANSMEM	2421	2422	143 SORCRILQAPDDIFAFPAFVAVMVKVVALGIFGKKCYLGDVNRDLDPFIVTAGMLEYSLD	QY			
FT	DOMAIN	2423	2424	130 SERCNLEAFAPAFIFAFPAFVAVMVKVVALGIFGKKCYLGDVNRDLDPFIVTAGMLEYSLD	QY			
FT	TRANSMEM	2425	2426	203 LQNVFSASVTRVRLRPLRINRVPMSRIITLLDLPMLGNVLLLCFFVFFIFGIVGV	QY			
FT	DOMAIN	2427	2428	190 GHNVLSLAIRTVRLRPLRINRVPMSRIITLLDLPMLGNVLLLCFFVFFIFGIVGV	QY			

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Db 1266 --CRSEAWALYFSPQNRFRVSCQKVIHMKFDHVVLFIFLNCVTIALERDIDPGST 1323
QY 1317 ERIFLTSNYIFTAVFLAETVVKVWALGWCFGBOAVLRSSMNVLDGLVLSIVIDLVSVM 1376
Db 1324 ERVFLSVSNVIFTAIFVAENWVAVVALLGSLGSHAYLQSSWNLLDGLLVLSVLDVWAM 1383
QY 1377 VDSGTGKILGMRLVRLRLTLRLRLVIRISRAQGLKLVVETIMSSLKPIGNIVWICCAFFII 1436
Db 1384 ASAGGAKILGLVRLRLTLRLRLVIRISRAQGLKLVVETIMSSLKPIGNIVWICCAFFII 1443
QY 1437 FGLGVQLFKGFVFCOGEDTRNITNKSDCABASYRWVRHKYNFNDNLGQALMSLFLVASK 1496
Db 1444 FGLGVQLFKGFVFCOGEDTRNITNKSDCABASYRWVRHKYNFNDNLGQALMSLFLVASK 1503
QY 1497 DGVVDIMYDGLDAVGDVQDQIMHNPWMLLYFTSPLLIIVAFVFLNMVGVVYENHFKCRQ 1556
Db 1504 DGVVDIMYDGLDAVGDVQDQIMHNPWMLLYFTSPLLIIVAFVFLNMVGVVYENHFKCRQ 1563
QY 1557 HQEAEARREKRLRLLEKRRSKEKQMAEACQKPYDYSRFRLLVHHLCTSHYLDLF 1616
Db 1564 HQEAEARREKRLRLLEKRRSKEKQMAEACQKPYDYSRFRLLVHHLCTSHYLDLF 1622
QY 1617 ITGVIGLVNWTAMSHYQOQLDEALKTCNYIFTIVFVESVFKLVAFAPRRFFQDRWN 1676
Db 1623 ITGVIGLVNWTAMSHYQOQLDEALKTCNYIFTIVFVESVFKLVAFAPRRFFQDRWN 1682
QY 1677 QLDLAIIVLLSGITIEIEVNLSPINPTIIRIMRVLRIRVLRVLRVLRVLRVLRVLRVLRV 1736
Db 1683 QLDLAIIVLLSGITIEIEVNLSPINPTIIRIMRVLRIRVLRVLRVLRVLRVLRVLRVLRV 1742
QY 1737 QOALPOVNGLGLFLLMFFIIFALGVLFGLDETHPCBGLGRHATFRNFGMAFLTF 1796
Db 1743 QOALPOVNGLGLFLLMFFIIFALGVLFGLDETHPCBGLGRHATFRNFGMAFLTF 1802
QY 1797 RVSTGDNWNGIMKOPSRDC---DQESTCYNVTISPIYFVSVFLTAQFVLVNVVIAVLMKH 1853
Db 1803 RVSTGDNWNGIMKOPSRDC---DQESTCYNVTISPIYFVSVFLTAQFVLVNVVIAVLMKH 1862
QY 1854 LEESNKAKEAEAELEAELEEMKTLSPHPSPLGSPFLWPGVEGVNSDPSKPGAPHTTA 1913
Db 1863 LEESNKAKEAEAELEAELEEMKTLSPHPSPLGSPFLWPGVEGVNSDPSKPGAPHTTA 1899
QY 1914 HIGASGFSLEHPTWPHPEVVPVLPGLDITVRKSGVSRTHSLPNDSPMYCNRNGSTA--- 1970
Db 1900 HIGASGFSLEHPTWPHPEVVPVLPGLDITVRKSGVSRTHSLPNDSPMYCNRNGSTA--- 1943
QY 1971 -----ERSLGRHGWGPKAQSGSILSVHSPADTSCILQPKDVH-----YLLQP 2015
Db 1944 HPRPLQEVEMETYGATP---LGSVASVHSPAPAESASLQIPLAVSSPARSGEPHALSP 2000
QY 2016 HGAPTGAIPKLPPLPPGSRPLAQRLRQAAIRTDSDLVQGLSGREDLLSEV---SGPSC 2071
Db 2001 RGT-----AESPSLSRLLCQEAHVHTDSLEGK-IDSPROTLDDPAEPEKTFVR 2047
QY 2072 PLTRSSFWGGSSIQVOORGGIOSKV--SKH-----IRLPAPCPGLEPSWAKDPPETRS 2123
Db 2048 PVTQ-----GGSLQPPRSPRPAASVTRKHTFGQRCVSRPAAPGEEAEADP----- 2096
QY 2124 SLELDTLSWISGDLPLP-SQOEPLP-----RDLKKCVSVTQSCRRRPPGWLDE 2173
Db 2097 ---ADEVSHITSACFWOATPEPHGPEASPVAGGERDLRLRLSVDAQGLDKPG-RADE 2152
QY 2174 QRHSTAVSCLDGSGOPRLCPSPSSILGGQPLGFP--GSRPKKLSPPSISIDPP-ESQGS 2230
Db 2153 QWRPSAE---LGSSE-----PGEAKWAG-PEAFALGARKKKKKSPPC-SVEPAEDEGS 2203
QY 2231 -RPPCSFG--VCLRRRAPA-----SDSKDPSVSSPLDSTAAS-----PSPKDLSL 2274
Db 2204 ARPSAAEGSGSTTLRRRTPSCATPHRDSLEPTBGSAGGDPAAKGERWQACRAEHLTV 2263
QY 2275 SGLSSDPTDM-----DP 2286

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Db 2264 PSFAFBLDLGVPSGDP 2280
CcAH MOUSE STANDARD; PRT; 2365 AA.
RESULT 12
ID CCAH_MOUSE STANDARD; PRT; 2365 AA.
AC O88427; Q9JKU5;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-
gated calcium channel alpha subunit Cav3.2).
GN Name-Cacnah; (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=BALEB/C;
RA Mittman S.;
RT "Exon organization of mouse Cacnah."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE OF 1823-1952 FROM N.A.
RC STRAIN=C57BL/6J;
RA Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
entry of calcium ions into excitable cells and are also involved
in a variety of calcium-dependent processes, including muscle
contraction, hormone or neurotransmitter release, gene expression,
cell motility, cell division and cell death. The isoform alpha-1H
gives rise to T-type calcium currents. T-type calcium channels
belong to the "low-voltage activated (LVA)" group and are strongly
blocked by nickel and mibefradil. A particularity of this type of
channels is an opening at quite negative potentials, and a
voltage-dependent inactivation. T-type channels serve pacemaking
functions in both central neurons and cardiac nodal cells and
support calcium signaling in secretory cells and vascular smooth
muscle. They may also be involved in the modulation of firing
patterns of neurons which is important for information processing
as well as in cell growth processes.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DOMAIN: Each of the four internal repeats contains five
hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
positively charged transmembrane segment (S4). S4 segments
probably represent the voltage-sensor and are characterized by a
series of positively charged amino acids at every third position.
CC -!- FM: In response to raising of intracellular calcium, the T-type
channels are activated by CaM-kinase II.
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
family.
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EMBL; AF226868; AAC21607.2; -.
EMBL; AY026385; AAC21607.2; JOINED.
EMBL; AF051947; AAC67240.1; -.
MGD; MGI:1928842; Cacnah.
InterPro; IPR001682; Ca/Na_pore.
InterPro; IPR002111; Cat channel_TripL.
InterPro; IPR005821; Ion trans.
InterPro; IPR005820; M+channel_nlg.
Pfam; PF00520; Ion trans; 4.
PRINTS; PR01629; TVDCCALPHAL.

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RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Copley V.E., Cole C.G., Collier R.E., Comor R.,
RA Corroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dowsorth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCormack B.J.,
RA McClellan J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.B., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissee S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Schett P., Walker C., Wansley A., Wohldmann P., Pepin K., Nelson J.,
RA Korff I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.B., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya E., Simon M.I., Dumanski J.P.,
RA Peyraud M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.B.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tikhunov Y., Wright H.,
RT "The DNA sequence of human chromosome 22."
RL Nature 402:489-495(1999).
RL [5]
RP SEQUENCE OF 1200-2223 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirasawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA Ohara O.;
RT "Characterization of cDNA clones selected by the GeneMark analysis
RT from size-fractionated cDNA libraries from human brain."
RT DNA Res. 6:329-336(1999).
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC entry of calcium ions into excitable cells and are also involved
CC in a variety of calcium-dependent processes, including muscle
CC contraction, hormone or neurotransmitter release, gene expression,
CC cell motility, cell division and cell death. Isoform alpha-11
CC gives rise to T-type calcium currents. T-type calcium channels
CC belong to the "low-voltage activated (LVA)" group and are strongly
CC blocked by nickel and mibefradil. A particularity of this type of
CC channels is an opening at quite negative potentials, and a
CC voltage-dependent inactivation. T-type channels serve pacemaking
CC functions in both central neurons and cardiac nodal cells and
CC support calcium signaling in secretory cells and vascular smooth
CC muscle. They may also be involved in the modulation of firing
CC patterns of neurons which is important for information processing
CC as well as in cell growth processes. Gates in voltage ranges
CC similar to, but higher than alpha 1G or alpha 1H (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=Delta36b;
CC IsoId=Q9P0X4-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9P0X4-2; Sequence=VSP_000951;
CC Name=3; Synonyms=Alpha11-a;
CC IsoId=Q9P0X4-3; Sequence=VSP_000950, VSP_000951;
CC

CC Name=4;
CC IsoId=Q9P0X4-4; Sequence=VSP_000950;
CC TISSUE SPECIFICITY: Brain specific.
CC -!- DOMAIN: Each of the four internal repeats contains five
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC positively charged transmembrane segment (S4). S4 segments
CC probably represent the voltage-sensor and are characterized by a
CC series of positively charged amino acids at every third position.
CC -!- PTM: In response to raising of intracellular calcium, the T-type
CC channels are activated by CaM-kinase II (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
CC -!- CAUTION: Ref.4 (CAB62996) sequence differs from that shown due to
CC erroneous gene model prediction.
CC

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CC EMBL; AF129133; AAD45251.1; -;
CC EMBL; AF142567; AAF25722.1; -;
CC EMBL; AF211189; AAF44626.1; -;
CC EMBL; AF393329; AAM67414.1; -;
CC EMBL; AL008716; CAA15494.1; -;
CC EMBL; AL022312; CAB62988.1; -;
CC EMBL; AL022319; CAB62996.1; ALT_SEQ.
CC EMBL; AL022319; CAD92536.1; -;
CC EMBL; AB032946; BAA86434.1; -;
CC Genew; HGNC:1396; CACNA1L.
CC MIM: 608230; -;
CC GO: GO:0005891; C:voltage-gated calcium channel complex; NAS.
CC GO: GO:0008332; F:low voltage-gated calcium channel activity; NAS.
CC GO: GO:0006816; P:calcium ion transport; NAS.
CC InterPro; IPR001682; Ca/Na_pore.
CC InterPro; IPR002077; Ca_Channel_alpha.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR005820; M4Channel_nlg.
CC Pfam; PF00520; Ion_trans; 4.
CC PRINTS; PR00167; CACHANNEL.
CC PRINTS; PR01629; TVDCCALPHA1.
CC Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;
CC Ion transport; Ionic channel; Multigene family; Phosphorylation;
CC Polymorphism; Repeat; Transmembrane; Voltage-gated channel.
CC REPEAT 66 401
CC I.
CC REPEAT 626 865
CC II.
CC REPEAT 1157 1434
CC III.
CC REPEAT 1472 1733
CC IV.
CC DOMAIN 79 99
CC TRANSMEM 100 120
CC DOMAIN 121 141
CC TRANSMEM 142 148
CC DOMAIN 149 168
CC TRANSMEM 169 173
CC DOMAIN 174 191
CC TRANSMEM 192 211
CC DOMAIN 212 232
CC TRANSMEM 233 377
CC DOMAIN 378 398
CC TRANSMEM 399 640
CC DOMAIN 641 661
CC TRANSMEM 662 676
CC DOMAIN 677 697
CC TRANSMEM 698 702
CC DOMAIN 703 721
CC TRANSMEM 722 729
CC DOMAIN 730 753
CC TRANSMEM 730 753

FT	DOMAIN	754	764	Cytoplasmic (Potential).
FT	TRANSMEM	765	785	S5 of repeat II (Potential).
FT	DOMAIN	786	841	Extracellular (Potential).
FT	TRANSMEM	842	862	S6 of repeat II (Potential).
FT	DOMAIN	863	1166	Cytoplasmic (Potential).
FT	TRANSMEM	1167	1187	S1 of repeat III (Potential).
FT	DOMAIN	1188	1209	Extracellular (Potential).
FT	TRANSMEM	1210	1230	S2 of repeat III (Potential).
FT	DOMAIN	1231	1244	Cytoplasmic (Potential).
Query Match				
Best Local Similarity 45.0%; Score 5418; DB 1; Length 2223;				
Matches 1235; Conservative 243; Mismatches 533; Indels 462; Gaps 68;				
QY	12	TPPLRGSRPSSDP-----	PGPRLARGWTRRRMERAPRSRSDSPVASRSTTCGPGCAAG	65
DB	6	SPSSSSAAAPAAEPGVITEQGPCR-----	SPSSPPGLEEPLDGA--	45
QY	66	AGSTKDPGSADSBAEGLYPALAPVVFYLSQDSRPSWCLRTVCNPFERSVLMVILL	125	
DB	46	-----DP-----	HVPFPLDPIAFCLFQRTTSPRNWCIMKVCNPFECVSLVILL	91
QY	126	NCVTGLMPERPCEDJACDSQRCLLQAFDDFIAPFAVEMVKQVALGIFGKCYKLGDTWN	185	
DB	92	NCVTGLMQYQDDMDCLSDRCKILQVDDFIFFAMEMVLKQVALGIFGKCYKLGDTWN	151	
QY	186	RLDFFIVIAGLMEXSLDLQNVSFSAVRTVRLPLRALNRVPSMRILVTLTLDTPMLGN	245	
DB	152	RLDFFIVMAGWEYSUDLQNLNLSAIRTVRLPLKALNRVPSMRILVNLGLDTPMLGN	211	
QY	246	VLLLCPPVFFITGVGVQLMAGLLNRCLFNPFSPLPSVLEPYQYOTENEDSPFICSQ	305	
DB	212	VLLLCPPVFFITGVGVQLMAGLLNRCLFLEENFTIQGDVALPPYQPEEDDEMPFICSL	271	
QY	306	PRENGMRSRCVPTLRGEGGGPPCSL-----	DYETYNSSNTT--CVNNQYNTNCSA	357
DB	272	SGDNGIMGCHIEIPPLEKQO---GRECCLSKDDVDFGAGRQDLNASGLCVNNRYYNVCRT	328	
QY	358	GEHNPFGAINFNDIGYAWIAIFQVITLEGVVDIMYFVMDAHSFYNTFYFILLIIVGSFF	417	
DB	329	GSANPHKGAINFNDIGYAWIVFOVITLGGWEIMYVMDAHSFYNTFYFILLIIVGSFF	388	
QY	418	MINICLVVIATQSETKQBSQLMREQRVFTLSNASTLASFPSCGYEELLKYLVILR	477	
DB	389	MINICLVVIATQSETKQREHRLMLEQRVYLS-SSTVASYAEPDGYEIEIFQVYCHILR	447	
QY	478	KAARLLAQVSRALGVVAGLLSSPVARSQGPQSPGSCITRSHRLSVHHLVHHHHHHHHY	537	
DB	448	KAKERALGLYQALQSRQAL--GPEAPAPAKPGP-----	HAKEPRHY	487
QY	538	H---LNGTLRLVRPRASPEIQDRDAN--GSRRLM--LPPSTPTPGGPPRGAESVHSFYHAD	592	
DB	488	HGKTKGQO-----	DEGRHLGSRHCQTLHGASP---GNHDSGRE-----	523
QY	593	CHLEPVRCQAPPRCPSEASGRVVGSKVPTVHTSPPEILKDKALVEVAPSGPPTLT	652	
DB	524	-----LC---FOHSLPDA-----	TPHT-----LVQ---PIPATLA	547
QY	653	SENIIPGPFSSMHKLELTQSTGAC--HSSCKISPCSKADSGACGPDSCPYCARTGAGEPE	711	
DB	548	S-----	DPASCPCQEHEDGRPPSLGSLTSDSGSGS-----GSSAGGEDE	588
QY	712	SADHVPDSDSEAVYFTQDAQSHDLRPHSRRRQRSLGDAEPSSVLA--FWLLICDTF	769	
DB	589	A-----DGDGA--	RSSEDDGASSELGKEEEEQ-----ADGAVWLGVVWRETRAKL	633
QY	770	RKIVDSKYFGRGIMAILNVTLSMGIEYHEQPEELTNALIEISNIVFTSLFALEMLIKLV	829	
DB	634	RGIVDSKYFNGIMAILNVTSMGIEHEQPEELTNILEICNVVFTSMFALEMLIKLAA	693	
QY	830	YGFPGYIKPNYINFDGVIVLWSVEIVGQGGGLSVLRTFLMRVLKLVRFPLAQRLV	889	
DB	694	FGLFDYLRPNYINFDGVIVLWSVEIVGQGGGLSVLRTFLRLVLKLVRFMPALRRQLV	753	

QY	890	VLMKTMNDNVATFCMLMLMFIFISILGMHLFGCKFASERD--GDTLPDRKNFDSLLWAIVT	948
DB	754	VLMKTMNDNVATFCMLMLMFIFISILGMHLFGCKFSLRDTGDTVPDRKNFDSLLWAIVT	813
QY	949	VFOILLTOEDNNKVLVNGMASTSSWAALYFIALMTFGNYVFLNLLVAILVEGFOAEGDATK	1008
DB	814	VFOILLTOEDNNVVLVNGMASTSPWASLYFVALMTFGNYVFLNLLVAILVEGFOAEGDANK	873
QY	1009	SESEPDFFPSV-----DGGDKRKLALVALGHAELRKSLLPPLIHT-----A	1054
DB	874	SYSDDEQSSNIIEEDFKLQEGLDSSGDPK--LCPIPTMPTNGHLDPSL--PLCGHLGPAGA	929
QY	1055	ATPMGHPKSSSTGVGEALGSGSRRTSSGSAPGAAHHEMKCPPSARSSPHSPWASAASW	1114
DB	930	AGPA--PRLSLQPDMLVALGSRKSSVMSL---GRMSYDQRSLSSRSRYYGFWGRSAAM	984
QY	1115	TSRRSRNSLGRAPSLKXPSGGERSSILSGE--GOESQDEBESSEE--DRASPAQSDH--	1169
DB	985	ASRRSSWN-----SLKHKPPSAEHSLSAERGGAARVCEVAADGPPRAAPLHTPHAH	1038
QY	1170	-----BHRGSLREAKSSFDLPDTLQVPGHRTASGRSS--ASEHQDCNKS	1214
DB	1039	HIHGHPLAHRHRHRTLSLDNRDSVDLAEIVPAVGAHPRAAAGAPAGHEDCNGRM	1098
QY	1215	ASGLARTLRTD--DPQLDGGDDNDDEGNLSKGERIQAWVRSLPACCRERDSWASYIFPPQ	1273
DB	1099	PS--IAKDVFTKMGDRGDRGEDEBEIDYTLCFRVRKMDVYKPDWCEVREDSVILFSE	1156
QY	1274	SRFLLCHRIITHKMFDEHVLVIIFLNCITITAMERPKIDPHSABRIFLTLSNYIFTAVFL	1333
DB	1157	NRFLVCQTTIAHKLFDYVWLAFIFLNCITITALEPQIEAGSTERIFLTVSNYIFTAIV	1216
QY	1334	AEMTVKVALGCFEGEQAYLRSSMNVLGDLVLISVIDILVSMVSDSGTKILGLMLVRL	1393
DB	1217	GEMTLKVSGLYFEGEQAYLRSSMNVLGDLGFLVFSIIDIVSLASAGAKILGLVRL	1276
QY	1394	LRLRLPRLVTSRQGLKLVVETLMSLLKPIGNIIVICAFPIIFGILGVOLFCKGFFVCQ	1453
DB	1277	LRLRLPRLVTSRAPGLKLVVETLMSLLKPIGNIIVICAFPIIFGILGVOLFCKGFFHCL	1336
QY	1454	GEOTRLTNKSDCAEASRYWRHKYNPDNI.GQALMSLFLVASKDGWVDIMYDGLDAYVD	1513
DB	1337	GVDTRLTNKSDCAEASRYWRHKYNPDNI.GQALMSLFLVASKDGWVNIWYNGLDVAVD	1396
QY	1514	QOPIMHNPWMLLYFISFLIIVAFFVLNMFVVVNFHCKROHQBEEERREKELRR	1573
DB	1397	QOPIVHNPNWMLLYFISFLIIVSVFFVLNMFVVVNFHCKROHQBEEERREKELRR	1456
QY	1574	LEKRRSKQMAEAOCKPYSDYSRFLVAHLHCTSHYLDLFTITGVIGLVNVTMAEHY	1633
DB	1457	LEKRR-----KAQRLPYATYCHTRLLIHSMTCTSHYLDLFTITCLNVNVTMSLEHY	1509
QY	1634	QOQILDEALKICNYITFVIFVFSYFKLVAFAPFRFFQDRWNQLDAIVLLSIMGITLE	1693
DB	1510	NQTSLETALKICNYMFTTFVLEAVLKLVAFLRFFFKDRWNQLDAIVLLSIMGITLE	1569
QY	1694	EIEVNLSPINPTIIRIMRVLRILARVLLKLVAGVWRALLHTVMOALPOVGNLGLFMLL	1753
DB	1570	EIEVNAALPINPTIIRIMRVLRILARVLLKLVAGVWRALLHTVMOALPOVGNLGLFMLL	1629
QY	1754	FIFPAALGVELFDLECDTHPCBGLGRHATFRNFGMAFLTFRVSTGNWNGIMKDPSSR	1813
DB	1630	FFIYAALGVELFDLVCNDENPCBGRHATFRNFGMAFLTFRVSTGNWNGIMKDTLR	1689
QY	1814	DC--DOESTCYNTV--ISPIYFVSFVLTAQFVLVNVVIAVLMKHEBSNKEAEAELEAE	1870
DB	1690	DCDTHERSCLSLQFVSPLYFVSFVLTAQFVLVNVVIAVLMKHEBSNKEAEAELEAE	1749
QY	1871	LELEM--KTLSPOPHSPGSP-----FLW-----	1892
DB	1750	LELEMAHGLGCPFLPTGSPGAPGPGAGGGGDTGGLCRRCYCSPAQENLWLDVSILI	1809

FT	TRANSMEM	688	711	S4 of repeat II (Potential).
FT	DOMAIN	712	722	Cytoplasmic (Potential).
FT	TRANSMEM	723	743	S5 of repeat II (Potential).
FT	DOMAIN	744	795	Extracellular (Potential).
FT	TRANSMEM	796	820	S6 of repeat II (Potential).
FT	DOMAIN	821	1125	Cytoplasmic (Potential).
FT	TRANSMEM	1126	1148	S1 of repeat III (Potential).
FT	DOMAIN	1149	1166	Extracellular (Potential).
FT	TRANSMEM	1167	1187	S2 of repeat III (Potential).
FT	DOMAIN	1188	1197	Cytoplasmic (Potential).
FT	TRANSMEM	1198	1217	S3 of repeat III (Potential).
FT	DOMAIN	1218	1231	Extracellular (Potential).
FT	TRANSMEM	1232	1253	S4 of repeat III (Potential).
FT	DOMAIN	1254	1263	Cytoplasmic (Potential).
FT	TRANSMEM	1264	1287	S5 of repeat III (Potential).
FT	DOMAIN	1288	1364	Extracellular (Potential).
FT	TRANSMEM	1365	1390	S6 of repeat III (Potential).
FT	DOMAIN	1391	1445	Cytoplasmic (Potential).
FT	TRANSMEM	1446	1466	S1 of repeat IV (Potential).
FT	DOMAIN	1467	1480	Extracellular (Potential).
FT	TRANSMEM	1481	1502	S2 of repeat IV (Potential).
FT	DOMAIN	1503	1509	Cytoplasmic (Potential).
FT	TRANSMEM	1510	1528	S3 of repeat IV (Potential).
FT	DOMAIN	1529	1542	Extracellular (Potential).
FT	TRANSMEM	1543	1566	S4 of repeat IV (Potential).
FT	DOMAIN	1567	1580	Cytoplasmic (Potential).
FT	TRANSMEM	1581	1601	S5 of repeat IV (Potential).
FT	DOMAIN	1602	1664	Extracellular (Potential).
FT	TRANSMEM	1665	1692	S6 of repeat IV (Potential).
FT	DOMAIN	1693	1835	Cytoplasmic (Potential).
FT	SITE	355	355	Calcium ion selectivity and permeability (By similarity).
FT	SITE	779	779	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1339	1339	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1637	1637	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	171	171	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	242	242	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	309	309	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1301	1301	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1304	1304	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	193	193	M -> V (in Ref. 3).
FT	CONFLICT	291	291	C -> L (in Ref. 3).
FT	CONFLICT	394	394	V -> L (in Ref. 3).
FT	CONFLICT	406	406	E -> N (in Ref. 3).
FT	CONFLICT	485	485	C -> S (in Ref. 3).
FT	CONFLICT	512	512	D -> Y (in Ref. 3).
FT	CONFLICT	558	558	S -> R (in Ref. 3).
FT	CONFLICT	683	683	G -> S (in Ref. 3).
FT	CONFLICT	691	691	F -> S (in Ref. 3).
FT	CONFLICT	739	740	MH -> ID (in Ref. 3).
FT	CONFLICT	833	833	C -> Y (in Ref. 3).
FT	CONFLICT	846	846	F -> L (in Ref. 3).
FT	CONFLICT	856	856	S -> R (in Ref. 3).
FT	CONFLICT	905	905	L -> R (in Ref. 3).
FT	CONFLICT	913	913	M -> YW (in Ref. 3).
FT	CONFLICT	936	936	W -> G (in Ref. 3).
FT	CONFLICT	996	996	A -> R (in Ref. 3).
FT	CONFLICT	1060	1060	I -> M (in Ref. 3).
FT	CONFLICT	1094	1094	D -> CC (in Ref. 3).
FT	CONFLICT	1197	1198	SS -> TD (in Ref. 3).
FT	CONFLICT	1229	1231	Missing (in Ref. 3).
FT	CONFLICT	1422	1422	K -> Y (in Ref. 3).
FT	CONFLICT	1623	1625	FGM -> SAR (in Ref. 3).
FT	CONFLICT	1656	1656	S -> T (in Ref. 3).
FT	CONFLICT	1737	1737	P -> A (in Ref. 3).
FT	SEQUENCE	1835	205348 MW; E6025E0F1BE80CCA CRC64	

Query Match 44.5%; Score 5354; DB 1; Length 1935;
 Best Local Similarity 55.4%; Pred. No. 1.6e-259;
 Matches 1138; Conservative 217; Mismatches 374; Indels 324; Gaps 45;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:06:00 ; Search time 186.635 Seconds
(without alignments)
4355.452 Million cell updates/sec

Title: US-09-611-257A-37

Perfect score: 11904

Sequence: 1 MDEEDGAGAESGQPRSF.....PKDVLISGLSSDPADLDP 2266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	11862.5	99.7	2273	4	Aae01019 Human T-t
2	11758.5	98.8	2243	2	Aay14589 Human T-t
3	11758.5	98.8	2243	7	Adj68819 Human T-t
4	11741	98.6	2250	2	Aay14586 Human T-t
5	11735.5	98.6	2261	2	Aay14587 Human T-t
6	11727	98.5	2268	2	Aay14588 Human T-t
7	11653	97.9	2266	4	Aab66481 Human T-t
8	11111	93.3	2428	3	Aay70720 Rat T-typ
9	10962.5	92.1	2247	2	Aay14593 Rat T-typ
10	10945	91.9	2254	2	Aay14590 Rat T-typ
11	10939.5	91.9	2265	2	Aay14591 Rat T-typ
12	10925	91.8	2272	2	Aay14592 Rat T-typ
13	10774	90.5	2287	4	Aab66475 Rat T-typ
14	6315.5	53.1	1207	4	Aau00474 Human T-t
15	6218	52.2	2359	4	Aab66476 Rat T-typ
16	6212	52.2	2352	4	Aay06299 Human T-t
17	6212	52.2	2353	6	Abp72254 Human T-t
18	6212	52.2	2353	7	Adj69322 Human T-t
19	6211	52.2	2353	7	Aay06298 Human T-t
20	6178	51.9	2353	5	Abg30840 Human T-t
21	5855.5	49.2	2038	2	Aay14595 Human T-t
22	5845.5	49.1	2044	2	Aay14594 Human T-t
23	5709.5	48.0	2034	2	Aay06300 Human T-t
24	5492.5	46.1	2175	5	Aau10535 Human T-t
25	5492.5	46.1	2175	6	Abu08511 Human T-t

26	5492.5	46.1	2175	8	ADH69265	Adh69265 Human T-t
27	5484	46.1	2188	5	AAU10536	Aau10536 Human T-t
28	5484	46.1	2188	6	ABU08512	Abu08512 Human T-t
29	5484	46.1	2188	8	ADH69267	Adh69267 Human T-t
30	5366	45.1	1835	2	AAy14597	Aay14597 Rat T-typ
31	5366	45.1	1835	8	ADH69268	Adh69268 Rat T-typ
32	5361.5	45.0	1823	2	AAy14596	Aay14596 Human T-t
33	5198.5	43.7	1792	4	AAb66477	Abb66477 Rat T-typ
34	5043.5	42.4	1854	2	AAW79161	Aaw79161 Human T-t
35	3959.5	33.3	1854	4	AAW79161	Aaw79161 Human T-t
36	3959.5	33.3	1854	4	AAW79161	Aaw79161 Human T-t
37	3442	28.9	2435	4	ABb60448	Abb60448 Human T-t
38	3427	28.8	644	4	ABb60448	Abb60448 Human T-t
39	3020.5	25.4	1859	4	ABG10954	Abg10954 Human T-t
40	1960	16.5	853	4	ADL31041	Adl31041 Human T-t
41	1960	16.5	853	4	ADL31041	Adl31041 Human T-t
42	1753	14.7	2264	8	ADM31026	Adm31026 Human T-t
43	1752.5	14.7	2339	2	AAZ33549	Aaz33549 Human T-t
44	1750.5	14.7	2343	2	AAZ33549	Aaz33549 Human T-t
45	1749	14.7	2337	2	AAW37878	Aaw37878 Human T-t

ALIGNMENTS

RESULT 1

AAE01019 ID AAE01019 standard; protein; 2273 AA.

XX AC AAE01019;

XX AC AAE01019;

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XX AC AAE01019;

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XX AC AAE01019;

PS Claim 11; Page 81-99; 115pp; English.

XX The invention relates to isoform of human T-type low voltage activated calcium channel (alpha1G-c) cDNA and protein. Cells transformed with calcium channel DNA to express calcium alpha1G-c channel protein are used to identify specific modulators (antagonists or agonists). These modulators are useful as therapeutic agents and are used for treating wide range of calcium alpha1G-c channel-mediated disorders, e.g. stress, epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease, endocrine disorders, respiratory disorder, peripheral muscle disorder, muscle excitability, fertilisation, contraception, disorders involving hypertension, neuronal firing regulation, potentiation of synaptic signals and cardiovascular disorders (e.g. atherosclerosis, cardiac hypertrophy, angina pectoris). Calcium alpha1G-c channel DNA is useful for isolating and identifying related molecule mutations. It is also optionally used as antisense sequences, in gene therapy. Calcium channel alpha1G-c DNA, protein and antibodies are useful for forensic analysis, diagnosis and epidemiological studies, by standard hybridisation or immunological assays. The present sequence is T-type low voltage activated calcium channel alpha1G-c protein

SQ Sequence 2273 AA;

Query Match 99.7%; Score 11862.5; DB 4; Length 2273;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 2260; Conservative 4; Mismatches 2; Indels 7; Gaps 1;

QY 1 MDEEDGAGAERSGQFRSMRLNDLSGAGRPGSAEKDPGSADEAGLPYPALAPV 60

DB 1 MDEEDGAGAERSGQFRSMRLNDLSGAGRPGSAEKDPGSADEAGLPYPALAPV 60

QY 61 FFLYQDSRPRWCLRTVCPNPFERISMLVILLNCVTILGMFPCCDIACDSORCILQAF 120

DB 61 FFLYQDSRPRWCLRTVCPNPFERISMLVILLNCVTILGMFPCCDIACDSORCILQAF 120

QY 121 DDFIAPFAFVAVKVAALGIFGKCYLGTWNRLDFFVIAGMLEYSLDLQNVFSYVR 180

DB 121 DDFIAPFAFVAVKVAALGIFGKCYLGTWNRLDFFVIAGMLEYSLDLQNVFSYVR 180

QY 181 TVRVLRLRAINRVPMSRILVTLTLLDTPMLGNVLLCFVFFIFGIVGVQVWAGLLNR 240

DB 181 TVRVLRLRAINRVPMSRILVTLTLLDTPMLGNVLLCFVFFIFGIVGVQVWAGLLNR 240

QY 241 CFLPENFSPLVDLERYQTENEDSPICQPRENGMRSCRSVPTLRGCGGGPPCGL 300

DB 241 CFLPENFSPLVDLERYQTENEDSPICQPRENGMRSCRSVPTLRGCGGGPPCGL 300

QY 301 DYEAYNSSNTTCVNNQYNTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM 360

DB 301 DYEAYNSSNTTCVNNQYNTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM 360

QY 361 YFMDAHSFYNYFTILLIVGFFMINCLVVIATQFSETKQRESQRLMREQVRFLSNA 420

DB 361 YFMDAHSFYNYFTILLIVGFFMINCLVVIATQFSETKQRESQRLMREQVRFLSNA 420

QY 421 STLASSEPGSCYEBELLKYLVTILKRAARLAQVSRAGVRLGSLSPAPLGQETOPSS 480

DB 421 STLASSEPGSCYEBELLKYLVTILKRAARLAQVSRAGVRLGSLSPAPLGQETOPSS 480

QY 481 SCRSRHRRLSVHLLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPPSTP 540

DB 481 SCRSRHRRLSVHLLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPPSTP 540

QY 541 ALSGAPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRVVGSKVYPTVHTSPPE 600

DB 541 ALSGAPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRVVGSKVYPTVHTSPPE 600

QY 601 TLKEKALVEVAASGPPTLTSLNTPCPYSSMHKLLTQSTGACQSCSKLSSPCLKADSG 660

DB 601 TLKEKALVEVAASGPPTLTSLNTPCPYSSMHKLLTQSTGACQSCSKLSSPCLKADSG 660

QY 661 ACPGDCPCYCARAGAGEVELADREMPDSDSEAVYFTQDAQHDLRDPHRRRQSLGPD 720

DB 661 ACPGDCPCYCARAGAGEVELADREMPDSDSEAVYFTQDAQHDLRDPHRRRQSLGPD 720

QY 721 EPSSVLAFWRILICDTERKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780

DB 721 EPSSVLAFWRILICDTERKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780

QY 781 VFTSLFALEMLLKLIVVPGFYIKNPYINPDGVIWISVWBIWVGOQGGGLSVLRTFLMR 840

DB 781 VFTSLFALEMLLKLIVVPGFYIKNPYINPDGVIWISVWBIWVGOQGGGLSVLRTFLMR 840

QY 841 VLKLVRELPALQROLVIMKTMNDVAFMCLMLFIETFSILGMHLFGCKEASERDGTLL 900

DB 841 VLKLVRELPALQROLVIMKTMNDVAFMCLMLFIETFSILGMHLFGCKEASERDGTLL 900

QY 901 PDRKNFSLWAIIVTFOILTQEDWNKVLVNGMASTSWAALYFIATMTFGYVLFNLV 960

DB 901 PDRKNFSLWAIIVTFOILTQEDWNKVLVNGMASTSWAALYFIATMTFGYVLFNLV 960

QY 961 AILVEGFOAEISKREDASGQLSCIQLPVDQGGDANKSESEDPFFSPSLDGDGRKKCL 1020

DB 961 AILVEGFOAEISKREDASGQLSCIQLPVDQGGDANKSESEDPFFSPSLDGDGRKKCL 1020

QY 1021 ALVSLGHEPRLKSLPLPILITHTAATPMSLPKSTGTGALGPASRTSSGSAEPGAA 1080

DB 1021 ALVSLGHEPRLKSLPLPILITHTAATPMSLPKSTGTGALGPASRTSSGSAEPGAA 1080

QY 1081 HEMKSPPARSPSPWASAASWTSRRSRNSLRAPSLKRRSPSGERRSLSGEQBSQ 1140

DB 1081 HEMKSPPARSPSPWASAASWTSRRSRNSLRAPSLKRRSPSGERRSLSGEQBSQ 1140

QY 1141 DEESSEERASPAQSDHHRGSLRREAKSPDLPTLQVPLHRTASGRSASHQDCN 1200

DB 1141 DEESSEERASPAQSDHHRGSLRREAKSPDLPTLQVPLHRTASGRSASHQDCN 1200

QY 1201 GKASGRRLARALRPDDPLDGDADDENLSKGERVRAIRARLPACYLERSWSAYIFP 1260

DB 1201 GKASGRRLARALRPDDPLDGDADDENLSKGERVRAIRARLPACYLERSWSAYIFP 1260

QY 1261 POSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYFTAV 1320

DB 1261 POSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYFTAV 1320

QY 1321 FLAEMTVKVALGWCFGQAYLRSSNVLDGLLVLISVIDILVSVSDSGTKILGMLRVL 1380

DB 1321 FLAEMTVKVALGWCFGQAYLRSSNVLDGLLVLISVIDILVSVSDSGTKILGMLRVL 1380

QY 1381 RLILRLRLRVLSRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVOLFKGKFFV 1440

DB 1381 RLILRLRLRVLSRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVOLFKGKFFV 1440

QY 1441 COGEDTRNITNKSDCAEASYRVRHKYNFDNLGOALMSLFLVASKDQWVDIMYDGLDVG 1500

DB 1441 COGEDTRNITNKSDCAEASYRVRHKYNFDNLGOALMSLFLVASKDQWVDIMYDGLDVG 1500

QY 1501 VDOQPMNHNPMWLLYFISFLILVAFVLMFVGVVVENFHKRQHQREERARRREKRL 1560

DB 1501 VDOQPMNHNPMWLLYFISFLILVAFVLMFVGVVVENFHKRQHQREERARRREKRL 1560

QY 1561 RLEKKER-----KAQCKPYSDYSRFRLLVHLLCTSHYLDLFTITVIGLNVWTWAME 1613

DB 1561 RLEKKERKEKQMAEQCKPYSDYSRFRLLVHLLCTSHYLDLFTITVIGLNVWTWAME 1620

QY 1614 HYQOQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLAIVLLSIMGIT 1673

DB 1614 HYQOQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLAIVLLSIMGIT 1680

QY 1674 LEBIEVNASLPINPTIIRIMRVLRARVLLKMAVMEALLDVTMOALPOVGNLGLLEM 1733

DB 1674 LEBIEVNASLPINPTIIRIMRVLRARVLLKMAVMEALLDVTMOALPOVGNLGLLEM 1740

QY 1734 LLFFPIFAALGVLELFGDLECDETHPCFGLGRHAFTRNFGMAFLTLFRVSTGDNWNGIMKDT 1793

DB 1741 LLFFPIFAALGVLELFGDLECDETHPCFGLGRHAFTRNFGMAFLTLFRVSTGDNWNGIMKDT 1800

QY 1794 LRDCQESTCYNTVTSPIYFVSVLTAQFVLVNVVIAVLMKHEESNKEAELEAEL 1853
DB 1801 LRDCQESTCYNTVTSPIYFVSVLTAQFVLVNVVIAVLMKHEESNKEAELEAEL 1860
QY 1854 ELEMKTLSQPHSPGLSGPFLWPGVGPDPSPDKPGALHHPAAHARSASHFSLHPTMQPH 1913
DB 1861 ELEMKTLSQPHSPGLSGPFLWPGVGPDPSPDKPGALHHPAAHARSASHFSLHPTMQPH 1920
QY 1914 PTELPGDLLTVRKSGVSRTHSLPNDYSYMRHGSTAEGLGHRGWLKPKAQSGLSVHS 1973
DB 1921 PTELPGDLLTVRKSGVSRTHSLPNDYSYMRHGSTAEGLGHRGWLKPKAQSGLSVHS 1980
QY 1974 QPADTSYIQLPKDAPHLLQPHSAPTWTGTPKLPPLPGSRPLAQRPLRQAAIRTDLSLDVQ 2033
DB 1981 QPADTSYIQLPKDAPHLLQPHSAPTWTGTPKLPPLPGSRPLAQRPLRQAAIRTDLSLDVQ 2040
QY 2034 GLGREDLLAEVSGSPPLARAYSWGOSSTQAQHSRSHSKI SKHMTTPAPCPGPEPNW 2093
DB 2041 GLGREDLLAEVSGSPPLARAYSWGOSSTQAQHSRSHSKI SKHMTTPAPCPGPEPNW 2100
QY 2094 GKGPPESTRSSLELDTLSWISGDLPLPGGQEPSPDLKKCYVSAQSCORRPTSMWLD 2153
DB 2101 GKGPPESTRSSLELDTLSWISGDLPLPGGQEPSPDLKKCYVSAQSCORRPTSMWLD 2160
QY 2154 QRRHSIAVCLDSGQPHLGTDPNLGGQPLGPGSRPKKLSPPSIITIDPPESQGRTP 2213
DB 2161 QRRHSIAVCLDSGQPHLGTDPNLGGQPLGPGSRPKKLSPPSIITIDPPESQGRTP 2220
QY 2214 PSPGICLRRRAPSSDSKDPPLASGPPDSMAASPSPKDVLSSGLSSDPADLDP 2266
DB 2221 PSPGICLRRRAPSSDSKDPPLASGPPDSMAASPSPKDVLSSGLSSDPADLDP 2273

RESULT 2
AA14589
ID AA14589 standard; protein; 2243 AA.
AC AA14589;
XX
XX 07-DEC-1999 (first entry)
XX Human T-type voltage-gated Ca channel alpha-1-G (hCavTid).
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX Homo sapiens.
XX WO9229847-A1.
XX
XX 17-JUN-1999.
XX
XX 30-OCT-1998; 98WO-US023161.
XX
XX 05-DEC-1997; 97US-00985809.
XX (LOYO) UNIV LOYOLA CHICAGO.
XX PA
XX Perez-Reyes E, Cribbs LL;
XX FI
XX WPI; 1999-394972/33.
XX DR N-PSDB; AAX83484.
XX
XX New T-type voltage-gated calcium channels.
XX Disclosure; Page 58-67; 138pp; English.
XX
XX This sequence represents a human T-type voltage-gated calcium (Ca)
XX channel alpha-1-G designated hCavTid. Voltage gated channels are membrane
XX bound glycosylated proteins formed of several subunits. The large alpha
XX subunits form a pore in the membrane that is selective for a given ionic
XX species. Each alpha subunit contains 4 domains (I, II, III and IV) and

CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC -type Ca channels are activated at a lower voltage than L- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC channels contains a putative IVS4 region comprising the amino acid
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect calcium
CC channels. Methods are also disclosed for treating a disease or disorder
CC associated with a deficiency in a native T-type calcium channel nucleic
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 2243 AA;

Query Match 98.8%; Score 11758.5; DB 2; Length 2243;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 1; Indels 23; Gaps 1;

QY 1 MDEEDGAGABESGQPSFMRNLNDLSGAGRPGSGAEKDPGSADSEAEGLPYPALAPVV 60
DB 1 MDEEDGAGABESGQPSFMRNLNDLSGAGRPGSGAEKDPGSADSEAEGLPYPALAPVV 60
QY 61 FFYLSQDSRPESWCLRTVCNPFERISMLVILLNCVTILGMPRPCEDIACDSQRCRILQAF 120
DB 61 FFYLSQDSRPESWCLRTVCNPFERISMLVILLNCVTILGMPRPCEDIACDSQRCRILQAF 120
QY 121 DDFIFAFVAVMVVMVALGIFGKKCYLGDWNLDFFIAGLMLEYSLDLQNVFSFAVR 180
DB 121 DDFIFAFVAVMVVMVALGIFGKKCYLGDWNLDFFIAGLMLEYSLDLQNVFSFAVR 180
QY 181 TVRVLRPLRAINRVPSMRILVTLLDTLPMGNVLLLCFFVFFIFGIVGQVWAGLLNR 240
DB 181 TVRVLRPLRAINRVPSMRILVTLLDTLPMGNVLLLCFFVFFIFGIVGQVWAGLLNR 240
QY 241 CFLPENFSLPLSDLEERYOTENEDSPFFCSPRENGMRSCRSVPTLRDGGGGGPPCGL 300
DB 241 CFLPENFSLPLSDLEERYOTENEDSPFFCSPRENGMRSCRSVPTLRDGGGGGPPCGL 300
QY 301 DYEAYNSSNTTCVNNQYNTCSAGEHNPFGKAINFDNIGYAWIAIFOVITLEGWVDIM 360
DB 301 DYEAYNSSNTTCVNNQYNTCSAGEHNPFGKAINFDNIGYAWIAIFOVITLEGWVDIM 360
QY 361 YFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLRQVRFLSNA 420
DB 361 YFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLRQVRFLSNA 420
QY 421 STLASFEPGSCVEELLKYLVLTKAARRLAQVSRAGVRVGLLSPPAPLGQETQPS 480
DB 421 STLASFEPGSCVEELLKYLVLTKAARRLAQVSRAGVRVGLLSPPAPLGQETQPS 480
QY 481 SCSRRRLSVHHLVHHHHHHHHVHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
DB 481 SCSRRRLSVHHLVHHHHHHHHVHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
QY 541 ALSGAPPGAESVHSFYHADCHLEPVRQAPPSPSEASGRTVSGSKYPTVHTSPPE 600
DB 541 ALSGAPPGAESVHSFYHADCHLEPVRQAPPSPSEASGRTVSGSKYPTVHTSPPE 600
QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGYSMSHKLLETQSTGACOSSCKISSPCIKADSG 660
DB 601 TLKEKALVEVAASSGPPTLTSLNIPPGYSMSHKLLETQSTGACOSSCKISSPCIKADSG 660
QY 661 ACGPDCPCYCARAGAGEVELADREMPDSDSAVYFTODAOHSDLRDPSRRORSIGPDA 720
DB 661 ACGPDCPCYCARAGAGEVELADREMPDSDSAVYFTODAOHSDLRDPSRRORSIGPDA 720
QY 721 BPSSVLAFWRLICDTFRKIVDSKYFGRGIMTIALVNTLSMGIEVHEQPEELTNALEISNI 780
DB 721 BPSSVLAFWRLICDTFRKIVDSKYFGRGIMTIALVNTLSMGIEVHEQPEELTNALEISNI 780
QY 781 VFTSLFALEMLKLLVYGPFGYIKNPYNIPOGVIVISVWEIVGQGGGLSVLRTFLMR 840

781 VFTSLFALEMLKLLVGPFGYIKNPYNIEDGVIVIVISVWEIVGQQGGLSVLRTFELMR 840 Db
841 VLKLVRLPALQRLVLMKTMNDVATFCMLLMFLFIFISILGMHLPCKCFASERDGTLL 900 Qy
841 VLKLVRLPALQRLVLMKTMNDVATFCMLLMFLFIFISILGMHLPCKCFASERDGTLL 900 Db
901 PDRKNFDSLWAIIVTFQILITQEDWNKVLNGMASTSSWAALYFIAMTGNVYVFNLLV 960 Qy
901 PDRKNFDSLWAIIVTFQILITQEDWNKVLNGMASTSSWAALYFIAMTGNVYVFNLLV 960 Db
961 AILVEGQAEHISKREDAAGQLSCIQLPVDVSGQDANKSEPEDFPSPSLDGDGRKKCL 1020 Qy
961 AILVEGQAEHISKREDAAGQLSCIQLPVDVSGQDANKSEPEDFPSPSLDGDGRKKCL 1020 Db
1021 ALVSLGHEPELRKILLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSGSAEPGAA 1080 Qy
1021 ALVSLGHEPELRKILLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSGSAEPGAA 1080 Db
998 ALVSLGHEPELRKILLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSGSAEPGAA 1057 Db
1081 HEMKSPSPASRSPSPWGAASWTSSRSRSLGRAPSLKRRSPSGERSLLSGEGQESQ 1140 Qy
1081 HEMKSPSPASRSPSPWGAASWTSSRSRSLGRAPSLKRRSPSGERSLLSGEGQESQ 1140 Db
1058 HEMKSPSPASRSPSPWGAASWTSSRSRSLGRAPSLKRRSPSGERSLLSGEGQESQ 1117 Db
1141 DEBESSHEERASBPAGSDHRRHGLSLEAKSGFDLPTLQVGLHRTASGRGSASEHODCN 1200 Qy
1141 DEBESSHEERASBPAGSDHRRHGLSLEAKSGFDLPTLQVGLHRTASGRGSASEHODCN 1200 Db
1118 DEBESSHEERASBPAGSDHRRHGLSLEAKSGFDLPTLQVGLHRTASGRGSASEHODCN 1177 Db
1201 GKSASGRALARALPDDPLDGDADDDEGNLSKGERVRAWIRARLPACVLERDSWSAYIFP 1260 Qy
1178 GKSASGRALARALPDDPLDGDADDDEGNLSKGERVRAWIRARLPACVLERDSWSAYIFP 1237 Db
1261 POSRPRLLCHRIITHKMFHDHVLVIFLNCITIAMERPKIDPHSAERIFLTLSNIFTAV 1320 Qy
1238 POSRPRLLCHRIITHKMFHDHVLVIFLNCITIAMERPKIDPHSAERIFLTLSNIFTAV 1297 Db
1321 FLAEMTVKVALGWCFGEQAYLRSSNVLDGLLVLSVIDILVMSVDSGTKILGMLRVL 1380 Qy
1298 FLAEMTVKVALGWCFGEQAYLRSSNVLDGLLVLSVIDILVMSVDSGTKILGMLRVL 1357 Db
1381 RLRLTLRLPLVRSRAGQLKLVVETLMSLKPIGNIVICAFPIIFGILGVQLFKGKPFV 1440 Qy
1358 RLRLTLRLPLVRSRAGQLKLVVETLMSLKPIGNIVICAFPIIFGILGVQLFKGKPFV 1417 Db
1441 CQGEDTRNTKSDCAEASRVRRHKYFNPDNLGOALMSLFLVLSKDGWDIMVDGLDVG 1500 Qy
1418 CQGEDTRNTKSDCAEASRVRRHKYFNPDNLGOALMSLFLVLSKDGWDIMVDGLDVG 1477 Db
1501 VDOQPMNNHPWMLLYFISFLLIIVAFVLMFVGVVVFHFKCRQHQEERARRBEKRL 1560 Qy
1478 VDOQPMNNHPWMLLYFISFLLIIVAFVLMFVGVVVFHFKCRQHQEERARRBEKRL 1537 Db
1561 RLLEKKRRKAQCKPYYSYRSRFLLVHLLCTSHYLDLFTGVGLNVVTWAMEHYOQPI 1620 Qy
1538 RLLEKKRRKAQCKPYYSYRSRFLLVHLLCTSHYLDLFTGVGLNVVTWAMEHYOQPI 1597 Db
1621 LDEALKICNVIPTVIFVLESVFLVAFGFRFRFQDRWNQDLDAIVLLSIMGITLEELEVN 1680 Qy
1598 LDEALKICNVIPTVIFVLESVFLVAFGFRFRFQDRWNQDLDAIVLLSIMGITLEELEVN 1657 Db
1681 ASLPINPTIIRIMRVLRARVLLKLMKAVGMRALDVTMOALFQVGNLGLLFLMFLPFA 1740 Qy
1658 ASLPINPTIIRIMRVLRARVLLKLMKAVGMRALDVTMOALFQVGNLGLLFLMFLPFA 1717 Db
1741 ALGVELFGDLECDTHPCBGLGRHATPRNFGMAFLTLFRYSTGDNWNGIMKDTLRDCDQE 1800 Qy
1718 ALGVELFGDLECDTHPCBGLGRHATPRNFGMAFLTLFRYSTGDNWNGIMKDTLRDCDQE 1777 Db
1801 STCVNTVISPITYFVSFVLTAQFVLNVVIVAVLMKHEESNKEAEAEAELEEMKTL 1860 Qy
1778 STCVNTVISPITYFVSFVLTAQFVLNVVIVAVLMKHEESNKEAEAEAELEEMKTL 1837 Db
1861 SPQHSPLGSPFLWFGVEGSDPSPKFGALHPAAHARSASHFSLHPTMQPHTLPGP 1920 Qy
1838 SPQHSPLGSPFLWFGVEGSDPSPKFGALHPAAHARSASHFSLHPTMQPHTLPGP 1897 Db

1921 DILLTVRKSGVSRTHSLPNDSYMCMRHGSGTAGBPLGHRGWGLPKAQSGSVLSVHSQPADTSY 1980 Qy
1898 DILLTVRKSGVSRTHSLPNDSYMCMRHGSGTAGBPLGHRGWGLPKAQSGSVLSVHSQPADTSY 1957 Db
1981 ILQIPKDAAPHLLQPHSAPTWTGTPKLPFGGSRPLAQRRLRQAARTDSDVQGLGSRD 2040 Qy
1958 ILQIPKDAAPHLLQPHSAPTWTGTPKLPFGGSRPLAQRRLRQAARTDSDVQGLGSRD 2017 Db
2041 LLAEVSGSPPLARAYFWGQSSTQAQOHSRSHSKISKHMTPTTAPCPGEPENWCKGPPET 2100 Qy
2018 LLAEVSGSPPLARAYFWGQSSTQAQOHSRSHSKISKHMTPTTAPCPGEPENWCKGPPET 2077 Db
2101 RSSLELDELTELISWISGDLPLPGGQEPSPRDLKCYVSAQSCORRPTSWLDEQRHSHIA 2160 Qy
2078 RSSLELDELTELISWISGDLPLPGGQEPSPRDLKCYVSAQSCORRPTSWLDEQRHSHIA 2137 Db
2161 VSCLDSSSQPHLGTDPNSLGGQPLGGGSRPKKLSPPSITIDPPESQGRTPPSPGICL 2220 Qy
2138 VSCLDSSSQPHLGTDPNSLGGQPLGGGSRPKKLSPPSITIDPPESQGRTPPSPGICL 2197 Db
2221 RRRAPSSDSKDPLASGPPDSMAASPSKPKOVLSLSGLSSDPADLDP 2266 Qy
2198 RRRAPSSDSKDPLASGPPDSMAASPSKPKOVLSLSGLSSDPADLDP 2243 Db

RESULT 3

ADJ68819
ID ADJ68819 standard; protein; 2243 AA.
XX
AC ADJ68819;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID625.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-038987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
XX
BU (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
PI Warnock DE;
XX
XX WPI; 2003-845369/78.
DR
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
XX
PS Claim 1; SEQ ID NO 625; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with

altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, liver's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytotatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.

XX Sequence 2243 AA;

CC	Query Match	98.8%;	Score 11758.5;	DB 7;	Length 2243;
CC	Best Local Similarity	98.9%;	Pred. No. 0;		
CC	Matches 2242;	Conservative 0;	Mismatches 1;	Indels 23;	Gaps 1;
QY	1	MDEEDGAGABESGQPRFMRINDLSGAGRPGPGSAEKDPGSADSEAGLPYPALAPV	60		
DB	1	MDEEDGAGABESGQPRFMRINDLSGAGRPGPGSAEKDPGSADSEAGLPYPALAPV	60		
QY	61	FFYLSQSRPRSWCLRTVCNPFWRISMLVILLNCVTILGMFRPCEDIAQDSQRCRILOAF	120		
DB	61	FFYLSQSRPRSWCLRTVCNPFWRISMLVILLNCVTILGMFRPCEDIAQDSQRCRILOAF	120		
QY	121	DDFPAFAFVEMVVMVALGFGKKCYLGDFTWNRDLFFIVTAGMLEYSLDIQNVSFAVR	180		
DB	121	DDFPAFAFVEMVVMVALGFGKKCYLGDFTWNRDLFFIVTAGMLEYSLDIQNVSFAVR	180		
QY	181	TVRVLRPLRAINRVPSMRILVTLLDLPMLGNVLLCCFFVFETFGVGVQLWAGLNR	240		
DB	181	TVRVLRPLRAINRVPSMRILVTLLDLPMLGNVLLCCFFVFETFGVGVQLWAGLNR	240		
QY	241	CFIPENFSLVDLERYOTENDESPFTCSQPRENGMRSCRSVPTLRDGGGGPPCGL	300		
DB	241	CFIPENFSLVDLERYOTENDESPFTCSQPRENGMRSCRSVPTLRDGGGGPPCGL	300		
QY	301	DYAYNSSNTTCVNNQYNTCSAGBNPFKGAINDNIGYAWIAIFQVITLEGWVDIM	360		
DB	301	DYAYNSSNTTCVNNQYNTCSAGBNPFKGAINDNIGYAWIAIFQVITLEGWVDIM	360		
QY	361	YFVMDAHSFYNFYIFILLIIVGSFFMNLCLVVIATQFSETKQESQLMREQVRFLSNA	420		
DB	361	YFVMDAHSFYNFYIFILLIIVGSFFMNLCLVVIATQFSETKQESQLMREQVRFLSNA	420		
QY	421	STLASSEPGSCYBELLKYLVIYLRKAARLAQVSRAGVRVGLLSSPAPLGGQETQPS	480		
DB	421	STLASSEPGSCYBELLKYLVIYLRKAARLAQVSRAGVRVGLLSSPAPLGGQETQPS	480		
QY	481	SCSRSHRRLSVHLLVHHHHHHHHYHLNGTLRAPASPEIQORDANGSRRLMLPPPTP	540		
DB	481	SCSRSHRRLSVHLLVHHHHHHHHYHLNGTLRAPASPEIQORDANGSRRLMLPPPTP	540		
QY	541	ALSGAPPGAGSVHSFYHADCHLEPVRCOAPPPSPSEASGRVTGSGKVPVTVHTSPPE	600		
DB	541	ALSGAPPGAGSVHSFYHADCHLEPVRCOAPPPSPSEASGRVTGSGKVPVTVHTSPPE	600		
QY	601	TLKXALVEVAASSGPPTLTSLNIPGPYSSMHKLETTOSTGACQSSCKISSPCLKADSG	660		
DB	601	TLKXALVEVAASSGPPTLTSLNIPGPYSSMHKLETTOSTGACQSSCKISSPCLKADSG	660		
QY	661	ACGPDSCPCARAGAGEVELAREMPDSDSEAVYEFTQDAQSHDLRDPHSRQRSIGPDA	720		
DB	661	ACGPDSCPCARAGAGEVELAREMPDSDSEAVYEFTQDAQSHDLRDPHSRQRSIGPDA	720		
QY	721	EPSSVLAFWRLLCDTFRKIVDSKYFGRGIMAILVNTLSMGIYEHQPEELTNALEISNI	780		
DB	721	EPSSVLAFWRLLCDTFRKIVDSKYFGRGIMAILVNTLSMGIYEHQPEELTNALEISNI	780		
QY	781	VFTSLFALEMLKLLIVYGFYIKNPYIFDGVIVVISWEIVGQGGGLSVLRTFLMR	840		

DB	781	VFTSLFALEMLKLLIVYGFYIKNPYIFDGVIVVISWEIVGQGGGLSVLRTFLMR	840		
QY	841	VILKLVRFALQORQVLWMLKMTNDVATCMLLMLEFIFISILGMHLFGCKFASERDGTIL	900		
DB	841	VILKLVRFALQORQVLWMLKMTNDVATCMLLMLEFIFISILGMHLFGCKFASERDGTIL	900		
QY	901	PDRKNFDSLLMAIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLIV	960		
DB	901	PDRKNFDSLLMAIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLIV	960		
QY	961	AILVEGFOAEISIKREDASGQLSCIQLPVDGQGDANKSESEPDPFSPSLDGDGDRKKCL	1020		
DB	961	AILVEGFOAEISIKREDASGQLSCIQLPVDGQGDANKSESEPDPFSPSLDGDGDRKKCL	997		
QY	1021	ALVSLGEHPERKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSGSAEPGAA	1080		
DB	998	ALVSLGEHPERKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSGSAEPGAA	1057		
QY	1081	HEMKSPPSARSPHSPMSAASWTSRRSRNSLGRAPSLKERSPSGERRSLLSGEGQESQ	1140		
DB	1058	HEMKSPPSARSPHSPMSAASWTSRRSRNSLGRAPSLKERSPSGERRSLLSGEGQESQ	1117		
QY	1141	DEESSEERASPASGSDHRRHRSLEREAKSFDLPDTLOVPLHRTASGRGSAEHQDCN	1200		
DB	1118	DEESSEERASPASGSDHRRHRSLEREAKSFDLPDTLOVPLHRTASGRGSAEHQDCN	1177		
QY	1201	GKSASGRALARALRPDDPDLQDDADDDEGNLSKGRVRVAMIRARLPACCLERDSWSAIFP	1260		
DB	1178	GKSASGRALARALRPDDPDLQDDADDDEGNLSKGRVRVAMIRARLPACCLERDSWSAIFP	1237		
QY	1261	PQSRFRLLCHRIITHKMFHDVHLVILFNCITTIAMERPKIDPHSAERIFLTSNYIETAV	1320		
DB	1238	PQSRFRLLCHRIITHKMFHDVHLVILFNCITTIAMERPKIDPHSAERIFLTSNYIETAV	1297		
QY	1321	FLAEMTVKVALGWCGEQAYLRSSNVLDGLLVLSVIDILVSMVSDSCTKILGMLRVL	1380		
DB	1298	FLAEMTVKVALGWCGEQAYLRSSNVLDGLLVLSVIDILVSMVSDSCTKILGMLRVL	1357		
QY	1381	RLRLTLRLRVISRAOGLKLVVETLMSLKPIGNIVVICAFIIFGILGVQFKGKFFV	1440		
DB	1358	RLRLTLRLRVISRAOGLKLVVETLMSLKPIGNIVVICAFIIFGILGVQFKGKFFV	1417		
QY	1441	CQEDTRNITNKSDCAEASYRWYRHKYFNFDNLQALMSLFLVASKDGVWDIMVDGLDVG	1500		
DB	1418	CQEDTRNITNKSDCAEASYRWYRHKYFNFDNLQALMSLFLVASKDGVWDIMVDGLDVG	1477		
QY	1501	VDOOPTMHNHPWMLLYFISFLIIVAFVLMFVGVVVENFHKCRQHOEBEERREKRL	1560		
DB	1478	VDOOPTMHNHPWMLLYFISFLIIVAFVLMFVGVVVENFHKCRQHOEBEERREKRL	1537		
QY	1561	RLLEKKRRKAQCKPYYSYDYSRFRLLVHLLCTSHYLDLFTGVIGLNVVWMAHEHYOQPI	1620		
DB	1538	RLLEKKRRKAQCKPYYSYDYSRFRLLVHLLCTSHYLDLFTGVIGLNVVWMAHEHYOQPI	1597		
QY	1621	LDEALKICNYIFTVIVLESVFKLVAFGFRFRFQDRWNOLDLAI VLLSIMGITLBEIEVN	1680		
DB	1598	LDEALKICNYIFTVIVLESVFKLVAFGFRFRFQDRWNOLDLAI VLLSIMGITLBEIEVN	1657		
QY	1681	ASLIPNPTIIRIMVLRITARVLKLLKMAVGMALLDTVMQALPQVGNLGLLPMLLFFIFA	1740		
DB	1658	ASLIPNPTIIRIMVLRITARVLKLLKMAVGMALLDTVMQALPQVGNLGLLPMLLFFIFA	1717		
QY	1741	ALGVLFGLDCEDETHPCBEGLRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCQE	1800		
DB	1718	ALGVLFGLDCEDETHPCBEGLRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCQE	1800		
QY	1801	STCYNTVISPFIYFVSFLVTAQFVLNVVIAVLMKHLSESNKEAEAELELEMEKTL	1860		
DB	1778	STCYNTVISPFIYFVSFLVTAQFVLNVVIAVLMKHLSESNKEAEAELELEMEKTL	1837		
QY	1861	SPQHSPLGSPFLWPGVEGPDSPSPKGAALHPAAHARSASHFSLEHPTMOPHTLPGP	1920		

1838 SPQFHSPLGSPFLWPGVEGSDPSDPKPGALHPAAHARSASHFSLEHPTMQPHTLP 1897
1921 DLLTVRSGVSRTHSLPNDSTYMCRHGTAEGPLGHRGWLKPAQSGSVLSVHSQADTSY 1980
1898 DLLTVRSGVSRTHSLPNDSTYMCRHGTAEGPLGHRGWLKPAQSGSVLSVHSQADTSY 1957
1981 ILQPKDAPHLLQPHSAPTWTGTPKLPPLPGSRPLAQRPLRQAAIRTDLSLVQGLGRED 2040
1958 ILQPKDAPHLLQPHSAPTWTGTPKLPPLPGSRPLAQRPLRQAAIRTDLSLVQGLGRED 2017
2041 LLAIVSGSPPLARAYSPWGSSTQAQOHSRSHSKISKHMTTPAPCPGPEPNWKGPPET 2100
2018 LLAIVSGSPPLARAYSPWGSSTQAQOHSRSHSKISKHMTTPAPCPGPEPNWKGPPET 2077
2101 RSSLELDELTSWISGDLPLPGQOEPPSPRDLKKCYVSAQSCQRRPTSWLDEQRHSIA 2160
2078 RSSLELDELTSWISGDLPLPGQOEPPSPRDLKKCYVSAQSCQRRPTSWLDEQRHSIA 2137
2161 VSCLDGSGQPHLGTDPNSVGGPLGGGSRPKKLSPPSITIDPPESQGPRTPPSPGICL 2220
2138 VSCLDGSGQPHLGTDPNSVGGPLGGGSRPKKLSPPSITIDPPESQGPRTPPSPGICL 2197
2221 RRRAPSSDSKDLASGPPDSMAASPSPKKDVLSLGLSDPADLDP 2266
2198 RRRAPSSDSKDLASGPPDSMAASPSPKKDVLSLGLSDPADLDP 2243

RESULT 4
AAY14586
ID AAY14586 standard; protein; 2250 AA.
XX AAY14586;
AC
XX
DT 07-DEC-1999 (first entry)
XX Human T-type voltage-gated Ca channel alpha-1-G (hCav1a).
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
KW Homo sapiens.
OS
XX W09299847-A1.
PN
XX
PD 17-JUN-1999.
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
PI Perez-Reyes E, Cribbs LL;
XX
XX WPI; 1999-394972/33.
DR N-PSDB; AAX83481.
XX
XX New T-type voltage-gated calcium channels.
XX
XX Disclosure; Page 31-40; 138pp; English.
XX This sequence represents a human T-type voltage-gated calcium (Ca)
CC channel alpha-1-G designated hCav1a. Voltage gated channels are membrane
CC bound glycosylated proteins formed of several subunits. The large alpha
CC subunits form a pore in the membrane that is selective for a given ionic
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC -type Ca channels are activated at a lower voltage than L- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC -channels contains a putative IVS4 region comprising the amino acid

sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect calcium
CC channels. Methods are also disclosed for treating a disease or disorder
CC associated with a deficiency in a native T-type calcium channel nucleic
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 2250 AA;
Query Match 98.6%; Score 11741; DB 2; Length 2250;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2241; Conservative 1; Mismatches 1; Indels 30; Gaps 2;
QY 1 MDEEDGAGAESQSPRSFMRNLDSGAGRPGPSAEKDPGSADSAEGSLYPALAPVV 60
DB 1 MDEEDGAGAESQSPRSFMRNLDSGAGRPGPSAEKDPGSADSAEGSLYPALAPVV 60
QY 61 PFYLSQDSRPSWCLRTVCNPFERISMLVTLLNCVTLGMFPCEDIAQDSQRCRILQAF 120
DB 61 PFYLSQDSRPSWCLRTVCNPFERISMLVTLLNCVTLGMFPCEDIAQDSQRCRILQAF 120
QY 121 DDF1FAFFAVEMVVMVALGIFGKCYLGDWTNRDLDPFIVIAAGMLEYSLDLQNVFSFSAVR 180
DB 121 DDF1FAFFAVEMVVMVALGIFGKCYLGDWTNRDLDPFIVIAAGMLEYSLDLQNVFSFSAVR 180
QY 181 TVRVLRPLRAINRVPMSRILVTLLDTPMLGNVLLLCFFEVFFIFGIVGVQLWAGLLNR 240
DB 181 TVRVLRPLRAINRVPMSRILVTLLDTPMLGNVLLLCFFEVFFIFGIVGVQLWAGLLNR 240
QY 241 CFLPENFSLPLSVDLERYOTENEDSPFICSPQRENGMRSCRSVPTLRGDCGGPPCGL 300
DB 241 CFLPENFSLPLSVDLERYOTENEDSPFICSPQRENGMRSCRSVPTLRGDCGGPPCGL 300
QY 301 DYEAYNSSNTTCVNWNQYTNCSAGEHNPFGKAINFNDNIGYAWIAIFQVITLEGWVDIM 360
DB 301 DYEAYNSSNTTCVNWNQYTNCSAGEHNPFGKAINFNDNIGYAWIAIFQVITLEGWVDIM 360
QY 361 YFVMDAHSFYNIYIFILLIIVGSFFMINCLVVIATOFSETKQRESQLMREQVRFLSNA 420
DB 361 YFVMDAHSFYNIYIFILLIIVGSFFMINCLVVIATOFSETKQRESQLMREQVRFLSNA 420
QY 421 STLASFSEPGSCVEELLKYLVLKAAARLQVRAAGVRVGLLSAPLGOETQSPSS 480
DB 421 STLASFSEPGSCVEELLKYLVLKAAARLQVRAAGVRVGLLSAPLGOETQSPSS 480
QY 481 SCSRSRRLSVHLLVHHHHHHHHHHLNGTTRAPASPEIQDRDANGSERMLPPSTP 540
DB 481 SCSRSRRLSVHLLVHHHHHHHHHHLNGTTRAPASPEIQDRDANGSERMLPPSTP 540
QY 541 ALSGAPPGAESVHSFYHADCHLEPVRCQAPPSPSEASGRVTVGSKVYPTVHTSPPE 600
DB 541 ALSGAPPGAESVHSFYHADCHLEPVRCQAPPSPSEASGRVTVGSKVYPTVHTSPPE 600
QY 601 TLKEKALVEVAASSGPPTLTSINIPPGYSSMHKLLTQSTGACQSCSKTSSPCCLKADSG 660
DB 601 TLKEKALVEVAASSGPPTLTSINIPPGYSSMHKLLTQSTGACQSCSKTSSPCCLKADSG 660
QY 661 ACGPDSCTPCYCARAGAGEVELADREMPDSEAVYFTQDACHSDLRPHSRQBSLGPDA 720
DB 661 ACGPDSCTPCYCARAGAGEVELADREMPDSEAVYFTQDACHSDLRPHSRQBSLGPDA 720
QY 721 EPSSVLAFWELICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALEISNI 780
DB 721 EPSSVLAFWELICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALEISNI 780
QY 781 VFTSLFALEMLLKLIVYGPFGYIKNPYINIFDGVIVISVWEIVGQGGGLSVLTFRLMR 840
DB 781 VFTSLFALEMLLKLIVYGPFGYIKNPYINIFDGVIVISVWEIVGQGGGLSVLTFRLMR 840
QY 841 VLKLVRLPALQRLQVLVLMKTMNDVATFCMLLMFIFESTLGMHFGCKFASRDGDTL 900
DB 841 VLKLVRLPALQRLQVLVLMKTMNDVATFCMLLMFIFESTLGMHFGCKFASRDGDTL 900
QY 901 PDRKNFDSLLWAIIVTFVQLTQEDWNKVLVNGMASTSWAALYFIALMTFGNYVLFNLIV 960

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901 PRKKNFSLMAIVTVFQILTOEDMKNVLYNGMASTSSWAALFYIALMTFGNVVLENLIV 960
961 AILVGFQAEIISKREDASQSLCIQLPVDSQGGDANKSESEPDREPSISLDGGRKKCL 1020
961 AILVGFQAEIISKREDASQSLCIQLPVDSQGGDANKSESEPDREPSISLDGGRKKCL 997
1021 ALVSLGEHPLELKSLLPPII IHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSAEPGAA 1080
998 ALVSLGEHPLELKSLLPPII IHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSAEPGAA 1057
1081 HEMKPPSARSPHSPWSAASWTSSRNSRLGRAPSLKRSPGERRSLLSGEGQESQ 1140
1058 HEMKPPSARSPHSPWSAASWTSSRNSRLGRAPSLKRSPGERRSLLSGEGQESQ 1117
1141 DEESSEERASPDGHRHRSLEAKSSFDLPDTLQVPGHRTASGRGASSHQDCN 1200
1118 DEESSEERASPDGHRHRSLEAKSSFDLPDTLQVPGHRTASGRGASSHQDCN 1177
1201 GKSASGRALARLPDDPPLDGDADDEGNLSKGERVRAWRARLPACCLERDSWYIYP 1260
1178 GKSASGRALARLPDDPPLDGDADDEGNLSKGERVRAWRARLPACCLERDSWYIYP 1237
1261 POSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
1238 POSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1297
1321 FLAEMTVKVALGWCFCGQAYLRSSNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVL 1380
1298 FLAEMTVKVALGWCFCGQAYLRSSNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVL 1357
1381 RLTLRLPLRVSRAQGLKLVETLMSLKPIGNIVICCAFFIIFGLGVQLFKGPFV 1440
1358 RLTLRLPLRVSRAQGLKLVETLMSLKPIGNIVICCAFFIIFGLGVQLFKGPFV 1417
1441 COGEDTRNITNKSOCASRYWVRHKYFNDFNLGQALMSFLVLSKDGWVDIMYDGLDVG 1500
1418 COGEDTRNITNKSOCASRYWVRHKYFNDFNLGQALMSFLVLSKDGWVDIMYDGLDVG 1477
1501 VDQOPIIMNHPMMLLYIFISFLLIIVAFVFLNMFVGVVVENFHKCHQOESEAREERKRL 1560
1478 VDQOPIIMNHPMMLLYIFISFLLIIVAFVFLNMFVGVVVENFHKCHQOESEAREERKRL 1537
1561 RLLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYDLFITGVGLNVVTWAME 1613
1538 RLLEKKRRSEKQMAEQAQCKPYSDYSRFRLLVHHLCTSHYDLFITGVGLNVVTWAME 1597
1614 HYQOQOILDEALKICNVIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLAIVLLSIMGIT 1673
1598 HYQOQOILDEALKICNVIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLAIVLLSIMGIT 1657
1674 LEBIEVNASLPINPTIIRIMRVLRIARVLKLLKQAVGMRALLOTVMQALPOVGNLGLFM 1733
1658 LEBIEVNASLPINPTIIRIMRVLRIARVLKLLKQAVGMRALLOTVMQALPOVGNLGLFM 1717
1734 LUFFIIPAAALGVELFGLDECDTHPCBGLGHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1793
1718 LUFFIIPAAALGVELFGLDECDTHPCBGLGHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1777
1794 LRDCDQESTCYNTVISPFIYFVSFVLTAQFVLVNVVIAVLMKHLSEENKEAKEAELEAEL 1853
1778 LRDCDQESTCYNTVISPFIYFVSFVLTAQFVLVNVVIAVLMKHLSEENKEAKEAELEAEL 1837
1854 ELEMKTLSQPSPHSPGLSPFMPGVEGPDSPDKPCGALHPAAHARSASHFSLEHPTMQPH 1913
1838 ELEMKTLSQPSPHSPGLSPFMPGVEGPDSPDKPCGALHPAAHARSASHFSLEHPTMQPH 1897
1914 PTELPGPDLLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLHGRGWLKPAQSGSVLSVHS 1973
1898 PTELPGPDLLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLHGRGWLKPAQSGSVLSVHS 1957
1974 QPADTSYIILQPKADPHILOPHSAFTWGTIPKLPPEGRSPLAQRPLRQAAITDSDLVQ 2033
1958 QPADTSYIILQPKADPHILOPHSAFTWGTIPKLPPEGRSPLAQRPLRQAAITDSDLVQ 2017
2034 GLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKISHMTTPAPCPGPEPNW 2093
2018 GLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKISHMTTPAPCPGPEPNW 2077
2094 GKGPETRSLSLELDELTELWSISGDLPLPGQOEPPSPRDLKKCYVSAQSCORRPTSWLDE 2153
2078 GKGPETRSLSLELDELTELWSISGDLPLPGQOEPPSPRDLKKCYVSAQSCORRPTSWLDE 2137
2154 QRHHSIAVSCLDGSGOPHLGTDPSNLGGOPLGPGSRPKKLSPPSIITIDPPESQGRPTP 2213
2138 QRHHSIAVSCLDGSGOPHLGTDPSNLGGOPLGPGSRPKKLSPPSIITIDPPESQGRPTP 2197
2214 PSPGICLRRARRPSSDSKOPLASGPPDSMAASPSPKKDVLSLGLSSDPADLDP 2266
2198 PSPGICLRRARRPSSDSKOPLASGPPDSMAASPSPKKDVLSLGLSSDPADLDP 2250

RESULT 5
AAV14587
ID AAV14587 standard; protein; 2261 AA.
XX
AC AAV14587;
XX
DT 07-DEC-1999 (first entry)
DE Human T-type voltage-gated Cc channel alpha-1-G (hcav1b).
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS Homo sapiens.
XX
PN WO9923847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
XX
DR N-PSDB; AAX83482.
XX
PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 40-49; 138pp; English.
XX
CC This sequence represents a human T-type voltage-gated calcium (Ca)
channel alpha-1-G designated hcav1b. Voltage gated channels are membrane
bound glycosylated proteins formed of several subunits. The large alpha
subunits form a pore in the membrane that is selective for a given ionic
species. Each alpha subunit contains 4 domains (I, II, III and IV) and
each domain contains 6 putative transmembrane helical segments (S1-S6). T
-type Ca channels are activated at a lower voltage than L- or N-type
channels. Characteristics of T-type channels include short current time,
slow activation kinetics near threshold, fast inactivation kinetics and
slow tail current. The sequences AAX83481-X83492 represent novel T-type
voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
channels contains a putative IVS4 region comprising the amino acid
sequence AAV14598. Cells expressing the T-type voltage-gated calcium
channel proteins can be used to screen for drugs which affect calcium
channels. Methods are also disclosed for treating a disease or disorder
associated with a deficiency in a native T-type calcium channel nucleic
acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 2261 AA;
```

Query Match 98.6%; Score 11735.5; DB 2; Length 2261; Best Local Similarity 98.1%; Pred. No. 0; Matches 2241; Conservative 1; Mismatches 1; Indels 41; Gaps 2;									
QY	1	MDEEDGAGAEBSQPRSPFNLNDLSGAGGPGPGSAEKDPGSADSAEAGLPPALAPVV	60	Db	998	ALVSLGHPHSLRSLLEPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA	1057		
Db	1	MDEEDGAGAEBSQPRSPFNLNDLSGAGGPGPGSAEKDPGSADSAEAGLPPALAPVV	60	QY	1081	HEMKSPPSARSSPHSPWSAASSWTSRRSSNSLGRAPSLKRRSPSGRRSSLLSGEGESQ	1140		
QY	61	FFYLSQDSRPSWCLRTVCNPFERISMLVILLNCVTILGMPRPCEDIACDSORCRLQAF	120	Db	1058	HEMKSPPSARSSPHSPWSAASSWTSRRSSNSLGRAPSLKRRSPSGRRSSLLSGEGESQ	1117		
Db	61	FFYLSQDSRPSWCLRTVCNPFERISMLVILLNCVTILGMPRPCEDIACDSORCRLQAF	120	QY	1141	DEESSBEERASPAAGSDHRRGSLERBAKSFDPDLTQVPLGHRHTASGRSASEHQDCN	1200		
QY	121	DDFIFAFPAVEVMVQWALGIPGKKCYLGDWNRLLDFFIVAGMLEYSLDLQNVSFAVR	180	Db	1118	DEESSBEERASPAAGSDHRRGSLERBAKSFDPDLTQVPLGHRHTASGRSASEHQDCN	1177		
Db	121	DDFIFAFPAVEVMVQWALGIPGKKCYLGDWNRLLDFFIVAGMLEYSLDLQNVSFAVR	180	QY	1201	GKSASGLARALRDPDDPLDGDADDGNGNSKGRVRAWIRARLPACVLEEDSDNSAYIFP	1260		
QY	181	TVRVLRPIRANRVPMSMRILVLLDTPMLGNVLLCFFVFPIFGIVGVQLWAGLLRNR	240	Db	1178	GKSASGLARALRDPDDPLDGDADDGNGNSKGRVRAWIRARLPACVLEEDSDNSAYIFP	1237		
Db	181	TVRVLRPIRANRVPMSMRILVLLDTPMLGNVLLCFFVFPIFGIVGVQLWAGLLRNR	240	QY	1261	POSFRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLNFIYFVAV	1320		
QY	241	CPLPENFSLPLSVDLERYQTENEDESPFCISQPRENGMRSRCSVPTLRGDCGGPPCGL	300	Db	1238	POSFRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLNFIYFVAV	1297		
Db	241	CPLPENFSLPLSVDLERYQTENEDESPFCISQPRENGMRSRCSVPTLRGDCGGPPCGL	300	QY	1321	FLAEMTVKVVALGMCFGQAYLRSSWNVDGLLVLSVIDILVMSVSDGTKILGMLRVL	1380		
QY	301	DYEAYNSSNTTCVNWNQYITNCAGEHNPFGKAINFDNIGYAWIAIFQVITLGGWVDIM	360	Db	1298	FLAEMTVKVVALGMCFGQAYLRSSWNVDGLLVLSVIDILVMSVSDGTKILGMLRVL	1357		
Db	301	DYEAYNSSNTTCVNWNQYITNCAGEHNPFGKAINFDNIGYAWIAIFQVITLGGWVDIM	360	QY	1381	RLLRTLRLRVISRAQGLKLVVETLMSLKPIGNIWVICCAFFIIFGLGVQLFKGKPFV	1440		
QY	361	YFVMDAHSFYNYFIYFILLIIVGSPFMINCLVVIATQFSETKQRESQMRQVRFLSNA	420	Db	1358	RLLRTLRLRVISRAQGLKLVVETLMSLKPIGNIWVICCAFFIIFGLGVQLFKGKPFV	1417		
Db	361	YFVMDAHSFYNYFIYFILLIIVGSPFMINCLVVIATQFSETKQRESQMRQVRFLSNA	420	QY	1441	COGEDTRNITNKSDCAEASYSRWVRHKYNFDNLGOALMSLFVLASKDGVVDIMYDGLDAVG	1500		
QY	421	STLASFSBPGSCYEELLKVLVILRKAARLAQVSRAGVVRGVLSSPAPLGQEQTPSS	480	Db	1418	COGEDTRNITNKSDCAEASYSRWVRHKYNFDNLGOALMSLFVLASKDGVVDIMYDGLDAVG	1477		
Db	421	STLASFSBPGSCYEELLKVLVILRKAARLAQVSRAGVVRGVLSSPAPLGQEQTPSS	480	QY	1501	VDOQPIMNHNPMWLLYFISFILLIIVAFVLNMFVGVVFNHFKRCHQHOEEERARRREKEL	1560		
QY	481	SCSRSHRRLSVHLLVHHHHHHHHYHLNGTLRAPRASPEIQORDANGSRRLMLPPSTP	540	Db	1478	VDOQPIMNHNPMWLLYFISFILLIIVAFVLNMFVGVVFNHFKRCHQHOEEERARRREKEL	1537		
Db	481	SCSRSHRRLSVHLLVHHHHHHHHYHLNGTLRAPRASPEIQORDANGSRRLMLPPSTP	540	QY	1561	RRLEKKRR-----KAOCKPYSDYSRFRLLVHHLCTSHVLDLFTIGV	1602		
QY	541	ALSGAPPGAESVHSFYHADCHLEPVRCAOPPRSPSEASGRIVGSGKVYPTVHTSPPE	600	Db	1538	RRLEKKRRMLDDVITASGSSASAASEAOCKPYSDYSRFRLLVHHLCTSHVLDLFTIGV	1597		
Db	541	ALSGAPPGAESVHSFYHADCHLEPVRCAOPPRSPSEASGRIVGSGKVYPTVHTSPPE	600	QY	1603	IGLVNVTMAHEHYQOQPIIDLEALKICNYIFTVIFVLESVFKLVAFGFRFPFQDRWNQDL	1662		
QY	601	TLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLTQSTGACQSSCKLSSPCLKADSG	660	Db	1598	IGLVNVTMAHEHYQOQPIIDLEALKICNYIFTVIFVLESVFKLVAFGFRFPFQDRWNQDL	1657		
Db	601	TLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLTQSTGACQSSCKLSSPCLKADSG	660	QY	1663	AIVLLSIMGITLLEEVNASLPINPTIIRIMRVLRARVLKILKMAVGMALLDVTMOAL	1722		
QY	661	ACGPDSCPYCARAGAGVELADREMPDSDSEAVVEFTQDAQHSDLRDPHRSRQSLGPD	720	Db	1658	AIVLLSIMGITLLEEVNASLPINPTIIRIMRVLRARVLKILKMAVGMALLDVTMOAL	1717		
Db	661	ACGPDSCPYCARAGAGVELADREMPDSDSEAVVEFTQDAQHSDLRDPHRSRQSLGPD	720	QY	1723	POYGNLGLLPMILFFIFAALGVLELFGDLECDETHPCBGLGRHATFRNFGMAFLTLPVST	1782		
QY	721	EPSSVLAFWRLLCOTFRKIVDSKYFGRGIMAILVNTLSMGEIYHEQPELTNALEISNI	780	Db	1718	POYGNLGLLPMILFFIFAALGVLELFGDLECDETHPCBGLGRHATFRNFGMAFLTLPVST	1777		
Db	721	EPSSVLAFWRLLCOTFRKIVDSKYFGRGIMAILVNTLSMGEIYHEQPELTNALEISNI	780	QY	1783	GDNNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVTAVLMKHEESNKE	1842		
QY	781	VFTSIFALEMLLKLVLVGPFGYIKNPYNIIFGVIVIVISWEIIVQOQGGGLSVLTFRLMR	840	Db	1778	GDNNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVTAVLMKHEESNKE	1837		
Db	781	VFTSIFALEMLLKLVLVGPFGYIKNPYNIIFGVIVIVISWEIIVQOQGGGLSVLTFRLMR	840	QY	1843	AKAEAELEAELEEMTKLSPQPHSPGSPFLWPGVEGPDSPDKPCALHAAHARSASH	1902		
QY	841	VKLIVRFPAIQORQLVLMKTMQNVATFCMLMLFIFFITLGMHLFGCKFASERDGTLL	900	Db	1838	AKAEAELEAELEEMTKLSPQPHSPGSPFLWPGVEGPDSPDKPCALHAAHARSASH	1897		
Db	841	VKLIVRFPAIQORQLVLMKTMQNVATFCMLMLFIFFITLGMHLFGCKFASERDGTLL	900	QY	1903	FSLEHPTMQPHTELPDGLLTVRKSGVSRTHSLPNDSYMCRHSGSTAEGLPHGRGWGLPK	1962		
QY	901	PDRKNFDSILLWAVTVFQILTOEDWNKVLNMGMASTSSWAALYFIALTMFGNYVLFNLLV	960	Db	1898	FSLEHPTMQPHTELPDGLLTVRKSGVSRTHSLPNDSYMCRHSGSTAEGLPHGRGWGLPK	1957		
Db	901	PDRKNFDSILLWAVTVFQILTOEDWNKVLNMGMASTSSWAALYFIALTMFGNYVLFNLLV	960	QY	1963	AQSGSVLSVHSQPADTSYIQLPKDAPHLLOPHSAPTWTGTPKLPPIPPGRSPLAORPLRRQ	2022		
QY	961	AILVEGFQABEISKREDASGQSLQLPVDSOGGDANKSESEPPFSPSLDGDGRKKCL	1020	Db	1958	AQSGSVLSVHSQPADTSYIQLPKDAPHLLOPHSAPTWTGTPKLPPIPPGRSPLAORPLRRQ	2017		
Db	961	AILVEGFQABEISKREDASGQSLQLPVDSOGGDANKSESEPPFSPSLDGDGRKKCL	1020	QY	2023	AAITDSDJVOGLGSRDRELLAEVSGSPPLAARAYFWGQSSTOAOQHRSRSHSKISXMTWP	2082		
QY	1021	ALVSLGHPHSLRSLLEPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA	1080	Db	2018	AAITDSDJVOGLGSRDRELLAEVSGSPPLAARAYFWGQSSTOAOQHRSRSHSKISXMTWP	2077		
Db	1021	ALVSLGHPHSLRSLLEPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA	1080	QY	2083	PAPCPGPENNKGPPEPTRSLELDTLSWISGDLPPFGQGEPPSPDLKKCKSVFAQS	2142		

Db 2078 PAPCPGPNWCKGPETRSSLELDTLWISGDLPLPGQGEPPSPRDLKKCYSEVAQS 2137
 QY 2143 CORRTSWLDEQRHSHIAVSCLDGSGQPHLGTDPNSLGGQPLGGGSRPKKXLSPESTIT 2202
 Db 2138 CORRTSWLDEQRHSHIAVSCLDGSGQPHLGTDPNSLGGQPLGGGSRPKKXLSPESTIT 2197
 QY 2203 DPESQGRTPSPGICLRRAPSSDSKDFLASGPPDSMAASPSPKKDVLSLGSDDPA 2262
 Db 2198 DPESQGRTPSPGICLRRAPSSDSKDFLASGPPDSMAASPSPKKDVLSLGSDDPA 2257
 QY 2263 DLDP 2266
 Db 2258 DLDP 2261

RESULT 6
 ID AAY14588
 AC AAY14588
 XX
 DT 07-DEC-1999 (first entry)
 DE Human T-type voltage-gated Ca channel alpha-1-G (hCav1.1c).
 KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
 KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
 OS Homo sapiens.
 XX
 XX W09929847-A1.
 FN 17-JUN-1999.
 PD 30-OCT-1998; 98WO-US023161.
 PF 05-DEC-1997; 97US-00985809.
 PR (LOYO) UNIV LOYOLA CHICAGO.
 PA Perez-Reyes E, Cribbs LL;
 PI WPI; 1999-394972/33.
 DR N-PSDB; AAX83483.
 XX
 PT New T-type voltage-gated calcium channels.
 PS Disclosure; Page 49-58; 138pp; English.
 XX
 CC This sequence represents a human T-type voltage-gated calcium (Ca)
 CC channel alpha-1-G designated hCav1.1c. Voltage gated channels are membrane
 CC bound glycosylated proteins formed of several subunits. The large alpha
 CC subunits form a pore in the membrane that is selective for a given ionic
 CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
 CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
 CC -type Ca channels are activated at a lower voltage than L- or N-type
 CC channels. Characteristics of T-type channels include short current time,
 CC slow activation kinetics near threshold, fast inactivation kinetics and
 CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
 CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
 CC channels contains a putative IVS4 region comprising the amino acid
 CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
 CC channel proteins can be used to screen for drugs which affect calcium
 CC channels. Methods are also disclosed for treating a disease or disorder
 CC associated with a deficiency in a native T-type calcium channel nucleic
 CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
 XX
 SQ Sequence 2268 AA;

Query Match 98.5%; Score 11727; DB 2; Length 2268;
 Best Local Similarity 97.8%; Pred. No. 0;
 Matches 2240; Conservative 1; Mismatches 2; Indels 48; Gaps 2;

QY 1 MDEEDGAGAESGQPSRSMRLNDLSGAGRPGPSAEKDPGSADSEAGLPYPALAPVV 60
 Db 1 MDEEDGAGAESGQPSRSMRLNDLSGAGRPGPSAEKDPGSADSEAGLPYPALAPVV 60
 QY 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLLGMFRPCEDICDSQRCRILOAF 120
 Db 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLLGMFRPCEDICDSQRCRILOAF 120
 QY 121 DDFIFAFPAFVAVMVKWVALGIFGKCYLGDWTNRDLDDFFVIAGMLEYSLDLQNVFSAYR 180
 Db 121 DDFIFAFPAFVAVMVKWVALGIFGKCYLGDWTNRDLDDFFVIAGMLEYSLDLQNVFSAYR 180
 QY 181 TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFIFGIVGVQWAGLLRNR 240
 Db 181 TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFIFGIVGVQWAGLLRNR 240
 QY 241 CFLPENFSLPLSVLDLERYQTENEDESPFICSPRENGMRCRSVPTLRGDDGGGPPCGL 300
 Db 241 CFLPENFSLPLSVLDLERYQTENEDESPFICSPRENGMRCRSVPTLRGDDGGGPPCGL 300
 QY 301 DYEAYNSSNTTCVNNWQYITNC SAGEHNPFKGAIFNFIQVITLEGWVDM 360
 Db 301 DYEAYNSSNTTCVNNWQYITNC SAGEHNPFKGAIFNFIQVITLEGWVDM 360
 QY 361 YFVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
 Db 361 YFVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
 QY 421 STLASFSEPGSCYBELLYLVIILKKAARLAQVSRAGVGVGLSSPAPVGGGQETQSS 480
 Db 421 STLASFSEPGSCYBELLYLVIILKKAARLAQVSRAGVGVGLSSPAPVGGGQETQSS 480
 QY 481 SCSRSRRRLSVHLLVHHHHHHHHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
 Db 481 SCSRSRRRLSVHLLVHHHHHHHHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
 QY 541 ALSGAPPGGAESVHSFYHADCHLEPVTCQAPPRSPSEAGRTVGSQKVPTVHTSPPE 600
 Db 541 ALSGAPPGGAESVHSFYHADCHLEPVTCQAPPRSPSEAGRTVGSQKVPTVHTSPPE 600
 QY 601 TLKEKALVEVAASGPPPTLSLNIIPGPYSSMHKLLTQSTGACOSSCKLSSPCLKADSG 660
 Db 601 TLKEKALVEVAASGPPPTLSLNIIPGPYSSMHKLLTQSTGACOSSCKLSSPCLKADSG 660
 QY 661 ACPDSCPYCARAGAGEVELADREMPDSDSEAVYFTQDAHQHSDLRDPHSRRORS LGPDA 720
 Db 661 ACPDSCPYCARAGAGEVELADREMPDSDSEAVYFTQDAHQHSDLRDPHSRRORS LGPDA 720
 QY 721 EPSSVLAFWRLICDTRFKIVDSKYFGRGIMIALVNTLSMGIBYHQPELTNVALEISNI 780
 Db 721 EPSSVLAFWRLICDTRFKIVDSKYFGRGIMIALVNTLSMGIBYHQPELTNVALEISNI 780
 QY 781 VFTSLFALEMLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMR 840
 Db 781 VFTSLFALEMLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMR 840
 QY 841 VLKLVFLPALQQLVLMKTMNDNVATFCMLLMFIFISILGMHLFGCKFASERDGLTL 900
 Db 841 VLKLVFLPALQQLVLMKTMNDNVATFCMLLMFIFISILGMHLFGCKFASERDGLTL 900
 QY 901 PORKNFDLSLLMAIVTVFQILTOEDNKNVLYNGMASTSSWAALYFIALMTFGNYVFNLLV 960
 Db 901 PORKNFDLSLLMAIVTVFQILTOEDNKNVLYNGMASTSSWAALYFIALMTFGNYVFNLLV 960
 QY 961 AILVGEFQAEIISKREDASGQLSQLPVDQSOGGANKSESPDFPSLDGDKGKKCL 1020
 Db 961 AILVGEFQAEIISKREDASGQLSQLPVDQSOGGANKSESPDFPSLDGDKGKKCL 997
 QY 1021 ALVSTGEHPPELRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRSSSGSAPGAA 1080
 Db 998 ALVSTGEHPPELRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRSSSGSAPGAA 1057
 QY 1081 HEMKSPPSARSSPHSPWAAASWTSRRSRNSLGRAPSLKRRSPGERRSLLSGEGQESQ 1140

Db	1058	HEMKSPPSARSSPSPWASASMTSRSSRSNLGRAPSLKRRSPGRRSLLSGEQBSQ	1117	Db	2138	YSVEAQSCORRPTSWLDEQRHSTAVSCLDSGSGPHLGTDFSNLGGQPLGGPGRPKKL	2197
Qy	1141	DEESSSEERASPGSDHRRHGSLEAKSFDLPDITLQVPLHRTASGRGASAEHQDN	1200	Qy	2196	SPPSITIDPESQGRTPPPGICLRRRAPSSDSKDLASGPPDSMAASPPKDVLSLS	2255
Db	1118	DEESSSEERASPGSDHRRHGSLEAKSFDLPDITLQVPLHRTASGRGASAEHQDN	1177	Db	2198	SPPSITIDPESQGRTPPPGICLRRRAPSSDSKDLASGPPDSMAASPPKDVLSLS	2257
Qy	1201	GKSASGRILARALRPPDPLDGDADDGCLNLSKGRVRAIRARLPACVLERDSWSAYIFP	1260	Qy	2256	GLSSDDPADLDP	2266
Db	1178	GKSASGRILARALRPPDPLDGDADDGCLNLSKGRVRAIRARLPACVLERDSWSAYIFP	1237	Db	2258	GLSSDDPADLDP	2268
Qy	1261	QPSRFLLCRIITHKMDHVLVITFLNCITIAMERKIDPHSAERIFLTLNVIPTAV	1320	RESULT 7			
Db	1238	QPSRFLLCRIITHKMDHVLVITFLNCITIAMERKIDPHSAERIFLTLNVIPTAV	1297	ID	AAB66481	standard; protein; 2266 AA.	
Qy	1321	FLAEMTVKVALGWCFGEQAYLRSSNVDLGLLVISVIDILVMSVSDGTKILGMLRVL	1380	XX	AAB66481;		
Db	1298	FLAEMTVKVALGWCFGEQAYLRSSNVDLGLLVISVIDILVMSVSDGTKILGMLRVL	1357	XX	09-APR-2001	(first entry)	
Qy	1381	RLRLTLRLVISAQGLKLVVETIMSSLKPTGNIVVICCAPIIFGILGVOLFPGKFPV	1440	XX	Human alpha-IG T-type calcium channel protein.		
Db	1358	RLRLTLRLVISAQGLKLVVETIMSSLKPTGNIVVICCAPIIFGILGVOLFPGKFPV	1417	XX	Human; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic;		
Qy	1441	COGEDTRNITKSDCAEASRVRKYNFDNLGOALMSLFLVASKDGVDMYDGLDVG	1500	KW	T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;		
Db	1418	COGEDTRNITKSDCAEASRVRKYNFDNLGOALMSLFLVASKDGVDMYDGLDVG	1477	KW	hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel.		
Qy	1501	VQOQPMHNPWMLLYFTSLFVIAFFVLNMFVGVVFNHRCRQHQEERARREKRL	1560	XX	Homo sapiens.		
Db	1478	VQOQPMHNPWMLLYFTSLFVIAFFVLNMFVGVVFNHRCRQHQEERARREKRL	1537	XX	WO200102561-A2.		
Qy	1561	RRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYL	1595	XX	11-JAN-2001.		
Db	1538	RRLEKKRRSKEKOMADMLDDLVIASGSSASAAEQCKPYSDYSRFRLLVHHLCTSHYL	1597	XX	04-JUL-2000; 2000WO-CA0000794.		
Qy	1596	DLFITGVIGLVNVTWAMEHYQOQILDEALKICNYITFTVFLVESFKLVAFGRFRFFQD	1655	XX	02-JUL-1999; 99US-00346794.		
Db	1598	DLFITGVIGLVNVTWAMEHYQOQILDEALKICNYITFTVFLVESFKLVAFGRFRFFQD	1657	XX	(NEUR-) NEUROMED TECHNOLOGIES INC.		
Qy	1656	RNQLDLAIVLLSINGITLLEEIEVNASLPINPTIIRIMRVLRARVLKLLKMAVGMRL	1715	XX	Snutch TP, Baillie DL;		
Db	1658	RNQLDLAIVLLSINGITLLEEIEVNASLPINPTIIRIMRVLRARVLKLLKMAVGMRL	1717	XX	WPI; 2001-123111/13.		
Qy	1716	DTVMQALPQVNLGLLFLMLFFITPAALGVFLPGDLECDETHPCCEGLGRHATFNFQAF	1775	XX	N-PSDB; AAF31684.		
Db	1718	DTVMQALPQVNLGLLFLMLFFITPAALGVFLPGDLECDETHPCCEGLGRHATFNFQAF	1777	XX	Novel T-type calcium channel alpha-1 subunit gene useful for treating		
Qy	1776	TLFRVSTGDNWNGIMKDTLDCDOESTCYNTVISPITYFVSFVLTAQFVLVNVVIAVLKMH	1835	XX	cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and		
Db	1778	TLFRVSTGDNWNGIMKDTLDCDOESTCYNTVISPITYFVSFVLTAQFVLVNVVIAVLKMH	1837	XX	epilepsy.		
Qy	1836	LEESNKEAEEAELEEMKTLSPQHPSPGLSGPFLMPGVGPDSPDGPALHPAA	1895	XX	Example 3; Fig 6; 103pp; English.		
Db	1838	LEESNKEAEEAELEEMKTLSPQHPSPGLSGPFLMPGVGPDSPDGPALHPAA	1897	XX	The present sequence is given in a specification providing sequences and		
Qy	1896	HARSASHFSLEHPTMQPHTELPGDILLTVRKSVSRTHSLPNDVSNWCRGSAEGLPHG	1955	XX	partial sequences for three types of mammalian (human and rat) T-type		
Db	1898	HARSASHFSLEHPTMQPHTELPGDILLTVRKSVSRTHSLPNDVSNWCRGSAEGLPHG	1957	XX	calcium channel subunits. An expression cassette has been generated which		
Qy	1956	RGWGLPKAQSGSVLSVHSQADTSYIQLPKDAPHLQPHSAPTWGITPKLPFGPSPLA	2015	XX	comprises a nucleotide sequence encoding a T-type calcium channel alpha_1		
Db	1958	RGWGLPKAQSGSVLSVHSQADTSYIQLPKDAPHLQPHSAPTWGITPKLPFGPSPLA	2017	XX	subunit operably linked to control sequences to effect its expression.		
Qy	2016	QRPLRQAAIRTDLSVQGLSREDLLAEVSGSPPLARAYSFVWGQSTQAOQHSRSHK	2075	XX	The novel calcium channel nucleic acids and proteins are useful for		
Db	2018	QRPLRQAAIRTDLSVQGLSREDLLAEVSGSPPLARAYSFVWGQSTQAOQHSRSHK	2077	XX	treating conditions characterised by undesirable levels of T-type calcium		
Qy	2076	ISKHMTTAPCPGEPNWKGPBTRSLDTELMTSGDLLPPGGQEEPPSPDLKKC	2135	XX	channel activity such as cardiac hypertrophy, cardiac arrhythmia,		
Db	2078	ISKHMTTAPCPGEPNWKGPBTRSLDTELMTSGDLLPPGGQEEPPSPDLKKC	2137	XX	hypertension, sleep disorder and epilepsy		
Qy	2136	YSVEAQSCORRPTSWLDEQRHSTAVSCLDSGSGPHLGTDFSNLGGQPLGGPGRPKKL	2195	XX	Sequence 2266 AA;		
				XX	Query Match	97.9%;	Score 11653; DB 4; Length 2266;
				XX	Best Local Similarity	98.8%;	Pred. No. 0;
				XX	Matches 2239; Conservative	7;	Mismatches 20; Indels 0; Gaps 0;
Qy	1	MDEEDGAGAEESQPSRFMLNDLSCAGGRPGSGAEKDPGSAESAEGLPYPALAPV	60	Qy	1	MDEEDGAGAEESQPSRFMLNDLSCAGGRPGSGAEKDPGSAESAEGLPYPALAPV	60
Db	1	MDEEDGAGAEESQPSRFMLNDLSCAGGRPGSGAEKDPGSAESAEGLPYPALAPV	60	Db	61	FFYLSQDSRPSRWCILRTVCPNWPFERISMLVILLNCVILGMRPCEDTACDSQRCLIQAF	120
Qy	61	FFYLSQDSRPSRWCILRTVCPNWPFERISMLVILLNCVILGMRPCEDTACDSQRCLIQAF	120	Qy	61	FFYLSQDSRPSRWCILRTVCPNWPFERISMLVILLNCVILGMRPCEDTACDSQRCLIQAF	120
Db	61	FFYLSQDSRPSRWCILRTVCPNWPFERISMLVILLNCVILGMRPCEDTACDSQRCLIQAF	120	Db	121	DDFIFAFVAVMVVNVVALGIFGKCYLGDITWNRDLDFPIVIAVGLMLEYSLDLQNVFSFAVR	180

121 DDFIAFAFVAVMVKNVALGIFGKCYLGTDTNNRLDFFVIAGMLEYSLDLQNVSPSAVR 180
181 TVRVLRLRAINRPSMRILVLLDLDLPMGNVLLCCFFVFFIIGVIGVOLWAGLLNR 240
181 TVRVLRLRAINRPSMRILVLLDLDLPMGNVLLCCFFVFFIIGVIGVOLWAGLLNR 240
241 CFLPENFSLPLSDVLERYYOTNEDESPFICQPRENGMRSCRSVPTLRGDGGGPPCGL 300
241 CFLPENFSLPLSDVLERYYOTNEDESPFICQPRENGMRSCRSVPTLRGDGGGPPCGL 300
301 DYEAVNSSNTTCVNNQYITNCSEHNPFGAINFDNIGYAWIAIQQVITLEGWVDIM 360
301 DYEAVNSSKTCVNNQYITNCSEHNPFGAINFDNIGYAWIAIQQVITLEGWVDIM 360
361 YFVMDAHFYNFIYFILAIIVGSPFMINCLVVIATQFSETKORESOLMREORVFLSNA 420
361 YFVMDAHFYNFIYFILAIIVGSPFMINCLVVIATQFSETKORESOLMREORVFLSNA 420
421 STLASFSPGSCYEBLLKYLVIILKAARRLAQVSRAAGVRGLLSPAPLGGOETOPSS 480
421 STLASFSPGSCYEBLLKYLVIILKAARRLAQVSRAAGVRGLLSPAPLGGOETOPSS 480
481 SCSRSRRLSVHLLVHHHHHHVHLGNGTLRAPRSPETQDRDANGSRRLMLPPSPTP 540
481 SCSRSRRLSVHLLVHHHHHHVHLGNGTLRAPRSPETQDRDANGSRRLMLPPSPTP 540
541 ALSGAPPGAESVHSFYHADCHLBPVRQOAPPPSPSEASGRTVSGKVYPTVNTSPPE 600
541 ALSGAPPGAESVHSFYHADCHLBPVRQOAPPPSPSEASGRTVSGKVYPTVNTSPPE 600
601 TLKEKALVEVAASGPPTLTSLNIPPGYSSMHKLETQSTGACQSSCKISSPCLKADSG 660
601 TLKERALVEVAASGPPTLTSLNIPPGYSSMHKLETQSTGACQSSCKISSPCLKADSG 660
661 ACGPDCPCYCARAGAVEADREMPDSDEAVYFTQDAQHSDLRDPHRSRQSLGPD 720
661 ACGPDCPCYCARAGAVEADREMPDSDEAVYFTQDAQHSDLRDPHRSRQSLGPD 720
721 EPSVLAFWRLICDTFRKIVDSKVFYRGIMAILVNTLSMGIEVHEQPEELTNALEISNI 780
721 EPSVLAFWRLICDTFRKIVDSKVFYRGIMAILVNTLSMGIEVHEQPEELTNALEISNI 780
781 VFTSLFALEMLKLLVYGPFGYIKNPYINFDGVIWISVWEIVGQGGGLSVLRTFLMR 840
781 VFTSLFALEMLKLLVYGPFGYIKNPYINFDGVIWISVWEIVGQGGGLSVLRTFLMR 840
841 VLKLVRLPALQQLVLMKTMONVATFCMLMLFIPIFISILGMHLPGCKFASERDGDTL 900
841 VLKLVRLPALQQLVLMKTMONVATFCMLMLFIPIFISILGMHLPGCKFASERDGDTL 900
901 PDRKNFDSLWAIWTVFQIILTQEDWKNKLYNGMASTSSMAALYFIALMTFGNVVLENLLV 960
901 PDRKNFDSLWAIWTVFQIILTQEDWKNKLYNGMASTSSMAALYFIALMTFGNVVLENLLV 960
961 ALIVEGFOABEISKREDAQSLSICILPVDQSGDANKSESEDFSPSIDGDGRKKCL 1020
961 ALIVEGFOABEISKREDAQSLSICILPVDQSGDANKSESEDFSPSIDGDGRKKCL 1020
1021 ALVSLGEHPELRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRSTSSGSAEPGAA 1080
1021 ALVSLGEHPELRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRSTSSGSAEPGAA 1080
1081 HEMKSPSARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPGERSLLSGEQESQ 1140
1081 HEMKSPSARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPGERSLLSGEQESQ 1140
1141 DEESESSEERAPAGSDHRRHROSLERAKSSFDLPDLTQVPLGHRHTASGRGSAEHQDCN 1200
1141 DEESESSEERAPAGSDHRRHROSLERAKSSFDLPDLTQVPLGHRHTASGRGSAEHQDCN 1200
1201 GKSASRLARALRPDDPLDGDADDDEGNLSKGERVRAMIRALPACYLERDSWSAYIFP 1260

1201 GKSASRLARALRPDDPLDGDADDDEGNLSKGERVRAMIRALPACYLERDSWSAYIFP 1260
1261 POSRFRLLCHRIITHKMFHDVHVLVIIIFLNCITIAMERPKIDPHSAERIFELTISNYIFTAV 1320
1261 POSRFRLLCHRIITHKMFHDVHVLVIIIFLNCITIAMERPKIDPHSAERIFELTISNYIFTAV 1320
1321 FLAEMTVKVALGWCFCGQAYLRSSNVLDGLLVLSIVDILVSMVSDSGTKILGMLRVL 1380
1321 FLAEMTVKVALGWCFCGQAYLRSSNVLDGLLVLSIVDILVSMVSDSGTKILGMLRVL 1380
1381 RLLRLRLPLRISRAQGLKLVVETLMSSIKPTIGNIWIWICCAFFIIFGILGVOLFPGKFPV 1440
1381 RLLRLRLPLRISRAQGLKLVVETLMSSIKPTIGNIWIWICCAFFIIFGILGVOLFPGKFPV 1440
1441 COGEDTRNITNKSDCAEASRVRHRYKYNFDNLGQALMSLFLVASKDGMVDIMYDGLDVG 1500
1441 COGEDTRNITNKSDCAEASRVRHRYKYNFDNLGQALMSLFLVASKDGMVDIMYDGLDVG 1500
1501 VDQOPIMNHNPMMLLYFISFLIIVAFVILNMFVGVVNFHFKROHQBEERAREEKL 1560
1501 VDQOPIMNHNPMMLLYFISFLIIVAFVILNMFVGVVNFHFKROHQBEERAREEKL 1560
1561 RRLEKRRKAKCKPYSDYSRFRLLVHHLCTSHVLDLFIITGVIGLVVTVMAHEHYQOQOI 1620
1561 RRLEKRRKAKCKPYSDYSRFRLLVHHLCTSHVLDLFIITGVIGLVVTVMAHEHYQOQOI 1620
1621 LDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRNQLDLAIVLLSIMGITILEEIEVN 1680
1621 LDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRNQLDLAIVLLSIMGITILEEIEVN 1680
1681 ASLPINPTIIRIMRVARIVLKLKMAVGRALLDTVMQALPOVGNLGLLMLFFIFA 1740
1681 ASLPINPTIIRIMRVARIVLKLKMAVGRALLDTVMQALPOVGNLGLLMLFFIFA 1740
1741 ALGVLEFGDLECEBTHPCBGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMKOTLRDCCOE 1800
1741 ALGVLEFGDLECEBTHPCBGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMKOTLRDCCOE 1800
1801 STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLAKHLEESNEKEAEAELELEMKTL 1860
1801 STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLAKHLEESNEKEAEAELELEMKTL 1860
1861 SPOPHSPGSPFLWPGVEGSDSPKPGALHAAHARSASHFSLEHPTMQPHTELPGP 1920
1861 SPOPHSPGSPFLWPGVEGSDSPKPGALHAAHARSASHFSLEHPTMQPHTELPGP 1920
1921 DLTIVRKSGVSRTHSLPNDSYMCRCRSTAGPLGRGWGLPKAQSGLSVLSVHSQPADTSY 1980
1921 DLTIVRKSGVSRTHSLPNDSYMCRCRSTAGPLGRGWGLPKAQSGLSVLSVHSQPADTSY 1980
1981 ILQLPKADPHLQPHSAPTWTGTIPKLPGRSPLAQRLRRQAAIRTDLSLDVOGLGSRED 2040
1981 ILQLPKADPHLQPHSAPTWTGTIPKLPGRSPLAQRLRRQAAIRTDLSLDVOGLGSRED 2040
2041 LLAEVSGSPPLARAYSFVWGQSTQAOQHSRSHSKISKHMTTPAPCPGPEPMKGKPPET 2100
2041 LLAEVSGSPPLARAYSFVWGQSTQAOQHSRSHSKISKHMTTPAPCPGPEPMKGKPPET 2100
2101 RSSLELDTLSWITSGDLLPPGGOEBPPSPRDLKKCVSEAOQCORRPTSWLDEORHSTA 2160
2101 RSSLELDTLSWITSGDLLPPGGOEBPPSPRDLKKCVSEAOQCORRPTSWLDEORHSTA 2160
2161 VSCLSGSGPHLGTDPFNLGGQPLGGQSRPKKLSPPSITIDPPESQGPRTPPSPGICL 2220
2161 VSCLSGSGPHLGTDPFNLGGQPLGGQSRPKKLSPPSITIDPPESQGPRTPPSPGICL 2220
2221 RERAPSSDKDPLASGPPDMSMAASPSPKDVLSLGLSSDPAADLP 2266
2221 RERAPSSDKDPLASGPPDMSMAASPSPKDVLSLGLSSDPAADLP 2266

CC channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid sequence to treat cardiomyopathy, epilepsy, etc

AA	Sequence 2247 AA;	Query Match Best Local Similarity Matches 2108; Conservative	92.1%; 92.8%; 33;	Score 10962.5; Pred. No. 0; Mismatches 101;	DB 2; Indels 29; Gaps 5;	Length 2247;
QY	1	MDDEEDGAGAESGGQPRSRFWRLNDLSAGGRPGPSAEKDPGSADEAGELFPYALAPV	60			
DB	1	MDDEEDGAGAESGGQPRSTQNLDSAGAGROGPSTKDPGSADEAGELFPYALAPV	60			
QY	61	FFYLSQDSRPRSCLRTVCNPNWPERISMLVILNCVTILGMFRPCEDIACDSORCILQAF	120			
DB	61	FFYLSQDSRPRSCLRTVCNPNWPERVSMVLILNCVTILGMFRPCEDIACDSORCILQAF	120			
QY	121	DDIFAFPAFVEMVVKVVALGIFGKKCYLGDWNRLDFFVIAGMLEYSLDLQNVSFSAVR	180			
DB	121	DDFIFAFPAFVEMVVKVVALGIFGKKCYLGDWNRLDFFVIAGMLEYSLDLQNVSESAVR	180			
QY	181	TVRVLRPLRAINVPMSRIILVTLLDTPMLGNVLLCFVFFIFGIVGVQVWAGLLRNR	240			
DB	181	TVRVLRPLRAINVPMSRIILVTLLDTPMLGNVLLCFVFFIFGIVGVQVWAGLLRNR	240			
QY	241	CFLPENFSLPSVDLERYOTENEDSDPFTCSOPRENGMRSCHSVTLACDGGGGPPCGI	300			
DB	241	CFLPENFSLPSVDLEPYOTENEDSDPFTCSOPRENGMRSCHSVTLRGGGGGGPPCSL	300			
QY	301	DYEAYNSSNTTCVNNQYVYTNCSAGBNPFGKAINFDNIKYAWIAIFQVITILEGWVDM	360			
DB	301	DYETYNSSNTTCVNNQYVYTNCSAGBNPFGKAINFDNIKYAWIAIFQVITILEGWVDM	360			
QY	361	YFVMDASFYNYFIILLIIVGSFFMINCLVVIATQFSETKQRESOLMEQRVRFLSNA	420			
DB	361	YFVMDASHFYNYFIILLIIVGSFFMINCLVVIATQFSETKQRESQMEQRVRFLSNA	420			
QY	421	STLASFSBPGSCYBELLYLWILRKAARLQAQVSRAGVRVGLSSPAPLGQEQTPSS	480			
DB	421	STLASFSBPGSCYBELLYLWILRKAARLQAQVSRAGVRLSSPAPVARSQEQPOPSG	480			
QY	481	SCSRSHRLSVHHLVHHHHHHHHVHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP	540			
DB	481	SCTRSHRLSVHHLVHHHHHHHHVHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTP	540			
QY	541	ALSGAPPGAGBSVHSFYHADCHLEBPVRQADPPRSPSEASGRTVGSGKVPVTHSTPPE	600			
DB	541	TPSGGPPRAGBSVHSFYHADCHLEBPVRQADPPRCPSEASGRTVGSGKVPVTHSTPPE	600			
QY	601	TLKEKALVEVAASGPPPLTTSINTPPGVPSMHKLIETQSTGACOSSCKSSPLCADSG	660			
DB	601	ILKDKALVEVAPSGPPPLTTSFNTPPGFSSMHKLIETQSTGACHSSCKLSSPCKADSG	660			
QY	661	ACGPDSPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRORSIGPD	719			
DB	661	ACGPDSPCYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRORSIGPD	720			
QY	720	AEPSVLAFAWRLICDTRFKIVDSKYFVGIMITAILVNTLSMGIEYHEQPEELTNALEISN	779			
DB	721	AEPSVLAFAWRLICDTRFKIVDSKYFVGIMITAILVNTLSMGIEYHEQPEELTNALEISN	780			
QY	780	IVFTSLFALEMLLKLLVYGPQYIKNPYNIPOGVIWISVWELIVGQQGGSLSVLRTFLRM	839			
DB	781	IVFTSLFALEMLLKLLVYGPQYIKNPYNIPOGVIWISVWELIVGQQGGSLSVLRTFLRM	840			
QY	840	RVLKLVREFTPALORQLVWLKMTMDNVATFCMLLMFLIFITPSILGMHLPGCKFASRDGDT	899			
DB	841	RVLLKLVREFTPALORQLVWLKMTMDNVATFCMLLMFLIFITPSILGMHLPGCKFASRDGDT	900			
QY	900	LPDRKPDFSLLWALIVTVFQILIQEDANKVLYNGMASTSSWAALYFIALMTFCNGYVLENLL	959			
DB	901	LPDRKPDFSLLWALIVTVFQILIQEDANKVLYNGMASTSSWAALYFIALMTFCNGYVLENLL	960			

QY	1080	A-HEMKSPPARSPHSPWASASWTGRRSRNSLGRAPSLKRRSPGERRSLLSGEGOE	1138
Db	1058	AHHEMKCPSARSPHSPWASASWTGRRSRNSLGRAPSLKRRSPGERRSLLSGEGOE	1117
QY	1139	SQDEEESSEERASPDGHRHRSLEAREAKSSFDLPTQVPGIHRHTASGRGASAEHOD	1198
Db	1118	SQDEEESSEERASPDGHRHRSLEAREAKSSFDLPTQVPGIHRHTASGRGASAEHOD	1177
QY	1199	CNGKSASGLARALPDDPPDGDGDDADDEGNLSKGERVRAIRARLPACYLERSWSAYI	1258
Db	1178	CNGKSASGLARALPDDPPDGDGDDADDEGNLSKGERIQAWVRSELPAACREEDSWSAYI	1237
QY	1259	FPQSRFRLLCHRIITHKMFDEHVLVLIIFLNCITITAMERPKIDPHSAERIFLTLNFIET	1318
Db	1238	FPQSRFRLLCHRIITHKMFDEHVLVLIIFLNCITITAMERPKIDPHSAERIFLTLNFIET	1297
QY	1319	AVFLAEMTKVVALGWCFCGEQAYLRSSWNVDGLLVLISVIDILYSMVSDSGTKILGMLR	1378
Db	1298	AVFLAEMTKVVALGWCFCGEQAYLRSSWNVDGLLVLISVIDILYSMVSDSGTKILGMLR	1357
QY	1379	VLRLRLTLRLPLRVISRAOGLKLWETLMSLSLPIGNIVVICCAFFIIFGILGVQLFKGF	1438
Db	1358	VURLRLTLRLPLRVISRAOGLKLWETLMSLSLPIGNIVVICCAFFIIFGILGVQLFKGF	1417
QY	1439	FVCOGEDTRNITKSDCAEASVVRVHKYNFNDLGOALMSLFLVASKDGMVIMYDGLDA	1498
Db	1418	FVCOGEDTRNITKSDCAEASVVRVHKYNFNDLGOALMSLFLVASKDGMVIMYDGLDA	1477
QY	1499	VGVDQOPINHNPMWLLYFISFLLIVAFVFLNMFVGVVVENPHKCHQHOEEERREBK	1558
Db	1478	VGVDQOPINHNPMWLLYFISFLLIVAFVFLNMFVGVVVENPHKCHQHOEEERREBK	1537
QY	1559	RLRLLEKKRR-----KAQCKEYYSYDYSRFRLLVHHLCTSHYLDLFTIGVIGLVVVTWA	1611
Db	1538	RLRLLEKKRRSKKQWAEQAQCKEYYSYDYSRFRLLVHHLCTSHYLDLFTIGVIGLVVVTWA	1597
QY	1612	MEHYQOQILDEALKICNYITFTVIFVLESVFKLVAFGRFRFFODRNQOLDLAVLSIMG	1671
Db	1598	MEHYQOQILDEALKICNYITFTVIFVLESVFKLVAFGRFRFFODRNQOLDLAVLSIMG	1657
QY	1672	ITLEETEVNASLPINPITIRIMVLRIARVLKLLKMAVGMRALDITVMOALPOVENIGLL	1731
Db	1658	ITLEETEVNASLPINPITIRIMVLRIARVLKLLKMAVGMRALDITVMOALPOVENIGLL	1717
QY	1732	FMLFFTFIIFALGVLFGLDCEDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK	1791
Db	1718	FMLFFTFIIFALGVLFGLDCEDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK	1777
QY	1792	DTLRDCQDETCYNTVISPFIYFVSFVLTAQFVLNVVVIAMKHLSESNKEAELEA	1851
Db	1778	DTLRDCQDETCYNTVISPFIYFVSFVLTAQFVLNVVVIAMKHLSESNKEAELEA	1837
QY	1852	ELEEMKTLSPQHPSPGSPPLWPGVGPDPSPKPGALHPAAHARSASHFSLEHPTMQ	1911
Db	1838	ELEEMKTLSPQHPSPGSPPLWPGVGPDPSPKPGALHPAAHARSASHFSLEHPTMQ	1897
QY	1912	PHPTPLP---GPDILLTVRKSGVSRTHSLPNDYSYMCRCRHSATAGPLGHRGWGLPKAQSGSV	1968
Db	1898	PHPREVPVPLGPDILLTVRKSGVSRTHSLPNDYSYMCRCRHSATAGPLGHRGWGLPKAQSGSV	1957
QY	1969	LSVHSQADTSTYIQLPKDAPELLLOPHSAPTWTGTPKLPBGRSPLAORPLRROAAIRTD	2028
Db	1958	LSVHSQADTSTYIQLPKDAPELLLOPHSAPTWTGTPKLPBGRSPLAORPLRROAAIRTD	2017
QY	2029	SIDVQGLSREDLLAEVSGPSPPLARAYSFWGQSSTQAOQHSRSHSKISKMTTPPAPCPG	2089
Db	2018	SIDVQGLSREDLLAEVSGPSPPLARAYSFWGQSSTQAOQHSRSHSKISKMTTPPAPCPG	2077
QY	2089	PEPNMGKPPETRSLELDELTELTSWISGDLPLPGGQEEPPSPDLKKCYSVQAQSCORPT	2148
Db	2078	LEPSWAKDPPETRSLELDELTELTSWISGDLPLPGGQEEPPSPDLKKCYSVQAQSCORPT	2136
QY	2149	SWLDEQRHRSIAVSCLSGSGSPHGLTDPNSLGGQPLGGPSPRKKLSPPSITIDPESQ	2208
Db	2137	FWLDEQRHRSIAVSCLSGSGSPHGLTDPNSLGGQPLGGPSPRKKLSPPSITIDPESQ	2196
QY	2209	GPRTPPGICLRRRAPSDDSKOPLAGPPDMSAASPSPKKDVLSLSGLSSDDPADLDP	2266
Db	2197	GSRPPCPGVCLRRRAPASDSKDPVSFPLDSTAASPSPKKDVLSLSGLSSDDPADLDP	2254

RESULT 11

AAV14591	AAV14591 standard; protein; 2265 AA.
XX	AAV14591;
AC	AAV14591;
DT	07-DEC-1999 (first entry)
XX	Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1b).
DE	Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW	activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX	Rattus sp.
OS	W09929847-A1.
XX	17-JUN-1999.
PD	30-OCT-1998; 98WO-US023161.
XX	05-DEC-1997; 97US-00985809.
PR	(LOYO) UNIV LOYOLA CHICAGO.
XX	Perez-Reyes E, Cribbs L;
PI	WPI; 1999-394972/33.
XX	N-PSDB; AAX83486.
DR	New T-type voltage-gated calcium channels.
XX	Disclosure; Page 76-85; 138pp; English.

This sequence represents a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCavT1b. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca channels contains a putative IVS4 region comprising the amino acid sequence AAV14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

Sequence 2265 AA;

Query Match	91.9%; Score 10939.5; DB 2; Length 2265;
Best Local Similarity	92.0%; Pred. No. 0;
Matches 2107; Conservative	34; Mismatches 101; Indels 47; Gaps 6;
QY	1 MDEEDGACAESGQPSRPFMLNDLSGAGRGPGSAEKDPGSADSEAEGLPYALAPVW 60
Db	1 MDEEDGACAESGQPSRPFMLNDLSGAGRGPGSAEKDPGSADSEAEGLPYALAPVW 60
QY	61 PFYLSQDSRPRSWCLRTVCNPFWRISMVLNLCVTLGMFRPCEDDACDSQRILQAF 120

Db 61 FFVLSQDSRPSRCLRTVCNPFWRVSMVLVILNCVTLMGFRPCEDIACDSQRCLIQAF 120
QY 121 DQIFAFVAVMVVXKVALGIFGKCYKLGDTWNRDLFFIVIAGLMBSYLDLQNVFSAYR 180
Db 121 DQIFAFVAVMVVXKVALGIFGKCYKLGDTWNRDLFFIVIAGLMBSYLDLQNVFSAYR 180
QY 181 TVRVLRPLRAINRPSMRILVILLDTLPMGNVLLLCFFVFFIGIVGVQLWAGLLNR 240
Db 181 TVRVLRPLRAINRPSMRILVILLDTLPMGNVLLLCFFVFFIGIVGVQLWAGLLNR 240
QY 241 CFLPENFSLPLVDLERYOTENEDSPICQPRENGMRSRSPVTLRGDGGGPPCGL 300
Db 241 CFLPENFSLPLVDLERYOTENEDSPICQPRENGMRSRSPVTLRGDGGGPPCGL 300
QY 301 DYEAVNSSTTCVNNQYITNCSSAGEHNPFFKGAINFONIGYAWIAI FQVITLGEWVDIM 360
Db 301 DYEAVNSSTTCVNNQYITNCSSAGEHNPFFKGAINFONIGYAWIAI FQVITLGEWVDIM 360
QY 361 YFVMDAHSFYNFIFILIIIVGSPFMINLCVVIATQFSETKQRESQLMRQVRFLSNA 420
Db 361 YFVMDAHSFYNFIFILIIIVGSPFMINLCVVIATQFSETKQRESQLMRQVRFLSNA 420
QY 421 STLASFSPGSCYBELLYVILKKAARLQAQVSRAAGVGLLSSPAPLGGQBTQSS 480
Db 421 STLASFSPGSCYBELLYVILKKAARLQAQVSRAAGVGLLSSPAPLGGQBTQSS 480
QY 481 SCSSHRRLSVHLLVHHHHHHHHYHNGTTRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db 481 SCSSHRRLSVHLLVHHHHHHHHYHNGTTRAPRASPEIQDRDANGSRRLMLPPSTP 540
QY 541 ALSGAPPGAGSVHSFVHADCHLEPVRQAPPPRSPSEASGRTVSGKVYVHTSPPE 600
Db 541 TPSGGPRGAGSVHSFVHADCHLEPVRQAPPPRSPSEASGRTVSGKVYVHTSPPE 600
QY 601 TLKEALVEVAASGPTLTSLNIPGPGYSMMHKLLETQSGACQSCCKISSPCLKADSG 660
Db 601 ILKDXALVEVAPGPTLTSLNIPGPGYSMMHKLLETQSGACQSCCKISSPCLKADSG 660
QY 661 ACPGDCPYCARAGAVELEADREMPDSDSEAVVEFTQDAQHSDLRDPHS - RQRSLGPD 719
Db 661 ACPGDCPYCARAGAVELEADREMPDSDSEAVVEFTQDAQHSDLRDPHS - RQRSLGPD 719
QY 720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQBEELTNALEISN 779
Db 721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQBEELTNALEISN 779
QY 780 IVFTSLFALEMLKJLVYGFYKPNYINFDGVIVVIVSWEIVGQGGGLSVLRTFRLM 839
Db 781 IVFTSLFALEMLKJLVYGFYKPNYINFDGVIVVIVSWEIVGQGGGLSVLRTFRLM 840
QY 840 RVILKLVRFPLAQRLVLMKMDNVATFCMLLMLEFIFISILGMHLFGCKPASERDGDT 899
Db 841 RVILKLVRFPLAQRLVLMKMDNVATFCMLLMLEFIFISILGMHLFGCKPASERDGDT 900
QY 900 LPDRKNFDSLWAIIVFOILTOEDWNKVLNGMASTSSWAALFYIALMTFGNYVLFNL 959
Db 901 LPDRKNFDSLWAIIVFOILTOEDWNKVLNGMASTSSWAALFYIALMTFGNYVLFNL 960
QY 960 VAILVEGFAEISIKREDASGQLSCIQLPVDGQGDANKSESEPPFSPSLDGDGRKCC 1019
Db 961 VAILVEGFAEISIKREDASGQLSCIQLPVDGQGDANKSESEPPFSPSLDGDGRKCC 997
QY 1020 LALVSLGHEPHEURKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA 1079
Db 998 LALVSLGHEPHEURKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA 1057
QY 1080 A-HEMKSPSPARSSPHSPWASAASWTSSRSRNSILGRAPSLKRRSPSGERRSLLSGEGOE 1138
Db 1058 AHHEMKSPSPARSSPHSPWASAASWTSSRSRNSILGRAPSLKRRSPSGERRSLLSGEGOE 1117
QY 1139 SQDEESSEERASAPAGDHRHRSGLEREAKSSFDLPDTLQVPGHLRTASGRGSAEHQD 1198
Db 1118 SQDEESSEERASAPAGDHRHRSGLEREAKSSFDLPDTLQVPGHLRTASGRGSAEHQD 1177

QY 1199 CNGKSASGLARALRDPDDPLDGDADDDEGNLSKGERVRAWIRARLPACVLYBDSMAYI 1258
Db 1178 CNGKSASGLARALRDPDDPLDGDADDDEGNLSKGERIQAWSRLPACCRERDSMAYI 1237
QY 1259 FPQSRERLLCHRIITHKMFHVILVIFLNCITTIAMERPDKIDPHSAERIFLTLSNYIFT 1318
Db 1238 FPQSRERLLCHRIITHKMFHVILVIFLNCITTIAMERPDKIDPHSAERIFLTLSNYIFT 1297
QY 1319 AVFLAEMTVKVALGWCQGEQAYLRSSNMVLDGLVLVLSVIDILVSMVSDSGTKILGMUR 1378
Db 1298 AVFLAEMTVKVALGWCQGEQAYLRSSNMVLDGLVLVLSVIDILVSMVSDSGTKILGMUR 1357
QY 1379 VLRLRLTRLPURVISAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQJFKGF 1438
Db 1358 VLRLRLTRLPURVISAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQJFKGF 1417
QY 1439 FVCOGEDTRNITNKSDCAEASYRWVRHKYNFDNLQALMSLVLASKDGWVDIMYDGLDA 1498
Db 1418 FVCOGEDTRNITNKSDCAEASYRWVRHKYNFDNLQALMSLVLASKDGWVDIMYDGLDA 1477
QY 1499 VGVDOQPIIMHNHPWMLLYFISFLILVAFVVLNMFVGVVFNPHKCRQHOEBEABRRREK 1558
Db 1478 VGVDOQPIIMHNHPWMLLYFISFLILVAFVVLNMFVGVVFNPHKCRQHOEBEABRRREK 1537
QY 1559 RLRLREKKRR-----KAQCKEYYSYDSRFRLLVHHLCTSHVLDLFT 1600
Db 1538 RLRLREKKRRMLMDDDVIAGSSASAASEAQCKEYYSYDSRFRLLVHHLCTSHVLDLFT 1597
QY 1601 GVILGNVVTWAMEHYQOPOILDEALKICNYIFTVIVLESVFKLVAFGPRFFFOQRNQL 1660
Db 1598 GVILGNVVTWAMEHYQOPOILDEALKICNYIFTVIVLESVFKLVAFGPRFFFOQRNQL 1657
QY 1661 DLAILVLSIMGITLEEVNLSPIINPTIIRIRVLRIRIARVILKLVAVGNRALLDTVMQ 1720
Db 1658 DLAILVLSIMGITLEEVNLSPIINPTIIRIRVLRIRIARVILKLVAVGNRALLDTVMQ 1717
QY 1721 ALPOVGNLGLFLLMFFIFAALGVLEFGDLECEDETHPCGELGRHATFRNFGMAFLTFRV 1780
Db 1718 ALPOVGNLGLFLLMFFIFAALGVLEFGDLECEDETHPCGELGRHATFRNFGMAFLTFRV 1777
QY 1781 STGDNNNGIMKOTLRDCDQESTCINTVISPITYFVSFVLTAQFVLVNVVIAVLMKHLEEN 1840
Db 1778 STGDNNNGIMKOTLRDCDQESTCINTVISPITYFVSFVLTAQFVLVNVVIAVLMKHLEEN 1837
QY 1841 KEAKEBAEAELELEBMKTLSPQHPSPGSPFLWPGVEGDPDSDPKGAPALHAAHARS 1900
Db 1838 KEAKEBAEAELELEBMKTLSPQHPSPGSPFLWPGVEGDPDSDPKGAPALHAAHARS 1897
QY 1901 SHPSLEHPTMQPHPTLP-----GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGLGHRG 1957
Db 1898 SGFSLHPTMVPHPEVPVPLGFDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGLGHRG 1957
QY 1958 WGLPKAQSGLSVHSQPADTSYIILQPKDAPHLLOPHSAPTWTGPTPKLPFPPGRSPLAQ 2017
Db 1958 WGLPKAQSGLSVHSQPADTSYIILQPKDAPHLLOPHSAPTWTGPTPKLPFPPGRSPLAQ 2017
QY 2018 PLRRQAARTDSDVQGLGSRREDLAEVSGSPPLARAYSFWGQSTQAOQHSRSHKITS 2077
Db 2018 PLRRQAARTDSDVQGLGSRREDLAEVSGSPPLARAYSFWGQSTQAOQHSRSHKITS 2077
QY 2078 KHMTPAPCPGPEPNWKGPPETRSSLELDTLSMISGDLPLPGQOEPPSPDRDLKKYCS 2137
Db 2078 KHMTPAPCPGPEPNWKGPPETRSSLELDTLSMISGDLPLPGQOEPPSPDRDLKKYCS 2136
QY 2138 VEAQSCQRRPTSWLDEQRHRSIAVCLDSGQPHLGTDPNLGGQPLGPGSRPKKLSLSP 2197
Db 2137 VEAQSCQRRPTSWLDEQRHRSIAVCLDSGQPHLGTDPNLGGQPLGPGSRPKKLSLSP 2196
QY 2198 PSITIDPESOGPRTPPSGICLRRAPSSDKPLASGPPDPSMAASPCKDVLISGL 2257
Db 2197 PSITIDPESOGPRTPPSGICLRRAPSSDKPLASGPPDPSMAASPCKDVLISGL 2256

QY	2258 SSDPADLDP 2266	Db	121	DDFIFFAFAVMVVMVALGIFGKCYLGDWNRDLDFIIVAGMLEYSLDLQNVFSVR	180
Db	2257 SSDPTMDP 2265	QY	181	TVRLPLRLAINRVPNMRILVTLTLLPMLGNVLLLCFFVPIFIVGVQLWAGLLNR	240
		Db	181	TVRLPLRLAINRVPNMRILVTLTLLPMLGNVLLLCFFVPIFIVGVQLWAGLLNR	240
		QY	241	CFLPENFSLPLSVLDLERYOTENEDSPFCSPQRENGMRCSPVTLRGDGGGPPCGL	300
		Db	241	CFLPENFSLPLSVLDLERYOTENEDSPFCSPQRENGMRCSPVTLRGDGGGPPCGL	300
		QY	301	DYEAYNSSNTTCVNNQYVTCNSAGHNPFGKAINFDNIGYAMIAIFQVITLGGWVIM	360
		Db	301	DYEAYNSSNTTCVNNQYVTCNSAGHNPFGKAINFDNIGYAMIAIFQVITLGGWVIM	360
		QY	361	YFVMDAHSFYNIYFILLIIVGSFFMINCLVVIATOFSETKQRESQMRQVRFLSNA	420
		Db	361	YFVMDAHSFYNIYFILLIIVGSFFMINCLVVIATOFSETKQRESQMRQVRFLSNA	420
		QY	421	STLASFSEPGSCYBELLKYLIVILRKAARRLAQVSRAGVRLSSPAPGGQGTOPSS	480
		Db	421	STLASFSEPGSCYBELLKYLIVILRKAARRLAQVSRAGVRLSSPAPGGQGTOPSS	480
		QY	481	SCSRSRRLSVHLLVHHHHHHHHVHLNGTLPRAPEIQDRDANGSRRLMLPPPTP	540
		Db	481	SCSRSRRLSVHLLVHHHHHHHHVHLNGTLPRAPEIQDRDANGSRRLMLPPPTP	540
		QY	541	ALSGAPPGARSVHSFYHADCHLEPVRQAPPPRSPSEASGRVTVSGKVTVHTSPPE	600
		Db	541	TPSGGPPRGAESVHSFYHADCHLEPVRQAPPPRSPSEASGRVTVSGKVTVHTSPPE	600
		QY	601	TLKEALVREVAASGPPPTLTSNIIPPGYSSMHKLETTQSTCACOSSCKISSPCLKADSG	660
		Db	601	ILKDKALVEVAPSPGPTLTSNIPPGYSSMHKLETTQSTCACOSSCKISSPCLKADSG	660
		QY	661	ACGPDSCPCYCARAGAVEVELADREMPDSDSEAVEFTQDAQHSRLDRPHS-RQBSLGD	719
		Db	661	ACGPDSCPCYCARAGAVEVELADREMPDSDSEAVEFTQDAQHSRLDRPHS-RQBSLGD	720
		QY	720	ABPSSVLAFWRLICDTRKIVDSKYFGRGIMTIALVNTLSMGIEVHEQBELTNALEISN	779
		Db	721	ABPSSVLAFWRLICDTRKIVDSKYFGRGIMTIALVNTLSMGIEVHEQBELTNALEISN	780
		QY	780	IVFTSLFALEMLKLLIVYGFPGYKPNYNIIDGVIVVISWEIVGQGGGLSVLRTFLM	839
		Db	781	IVFTSLFALEMLKLLIVYGFPGYKPNYNIIDGVIVVISWEIVGQGGGLSVLRTFLM	840
		QY	840	RVLKLVRELPALQRLVLMKTMNDVATFCMLLMLEFIFIPSLGMHLPGCKFASERDGT	899
		Db	841	RVLKLVRELPALQRLVLMKTMNDVATFCMLLMLEFIFIPSLGMHLPGCKFASERDGT	900
		QY	900	LPDRKNFDSLMLAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNVLPNLL	959
		Db	901	LPDRKNFDSLMLAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNVLPNLL	960
		QY	960	VAILVEGFQABEISKREDASGQSLCQLPVDVSGGQDANKSEBPPDFPSIDGDRKKC	1019
		Db	961	VAILVEGFQAE-----GDAKSEBPPDFPSIDGDRKKR	997
		QY	1020	LALVSLGHEPRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSAEPGA	1079
		Db	998	LALVSLGHEPRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSAEPGA	1057
		QY	1080	A-HEMKSPPSARSPHSPFWSAAASWTSRRSRNLGAPSLKRPSPGERESILSGGQ	1138
		Db	1058	AHEMKCPSPASRSPHSPFWSAAASWTSRRSRNLGAPSLKRPSPGERESILSGGQ	1117
		QY	1139	SODEESEEERAPAGSDHHRGSLREAKSSFDLPDQLQVGLHRTASGRSASHEQD	1198
		Db	1118	SODEESEEERAPAGSDHHRGSLREAKSSFDLPDQLQVGLHRTASGRSASHEQD	1177
		QY	1199	CNGKSASGLRALALEPDDPLDGDADDDEGNLKGKERVIRARLPCYLERSWSAYI	1258
		Db	1178	CNGKSASGLRALALEPDDPLDGDADDDEGNLKGKERVIRARLPCYLERSWSAYI	1237

QY 2258 SSDPADLDP 2266
 Db 2257 SSDPTMDP 2265
 RESULT 12
 AAY14592
 ID AAY14592 standard; protein; 2272 AA.
 AC AAY14592;
 XX 07-DEC-1999 (first entry)
 DT Rat T-type voltage-gated Ca channel alpha-1-g (rCavT1c).
 DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
 XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
 KW Rattus sp.
 XX WO9929847-A1.
 PN 17-JUN-1999.
 PD 30-OCT-1998; 98WO-US023161.
 PF 05-DEC-1997; 97US-00985809.
 PR (LOYO) UNIV LOYOLA CHICAGO.
 XX Perez-Reyes E, Cribbs LL;
 PI WPI: 1999-394972/33.
 DR N-PSDB; AAX83487.
 PT New T-type voltage-gated calcium channels.
 PS Disclosure; Page 85-94; 138pp; English.
 XX This sequence represents a rat T-type voltage-gated calcium (Ca) channel
 CC alpha-1-g designated rCavT1c. Voltage gated channels are membrane bound
 CC glycosylated proteins formed of several subunits. The large alpha
 CC subunits form a pore in the membrane that is selective for a given ionic
 CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
 CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
 CC -type Ca channels are activated at a lower voltage than L- or N-type
 CC channels. Characteristics of T-type channels include short current time,
 CC slow activation kinetics near threshold, fast inactivation kinetics and
 CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
 CC channels contains a putative IVS4 region comprising the amino acid
 CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
 CC channel proteins can be used to screen for drugs which affect calcium
 CC channels. Methods are also disclosed for treating a disease or disorder
 CC associated with a deficiency in a native T-type calcium channel nucleic
 CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
 XX Sequence 2272 AA;
 QY Query Match 91.8%; Score 10925; DB 2; Length 2272;
 Best Local Similarity 91.7%; Pred. No. 0;
 Matches 2106; Conservative 33; Mismatches 103; Indels 54; Gaps 6;
 QY 1 MDEEDGAGAESQPRSFMRNLDSGAGRGPGCSAFKDPGSDADSEAGLPYALAPV 60
 Db 1 MDEEDGAGAESQPRSFMRNLDSGAGRGPGCSAFKDPGSDADSEAGLPYALAPV 60
 QY 61 PFYLSQDRSRPSCVLCVTCNPFWRISMLVLLNCVTLGMFPCEDICDSQRCILQAF 120
 Db 61 PFYLSQDRSRPSCVLCVTCNPFWRISMLVLLNCVTLGMFPCEDICDSQRCILQAF 120
 QY 121 DDFIFFAFAVMVVMVALGIFGKCYLGDWNRDLDFIIVAGMLEYSLDLQNVFSVR 180

QY 1259 FPQSRFRLLCHRIITHKMPDHHVVLVIIFLNCITTIAMERPKIDPHSAERIFLTLSNYIFT 1318
Db 1238 FPQSRFRLLCHRIITHKMPDHHVVLVIIFLNCITTIAMERPKIDPHSAERIFLTLSNYIFT 1297
QY 1319 AVFLAEMTVKVALGWCCEQAYLRSSWNVLGDLVLIISVIDILVSMVSDSGTKILGMLR 1378
Db 1298 AVFLAEMTVKVALGWCCEQAYLRSSWNVLGDLVLIISVIDILVSMVSDSGTKILGMLR 1357
QY 1379 VLRLARTLRPLRVISRAQGLKLVETLMSLXPIGNIVVIVICCAFRIIGILGVQVFKGF 1438
Db 1358 VLRLARTLRPLRVISRAQGLKLVETLMSLXPIGNIVVIVICCAFRIIGILGVQVFKGF 1417
QY 1439 FVCGEDTRNITKSDCAEASRWVRHKYNFONLQALMSLFLVASKGWDVIMYDGLDA 1498
Db 1418 FVCGEDTRNITKSDCAEASRWVRHKYNFONLQALMSLFLVASKGWDVIMYDGLDA 1477
QY 1499 VGVDQOPTMNNPMLLYFISFLLIIVAFVLMFVGVVVENPHKCRHQEAEARRREK 1558
Db 1478 VGVDQOPTMNNPMLLYFISFLLIIVAFVLMFVGVVVENPHKCRHQEAEARRREK 1537
QY 1559 RLRLKRRR-----KAOCKPVYSDYSFRLLVHHLCTSH 1593
Db 1538 RLRLKRRRKEKQMDLMDDDVIASGSSASAASEAOCKPYSDYSFRLLVHHLCTSH 1597
QY 1594 YLDFITGVIGLVNVTWAMEHYQQPILDEALKICNYIFTVIFVLESVKLVAFGRFRFF 1653
Db 1598 YLDFITGVIGLVNVTWAMEHYQQPILDEALKICNYIFTVIFVLESVKLVAFGRFRFF 1657
QY 1654 QDRWNQDLALVLSIGITILEEVNASLPIINTIIRIMVLRIARVLKLLKMAVGMA 1713
Db 1658 QDRWNQDLALVLSIGITILEEVNASLPIINTIIRIMVLRIARVLKLLKMAVGMA 1717
QY 1714 LLDTVMQALPQVGNLGLLMLFFIFALGVELFGDLECDTHPCGGLGRHATERNFGMA 1773
Db 1718 LLDTVMQALPQVGNLGLLMLFFIFALGVELFGDLECDTHPCGGLGRHATERNFGMA 1777
QY 1774 FLTLFRVSTGDNWNGIMKDLRDCQDSTCYNTVISPFIYFVSFLTAQFVLNVNVIIVLM 1833
Db 1778 FLTLFRVSTGDNWNGIMKDLRDCQDSTCYNTVISPFIYFVSFLTAQFVLNVNVIIVLM 1837
QY 1834 KHLSESKAEAEAELEWMLKTLSPQHPGLSPFTLPWGVGPDSPDSPKPGALHP 1893
Db 1838 KHLSESKAEAEAELEWMLKTLSPQHPGLSPFTLPWGVGPDSPDSPKPGALHP 1897
QY 1894 AAHARSASHFSLHPTMQPHTLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHSTAE 1950
Db 1898 TAHIKAASGFSLEHPTMWPHEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRHSTAE 1957
QY 1951 GPLGHRGWGLPKAQSGLSVLSVHSQPADTSYIQLPKDAPHLQPHSAPTMTGTPKLPPLPG 2010
Db 1958 RSLGHRGWGLPKAQSGLSVLSVHSQPADTSYIQLPKDAPHLQPHSAPTMTGTPKLPPLPG 2017
QY 2011 RGPLAQRLRROAAIRTSIDVGLGSRDLLEAVSGPPPLARAYFWGQSQTAQOHS 2070
Db 2018 RGPLAQRLRROAAIRTSIDVGLGSRDLLEAVSGPPPLARAYFWGQSQTAQOHS 2077
QY 2071 RSHKTSKEMTPPAPCPGPEPNWKGPPETRSLSLELDTLSMTSGDLLPPGQEPSPR 2130
Db 2078 GTSKVSXKHLRPAKGLPSPWAKDPPETRSLSLELDTLSMTSGDLLPPGQEPSPR 2136
QY 2131 DLKCYSVFAQSCORRPTWLBQRRHSIAVSCLDGSGQPHLGTDPNSLGGQPLGGPSR 2190
Db 2137 DLKCYSVFAQSCORRPTWLBQRRHSIAVSCLDGSGQPHLGTDPNSLGGQPLGGPSR 2196
QY 2191 PKKLSPPSITIDPPESQCPPTPPSGICLRRAPSDDSKDPLAGPPDSMAASPPKDD 2250
Db 2197 PKKLSPPSITIDPPESQCPPTPPSGICLRRAPSDDSKDPLAGPPDSMAASPPKDD 2256
QY 2251 VLSLSGLSSDADLDP 2266
Db 2257 VLSLSGLSSDADLDP 2272

RESULT 13
AAB66475
ID AAB66475 standard; protein; 2287 AA.
XX AC AAB66475;
XX DT 09-APR-2001 (first entry)
XX DE Rat alpha-IG calcium channel protein.
XX KW Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;
KW hypotensive; cardiac; nootropic; T-type calcium channel subunit;
KW cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;
KW epilepsy; alpha-IG calcium channel.
XX OS Rattus sp.
XX PN WO200102561-A2.
XX PD 11-JAN-2001.
XX PF 04-JUL-2000; 2000WO-CA000794.
XX PR 02-JUL-1999; 99US-00346794.
XX PA (NEUR-) NEUROMED TECHNOLOGIES INC.
XX PI Snutch TP, Baillie DL;
XX DR WPI; 2001-123111/13.
XX DR N-PSDB; AAF31677.
XX PT Novel T-type calcium channel alpha-1 subunit gene useful for treating
XX PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
XX PT epilepsy.
XX PS Disclosure; Page 63-72; 103pp; English.
XX CC The present sequence is given in a specification providing sequences and
XX CC partial sequences for three types of mammalian (human and rat) T-type
XX CC calcium channel subunits. An expression cassette has been generated which
XX CC comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
XX CC subunit operably linked to control sequences to effect its expression.
XX CC The novel calcium channel nucleic acids and proteins are useful for
XX CC treating conditions characterised by undesirable levels of T-type calcium
XX CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
XX CC hypertension, sleep disorder and epilepsy
XX SQ Sequence 2287 AA;
Query Match 90.5%; Score 10774; DB 4; Length 2287;
Best Local Similarity 92.3%; Pred. No. 0;
Matches 2075; Conservative 33; Mismatches 105; Indels 36; Gaps 6;
QY 30 GRPGSABKPGSADSEAEGLYPALAPVVFYLLSQDSRPSWCLRTVCNPFERISML 89
Db 62 GAAGAGSTEKPGSADSEAEGLYPALAPVVFYLLSQDSRPSWCLRTVCNPFERISML 121
QY 90 VILLNCVTLGMFPCEDTACDSQRCRILOAFDDPTFAFFAVEMVVMVALGIFGKKCYLG 149
Db 122 VILLNCVTLGMFPCEDTACDSQRCRILOAFDDPTFAFFAVEMVVMVALGIFGKKCYLG 181
QY 150 DTWNRLDFFVIAGMLEYSLDLQNVSAFVTRVLRPLRINRVPVSMRILVTLTLLDLP 209
Db 182 DTWNRLDFFVIAGMLEYSLDLQNVSAFVTRVLRPLRINRVPVSMRILVTLTLLDLP 241
QY 210 MLGNVLLLCFFVFFITGIVGVQLWAGLLRNCFLPENFSLPLSVLDLERYQYENEDSPF 269
Db 242 MLGNVLLLCFFVFFITGIVGVQLWAGLLRNCFLPENFSLPLSVLDLERYQYENEDSPF 301
QY 270 ICSQPRENGMSCRVPFLTRGDGGGPGCGLDYDAYNSSNTTCVMNQYTNCSAGEHN 329

Db 302 ICSPRENGMRCRSPVTLRGGGGGPPCLDYETVYNSNTTVCNNVQYVYTNCSAGEHN 361
 Qy 330 PFKGAINFDNGVAMIAIFQVITLGGWVDIMYFVMDAHSFNFYIFILLIIVGSFFMINL 389
 Db 362 PFKGAINFDNGVAMIAIFQVITLGGWVDIMYFVMDAHSFNFYIFILLIIVGSFFMINL 421
 Qy 390 CLVVIATQFSETKQRESQLMREQRVRLSNASTLASPEGPCYBEELKYLIVYLKRAAR 449
 Db 422 CLVVIATQFSETKQRESQLMREQRVRLSNASTLASPEGPCYBEELKYLIVYLKRAAR 481
 Qy 450 RLAQVSRAGVRVGLLSPAPLGGQFTOPSSCSHRRLSVHHLVHHHHHHHHYHILGN 509
 Db 482 RLAQVSRAGVRVGLLSPAPLGGQFTOPSSCSHRRLSVHHLVHHHHHHHHYHILGN 541
 Qy 510 GTLRAPRASPEIQORDANGSRRLMLPPSTPALSGAPPGAESVHSFYHADCHLEPVRCQ 569
 Db 542 GTLRAPRASPEIQORDANGSRRLMLPPSTPALSGAPPGAESVHSFYHADCHLEPVRCQ 601
 Qy 570 APPRSPSEASGRTVSGKVYPTVHTSPPTLKEKALVEVNAASSGPTLTSLNIPPGPY 629
 Db 602 APPRSPSEASGRTVSGKVYPTVHTSPPTLKEKALVEVNAASSGPTLTSLNIPPGPY 661
 Qy 630 SSMKHLTOSTGACQSCCKISSPCLKADSGAGPDCPYCARAGAGVELADREMPDSD 689
 Db 662 SSMKHLTOSTGACQSCCKISSPCLKADSGAGPDCPYCARAGAGVELADREMPDSD 721
 Qy 690 SEAVVEFTQDAQHSDLRDPHS--RRORSILGPDAEPSVLAFWRLICDTFRKIVDSKYFGRG 748
 Db 722 SEAVVEFTQDAQHSDLRDPHS--RRORSILGPDAEPSVLAFWRLICDTFRKIVDSKYFGRG 781
 Qy 749 IMAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLKLLVYGPYIKNPYN 808
 Db 782 IMAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLKLLVYGPYIKNPYN 841
 Qy 809 IFDGVIVISVMEIVCQGGGLSVLRTFLMRVLKLVRLPALQRLVLMKTMNDVATF 868
 Db 842 IFDGVIVISVMEIVCQGGGLSVLRTFLMRVLKLVRLPALQRLVLMKTMNDVATF 901
 Qy 869 CMLLMFIFIFSLGMLHFGCKFASBERDGTLPDRKNFDSLWAIIVTVQILTOEDWNV 928
 Db 902 CMLLMFIFIFSLGMLHFGCKFASBERDGTLPDRKNFDSLWAIIVTVQILTOEDWNV 961
 Qy 929 LYNGMASTSSWAAIFYALMTFGNYVLNLLVAILVEGQAEBISKREDASGQLSCIQLP 988
 Db 962 LYNGMASTSSWAAIFYALMTFGNYVLNLLVAILVEGQAEBISKREDASGQLSCIQLP 1003
 Qy 989 VDSQGGDANKSESEDPFSLDGDGDRKKCLALVSLGHEPRLKSLPLLIHTAATPM 1048
 Db 1004 VDSQGGDANKSESEDPFSLDGDGDRKKCLALVSLGHEPRLKSLPLLIHTAATPM 1058
 Qy 1049 SLPKSTSTGLGEALGPASRTSSGSAEPGAA--HEMKSPPSARSGSPHSWASAASSWTSRR 1107
 Db 1059 SHPKSSTGVGEALGSGSRRTSSGSAEPGAAHEMKSPPSARSGSPHSWASAASSWTSRR 1118
 Qy 1108 SSRNLSGRAPSLKRSPSGERRSLLSGEGQESQDEESSERASPDGHRHUGSLERE 1167
 Db 1119 SSRNLSGRAPSLKRSPSGERRSLLSGEGQESQDEESSERASPDGHRHUGSLERE 1178
 Qy 1168 AKSFDLPDPTLOVPLHRTASGRGSAHQDCNKSASGRILARALRPDDPLDGDADDDE 1227
 Db 1179 AKSFDLPDPTLOVPLHRTASGRGSAHQDCNKSASGRILARALRPDDPLDGDADDDE 1238
 Qy 1228 GNLKSGRVRVAVIRARLPACYLERSMSAYIFPPQSRFLLCHRIITHKMPDHVVLVIF 1287
 Db 1239 GNLKSGRVIQAWRSRLPACCRDRMSAYIFPPQSRFLLCHRIITHKMPDHVVLVIF 1298
 Qy 1288 LNCITIAMERKIDPHSARIFLTLSNYIFTAVFLAEMTVKVALGWCFCGQAYLRSSWN 1347
 Db 1299 LNCITIAMERKIDPHSARIFLTLSNYIFTAVFLAEMTVKVALGWCFCGQAYLRSSWN 1358
 Qy 1348 VLDGLLVLSVTDIILVMSVSDSGTKILGMLRVLRLLRTPRLRVISRAQGLKLVVETILMS 1407
 Db 1359 VLDGLLVLSVTDIILVMSVSDSGTKILGMLRVLRLLRTPRLRVISRAQGLKLVVETILMS 1418

Qy 1408 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVQCQGBDTNINTKSDCAEASVWVHKY 1467
 Db 1419 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVQCQGBDTNINTKSDCAEASVWVHKY 1478
 Qy 1468 NFDNLGQALSLFVLASKQGWDMIDYDGLDAVGVDQOPIMNHNPMMLLYIFISFLIIVAFF 1527
 Db 1479 NFDNLGQALSLFVLASKQGWDMIDYDGLDAVGVDQOPIMNHNPMMLLYIFISFLIIVAFF 1538
 Qy 1528 VLNNFVGVVVENFHKCHQHEEERREERREKRLRLEKKRR-----KAQCKPYYSYDS 1580
 Db 1539 VLNNFVGVVVENFHKCHQHEEERREERREKRLRLEKKRRSKEKQMAEACKPYYSYDS 1598
 Qy 1581 RFRLLVHHLCTSHYLDLFTITGIVGLNVVTWAMEHYQQPILDEALKICNYIFTVIFVLES 1640
 Db 1599 RFRLLVHHLCTSHYLDLFTITGIVGLNVVTWAMEHYQQPILDEALKICNYIFTVIFVLES 1658
 Qy 1641 VFKLVAAGFRFRFQDRNQLDLAIVLSIMGITTEEVNASLNPINPIIRMLVRIAR 1700
 Db 1659 VFKLVAAGFRFRFQDRNQLDLAIVLSIMGITTEEVNASLNPINPIIRMLVRIAR 1718
 Qy 1701 VLKLLKMAVGRALLDTVMQALPOVGNLGLLFLMLFFIFAALGVLEFGDLECDTHPCBG 1760
 Db 1719 VLKLLKMAVGRALLDTVMQALPOVGNLGLLFLMLFFIFAALGVLEFGDLECDTHPCBG 1778
 Qy 1761 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTURDCQOESTCYNTVISPFIYFVFLTA 1820
 Db 1779 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTURDCQOESTCYNTVISPFIYFVFLTA 1838
 Qy 1821 QVVLNVVIAVLUMKHEESNKEAEAELEAELEEMKTLSPQHSPLGSPFLMWQVEGV 1880
 Db 1839 QVVLNVVIAVLUMKHEESNKEAEAELEAELEEMKTLSPQHSPLGSPFLMWQVEGV 1898
 Qy 1881 DSDPDKPCALHPAAHARSASHFSLEHTMQDPHTLP---GPDLLTVKSGVSRTHSLP 1937
 Db 1899 NSTDSFKPCGAPHTTHIGHAASGFSLEHTPMVPHPEEVPVPLGPDLLTVKSGVSRTHSLP 1958
 Qy 1938 NDSYMCNRHGSTAEGLPHRGWGLPKAQSGLSVLSHSQPADTYSIILPKDAPEHLOPHSA 1997
 Db 1959 NDSYMCNRHGSTAEGLPHRGWGLPKAQSGLSVLSHSQPADTYSIILPKDAPEHLOPHSA 2018
 Qy 1998 PTWGTIPKLPPLPPGRSLAORPLRQAAIIRTSIDVQGLGSRDILLAEVSGSPPLARAYS 2057
 Db 2019 PTWGTIPKLPPLPPGRSLAORPLRQAAIIRTSIDVQGLGSRDILLAEVSGSPPLARAYS 2078
 Qy 2058 FWSQSTQAOQHSRSHSKISKMTTPAPCPGPEPNMGKGPETPRSSLELDTLSWISGDL 2117
 Db 2079 FWSQSTQAOQHSRSHSKISKMTTPAPCPGPEPNMGKGPETPRSSLELDTLSWISGDL 2138
 Qy 2118 LPFGQGEPPSPRDLKKCYSVSAQSCORRPTSWLDEQRHSIAVSCLDGSGQHLGTDPS 2177
 Db 2139 L-PSSQGEPLFPRDLKKCYSVETQSCRRRPFGLWDEQRHSIAVSCLDGSGQHLGTDPS 2197
 Qy 2178 NLGQPLGGGSPGPKKLSPPSITIDPPESQGPRTTSPGICLRRRAPSDDSKDPLASGP 2237
 Db 2198 SLGQPLGGGSPGPKKLSPPSITIDPPESQGPRTTSPGICLRRRAPSDDSKDPLASGP 2257
 Qy 2238 PDGMAASPSPKDVLISGLSSDPADLDP 2266
 Db 2258 LDSTAASPSPKDVLISGLSSDPADLDP 2286

RESULT 14

AAU00474
 ID AAU00474 standard; protein; 1207 AA.

AC AAU00474;

DT 18-JUL-2001 (first entry)

DE Human T-type calcium channel CACNA1G protein.

XX Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
 KW

cellular proliferative disorder; colorectal cancer; age related disease; apolipoprotein B; APOB; caudal type homeobox transcription factor 2; CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1; MINT31; G protein-coupled receptor 37; GPR37; heat shock 70KD protein 6; HSP70B; HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2; PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL; patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4; chromosome 17.

XX Homo sapiens.

OS WO200119845-A1.

PN 22-MAR-2001.

PF 14-SEP-2000; 2000MO-US025479.

PR 15-SEP-1999; 99US-00398522.

PA (UYTO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Issa J;

PI WPI; 2001-244777/25.

DR N-PSDB; AAS01624.

XX New nucleic acid molecule for use as a marker for screening cancer, comprises the coding region for a T-type calcium channel and regulatory sequences associated with the channel.

PS Claim 9; Fig 3B; 125pp; English.

XX The present sequence representing a novel human T-type calcium channel CACNA1G maps to chromosome 17. The methylation state of specific regions within CpG islands associated with the CACNA1G gene correlate with several cancerous phenotypes involving various tissue and cell types. Since aberrant methylation of normally unmethylated CpG islands is often observed in immortalised and transformed cells, CACNA1G is implicated in cellular proliferative disorders e.g. leukaemia, colorectal, lung, breast and other cancers. The nucleic acid coding for CACNA1G is useful as a marker for screening cancer and age related diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for amplification of a CpG-containing nucleic acid, where the primer hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can be used for detecting aberrant methylation. The CpG island sequences (AAS01677-AAS01692) are selected from genes encoding CACNA1G, apolipoprotein B (APOB), caudal type homeobox transcription factor 2 (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G protein-coupled receptor 37 (GPR37), heat shock 70KD protein 6 (HSP70B; HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-activated receptor 2 (PAR2), paired-like homeodomain transcription factor 2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1; SDC4) or a MINT 31 sequence

XX Sequence 1207 AA;

Query Match 53.1%; Score 6315.5; DB 4; Length 1207;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1207; Conservative 0; Mismatches 0; Indels 23; Gaps 1;

QY	1	MBEEDGAGAEESGQPRSMRLNDLSCAGRPPGSAEKDPGSADEAGLPYPALAPVV	60
Db	1	MBEEDGAGAEESGQPRSMRLNDLSCAGRPPGSAEKDPGSADEAGLPYPALAPVV	60
QY	61	FFYLSQDSRPSRCLRTVCNPFERISMLVILLNCVTLGWFRCEDICDSORCRLQAF	120
Db	61	FFYLSQDSRPSRCLRTVCNPFERISMLVILLNCVTLGWFRCEDICDSORCRLQAF	120
QY	121	DDPIFAFFAVEMVVMWALGIFGKKCYLGGDTWNRLDFFIVAGMLEYSLDLQNVFSAYR	180
Db	121	DDPIFAFFAVEMVVMWALGIFGKKCYLGGDTWNRLDFFIVAGMLEYSLDLQNVFSAYR	180
QY	181	TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLCFVFFIFGIVGVQLWAGLLNR	240

RESULT 15
AAB66476

Db	181	TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLCFVFFIFGIVGVQLWAGLLNR	240
QY	241	CELPEFNSPLSVDLERYQYQTEDESPFICQPRENGMRSCRSVPTLRGDDGGPPCGL	300
Db	241	CELPEFNSPLSVDLERYQYQTEDESPFICQPRENGMRSCRSVPTLRGDDGGPPCGL	300
QY	301	DYEAYNSSNTTCVNMNQYITNCAGEHNPFKGAINFDMNIGYAWIAFQVITLEGWVDIM	360
Db	301	DYEAYNSSNTTCVNMNQYITNCAGEHNPFKGAINFDMNIGYAWIAFQVITLEGWVDIM	360
QY	361	YFVMDAHSFYNIYFILLIIVGSFFMINLCLVVIATOFSETKORESQLMREORVPLSNA	420
Db	361	YFVMDAHSFYNIYFILLIIVGSFFMINLCLVVIATOFSETKORESQLMREORVPLSNA	420
QY	421	STLASFSFGSCYEELLYVYLKKAARRLAQVRAAGVRVGLLSSPAPLGGQETQPS	480
Db	421	STLASFSFGSCYEELLYVYLKKAARRLAQVRAAGVRVGLLSSPAPLGGQETQPS	480
QY	481	SCSRSHRRLSVHLLVHHHHHHHHVHLNGTILRAPASPEIQDRDANGSRRLMLPPSTP	540
Db	481	SCSRSHRRLSVHLLVHHHHHHHHVHLNGTILRAPASPEIQDRDANGSRRLMLPPSTP	540
QY	541	ALSGAPPGCAESVHSFYHADCHLEPVRCAQAPPSPSEASGRTVSGKVPYTVHTSPPE	600
Db	541	ALSGAPPGCAESVHSFYHADCHLEPVRCAQAPPSPSEASGRTVSGKVPYTVHTSPPE	600
QY	601	TLKXKALVEVAASGPPTLTSLNIPPGYSSMHKLLTQSTGACOSSCKISSPCLKADSG	660
Db	601	TLKXKALVEVAASGPPTLTSLNIPPGYSSMHKLLTQSTGACOSSCKISSPCLKADSG	660
QY	661	ACGPDSCPYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRPHSRQRSLGPA	720
Db	661	ACGPDSCPYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRPHSRQRSLGPA	720
QY	721	EPSSVLAFWRLICDTFRKIVDSKYFGRGIMTALVNTLSMGIEVHEQPEELTNALEISNI	780
Db	721	EPSSVLAFWRLICDTFRKIVDSKYFGRGIMTALVNTLSMGIEVHEQPEELTNALEISNI	780
QY	781	VFTSLFALEMLLKLVLVYGPFGYIKNPYINFDGVTIVISVWEIVGQGGGLSVLRTFLMR	840
Db	781	VFTSLFALEMLLKLVLVYGPFGYIKNPYINFDGVTIVISVWEIVGQGGGLSVLRTFLMR	840
QY	841	VKLVRFLPALQRLVLMKTMQNVATFCMLLMFLIFIFSILGHLPGCKFASERDGTLL	900
Db	841	VKLVRFLPALQRLVLMKTMQNVATFCMLLMFLIFIFSILGHLPGCKFASERDGTLL	900
QY	901	PDRKNFDSLWLVAITVFOILTQEDWNKVLNGMASTSSWAALYFIALMTGNYVLNLLV	960
Db	901	PDRKNFDSLWLVAITVFOILTQEDWNKVLNGMASTSSWAALYFIALMTGNYVLNLLV	960
QY	961	AILVEGFAEIEISKREDASGQLSCIQLPVDSDQDANKSESEPDFTSPSLDGDGRKKCL	1020
Db	961	AILVEGFAEIEISKREDASGQLSCIQLPVDSDQDANKSESEPDFTSPSLDGDGRKKCL	1020
QY	1021	ALVSLGHEPELRKSLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSAEPGAA	1080
Db	998	ALVSLGHEPELRKSLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSAEPGAA	1057
QY	1081	HEMKSPSARSPPHSPWSAASWTSPRSNSIGRAPSLKRSPSGERRSLLSGEGQESQ	1140
Db	1058	HEMKSPSARSPPHSPWSAASWTSPRSNSIGRAPSLKRSPSGERRSLLSGEGQESQ	1117
QY	1141	DEESESSEERASPGSDHRRHRSLEAKSSFDLPTLQVPGHLHRTASGRGSAHQDCN	1200
Db	1118	DEESESSEERASPGSDHRRHRSLEAKSSFDLPTLQVPGHLHRTASGRGSAHQDCN	1177
QY	1201	GKSASGRALARALRPDDPLDGDADDEGNL	1230
Db	1178	GKSASGRALARALRPDDPLDGDADDEGNL	1207

Mon Nov 22 06:47:54 2004

ID AAB66476 standard; protein; 2359 AA.
XX AAB66476;
XX 09-APR-2001 (first entry)
DT
XX
XX Rat alpha-IH calcium channel protein.
DE
XX Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;
XX hypotensive; cardiac; nootropic; T-type calcium channel subunit;
KW cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;
KW epilepsy; alpha-IH calcium channel.
XX
OS Rattus sp.
XX
XX WO200102561-A2.
FN
XX
XX 11-JAN-2001.
PD
XX
XX 04-JUL-2000; 2000WO-CA000794.
PF
XX
XX 02-JUL-1999; 99US-00346794.
PR
XX
XX (NEUR-) NEUROMED TECHNOLOGIES INC.
PA
XX
XX Snutch TP, Baillie DL;
PI
XX
XX WPI; 2001-123111/13.
DR N-PSDB; AAF31678.
XX
XX Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT epilepsy.
XX
XX Disclosure; Page 75-85; 103pp; English.
PS
XX The present sequence is given in a specification providing sequences and
CC partial sequences for three types of mammalian (human and rat) T-type
CC calcium channel subunits. An expression cassette has been generated which
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC subunit operably linked to control sequences to effect its expression.
CC The novel calcium channel nucleic acids and proteins are useful for
CC treating conditions characterised by undesirable levels of T-type calcium
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC hypertension, sleep disorder and epilepsy
XX
SQ Sequence 2359 AA;
Query Match 52.2%; Score 6218; DB 4; Length 2359;
Best Local Similarity 56.4%; Pred. No. 0;
Matches 1369; Conservative 228; Mismatches 509; Indels 322; Gaps 62;
QY 2 DEEDGAGAESQPSRSMELNDLS-CAGGRP--GPGS---AEKDPGS---AD---SEA 48
DB 9 DEVRVPLUGAPPA-PAAPVRSASPAPGAPGOREGGSGSVLAPESPTECGADLGADEE 67
QY 49 EGLPYPALAPVVFYLLSQDSRPSWCLRTVCNPFERISMVILLNCVTLMGMPRCDIA 108
DB 68 QVPYPALAAATVFCLGQTTTPRSWCLRLVCNPFVHVMVIMLNCVTLMGMPRCDVE 127
QY 109 CDSORCRLQAFDDFIAPFAVENVMVAVGIGKCKYLGDTWNRDLDFVIAGMLEYS 168
DB 128 CRSERCILEAFDDFIAPFAVENVMVAVGIGKCKYLGDTWNRDLDFVIAGMLEYS 187
QY 169 LDIQWVSFAVTVRVRLPRAINRVPSMRILVTLTDLTLMGNVLLLCFFVFFIGIV 228
DB 188 LDGHKVSLSATRTVRVRLPRAINRVPSMRILVTLTDLTLMGNVLLLCFFVFFIGIV 247
QY 229 GYQWAGLLNRRCFLPENFSLPLSDV-LERYQTENEDESPFCSQPRENGMRSRCSVPT 287
DB 248 GYQWAGLLNRRCFLDSAFVRNNLTFLRPYQYTEGENPFICSSREDNGMQCKSHIPS 307
QY 288 ---LRGDGGGPPCGLDYEAY-----NSSNTTCVNNQYTYTNCSSAGEHNPKGAINF 337

DB RBRLR-----VQCTLGWEAYGQPAEDGGAGRNACINWQYVNVKSGSFNPENGAINF 361
QY 338 DNIGYAMIAIPOVITTEGWDIMYFVMDAHSFYNYFIYFILLIIVGSPFIMLCIVVIATQ 397
DB 362 DNIGYAMIAIPOVITTEGWDIMYFVMDAHSFYNYFIYFILLIIVGSPFIMLCIVVIATQ 421
XX
XX FSETKQRESOLMRQRVRFILSNASTLASFSPPGSCYBELLYVILURKAARRLAQVRA 457
XX 422 FSETKQRENQLMREQRARYLSNDSTLASFSPPGSCYBELLYVGHIFRKVKRRSLRYAR 481
DB 458 AGVRVGLLSSP-APLGGQETOPSSSCSRSHRR-LSVHHLV-HHHHHHHHHVHLNGTURA 514
QY 482 WQSRWRKXVDPSSTVHGO--GPGRRPRRAGRRTASVHHLVYHHHHHHHHVHFSGGRR 539
DB 515 PRASPEIQDRDANGSRRLM--LPPSTPALSGAPPGAESVHSFYHADCHLEPEVRCQAPP 572
QY 540 P--SPE-----PGAGNRLVRACAPSPSPGHPGPP-DSESVHSIVHADCHVEGPGQERARV 592
DB 573 PRSPSEASGRTVGSG--KVYPTVHTSPPTLKEKALVEVAASGSPPTLTSLNTP----- 625
XX 593 AHSIATAASLKLASGLGTWNYPTI--LPSGTVNSKG---GTSSRPKGLRGAGAPGA 645
DB 626 -----PGPYSSMHKLETTQSTGACQS-----SCKISSPCLKADSGAGCPDPCYC 670
QY 646 HSPLSLGSPRPYKIQDVVGEQGLGRASSHLSGLSVPCPLPSP--QAGTLTCELKSCPYC 703
DB 671 ABA-CAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDP-----HS--RRQSL 716
QY 704 ASALEDPFEPFSGSBSGSDAHGVTEFTQDVHGHGCRDPVQQPHVEVGTGHSNERRRTP 763
DB 717 GPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMIGIYHEQBELTNALE 776
XX 764 RXASQFGGIGHLWASFSGKLRIVDSKYENRGIMAILVNTLSMIGIYHEQBELTNALE 823
QY 777 ISNIVFTSLFALEMLKLLVYGPFGYIKPYNIPDGIWVVISWEIVGQGGSLVLRTF 836
DB 824 ISNIVFTSMFALEMLKLLACGFLGYIRPNYIFDGIWVVISWEIVGQGGSLVLRTF 883
QY 837 RLMRVLKVRFPALORQLVLMKTMNDVATFCMLMLFIFISILGMLHFGCKFASERD 896
DB 884 RLLRVLLKVRFPALRRQLVLMKTMNDVATFCMLMLFIFISILGMLHFGCKFSLKTD 943
QY 897 -GDTLPDRKNFDSLLWAIIVTFQILQEDWNKVLVNGMASTSSWAALYFIALMTFGNYVL 955
DB 944 SGTVPDRKNFDSLLWAIIVTFQILQEDWNKVLVNGMASTSSWAALYFIALMTFGNYVL 1003
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DB 1041 KLKDLRATRMKMTSLAVTPNGHLEGRLSPPLIITHTAATPMTPKS-SPNLDVAHALLD 1099
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DB 1100 SRRSSSGSVDPQLG-DQKSLASLRSSPCTPWPNSAGSSRRSSWNSILGRAPSLKRRSQCG 1158
QY 1127 ERKSLLSGEGQESODEESSEERAS-----PAGSDHRRHRSGLEREAKSFDL-- 1174
DB 1159 ERESLLSGEGKSTDD--AEDSRPSTGTTHPGASGPGPATPLRAESLDH--RSTLDLCP 1214
QY 1175 ----PDTLQVPLHRTASGRGSAHQPCNGKSASGLARALRDPDPLDGDADDEGNL 1230
DB 1215 PRPAPPVQV-----HDCNGQMVALPSEFFLRDHSKEDAAEFDDIED 1258
QY 1231 SKGERVAMTRARUAPCVLEKDDSWAIFPPQSRFLIICRILTHKMFHVLVILFNC 1290
DB 1259 SCCFRLHKVLEPYAPQWCRSRESWALYLPQPNRLRVSCQVIAHKMFHDVVLVIFLNC 1318
QY 1291 ITIAMERPDKIPHSARIFLTLNVITFAVLAEMTVKVALGWCFGQAYLRSSWVLD 1350

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:41 ; Search time 40.3132 Seconds
(without alignments)
3727.727 Million cell updates/sec

Title: US-09-611-257A-37

Perfect score: 11904

Sequence: 1 MDEEDGAGAESGQPRSF.....PKKDVLISGLSDPADLDP 2366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11862.5	99.7	2273	3	US-09-426-998-5
2	6315.5	53.1	1207	4	US-09-398-522-52
3	6211.5	52.2	2353	4	US-08-984-709A-50
4	5492.5	46.1	2175	3	US-09-404-650-2
5	5492.5	46.1	2175	4	US-09-935-541-2
6	5484	46.1	2188	3	US-09-404-650-4
7	5484	46.1	2188	4	US-09-935-541-4
8	5366	45.1	1835	3	US-09-404-650-5
9	5366	45.1	1835	4	US-09-935-541-5
10	1750.5	14.7	2343	3	US-09-268-163-4
11	1749	14.7	2337	3	US-08-713-118-2
12	1749	14.7	2337	3	US-09-452-007-2
13	1748.5	14.7	2339	1	US-08-455-543A-47
14	1748.5	14.7	2339	2	US-08-223-305C-47
15	1746.5	14.7	2339	3	US-09-268-163-6
16	1743	14.6	2237	1	US-08-455-543A-48
17	1743	14.6	2237	2	US-08-223-305C-48
18	1741	14.6	2237	3	US-09-268-163-8
19	1722	14.5	2236	3	US-09-268-163-10
20	1632.5	13.7	1873	1	US-08-435-675B-4
21	1622.5	13.6	1873	1	US-08-336-257A-7
22	1619.5	13.6	1984	3	US-08-836-325-10
23	1619.5	13.6	1984	4	US-09-457-571-10
24	1619.5	13.6	1985	4	US-09-495-714C-6
25	1616	13.6	1872	6	5386025-6
26	1615.5	13.6	1989	3	Patent No. 5386025
27	1615.5	13.6	1989	4	Sequence 12, Appl
28	1607.5	13.5	2516	3	US-08-374-077C-2
29	1607.5	13.5	2516	3	US-08-895-590-2
30	1607.5	13.5	2516	4	US-09-539-879A-2
31	1601	13.4	1977	4	US-09-495-714C-4
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33	1587	13.3	2016	4	US-09-514-907A-2
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35	1586	13.3	1969	3	US-08-836-325-16
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43	1569.5	13.2	1968	2	US-08-223-305C-45
44	1560.5	13.1	2161	1	US-08-455-543A-51
45	1560.5	13.1	2161	2	US-08-223-305C-51

ALIGNMENTS

RESULT 1

US-09-426-998-5
; Sequence 5, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: BELANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 5
; LENGTH: 2273
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-426-998-5

Query Match 99.7%; Score 11862.5; DB 3; Length 2273;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2260; Conservative 4; Mismatches 2; Indels 7; Gaps 1;

QY 1 MDEEDGAGAESGQPRSFMRNDLSGAGRPGSAEKDPGSADEAEGLFPALAPVY 60
Db 1 MDEEDGAGAESGQPRSFMRNDLSGAGRPGSAEKDPGSADEAEGLFPALAPVY 60

QY 61 RFLYSDSRPSRSCWLTVCNPFERISMLVILLNCVTGLMFRPCEDIACDSQRILQAF 120
Db 61 RFLYSDSRPSRSCWLTVCNPFERISMLVILLNCVTGLMFRPCEDIACDSQRILQAF 120

QY 121 DDFIFAFVAVENVKVALGIFGKCYLGDWTNRLDFFVIAGMLEYSLDLONVSFAVR 180
Db 121 DDFIFAFVAVENVKVALGIFGKCYLGDWTNRLDFFVIAGMLEYSLDLONVSFAVR 180

QY 181 TVRVLRLPRAINRVPMSRILVTLDDTLPLMGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
Db 181 TVRVLRLPRAINRVPMSRILVTLDDTLPLMGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

QY 241 CFLPENFSLPLSVDLERYQYOTENEDESPFICSPRENGMRSCRSVPTLRGGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYQYOTENEDESPFICSPRENGMRSCRSVPTLRGGGGPPCGL 300

QY 301 DYEAYNSSNTTCVNNQYITNCAGHNPFKGINFQNTAIQVITLLEGWVDIM 360
Db 301 DYEAYNSSNTTCVNNQYITNCAGHNPFKGINFQNTAIQVITLLEGWVDIM 360

QY 361 YFVMDAHSFYNYFYILLIIVGFFMINCLVVIATQFSTKQREBSQIMREQVRFLSNA 420
 Db 361 YFVMDAHSFYNYFYILLIIVGFFMINCLVVIATQFSTKQREBSQIMREQVRFLSNA 420
 QY 421 STLASFSEPGSCYBELLKYLVIILKKAARLAQVSRRAAGVRVGLSSPAPLGGQETOPSS 480
 Db 421 STLASFSEPGSCYBELLKYLVIILKKAARLAQVSRRAAGVRVGLSSPAPLGGQETOPSS 480
 QY 481 SCRSRRLS VHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
 Db 481 SCRSRRLS VHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
 QY 541 ALSGAPPGAESVHSFYHADCHLSPVRCQAPPPRSPSEASGRTVGSKVPTVHTSPPE 600
 Db 541 ALSGAPPGAESVHSFYHADCHLSPVRCQAPPPRSPSEASGRTVGSKVPTVHTSPPE 600
 QY 601 TLKEKALVEVAASSGPTLSTLNPFGPYSSMHKLETOQGACQSSCKISSPCLKADSG 660
 Db 601 TLKEKALVEVAASSGPTLSTLNPFGPYSSMHKLETOQGACQSSCKISSPCLKADSG 660
 QY 661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRPHSRQRSLGPD 720
 Db 661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRPHSRQRSLGPD 720
 QY 721 EPSSVLAFWRILCDTRFKIVDSKYFGRGIMTALVNTLSMGIYHQPEELTNALEISNI 780
 Db 721 EPSSVLAFWRILCDTRFKIVDSKYFGRGIMTALVNTLSMGIYHQPEELTNALEISNI 780
 QY 781 VFTSLFALEMLKLVVGPFGYIKNPYNI FGVIVIVISVWEIVGQGGGLSVLRTFLMR 840
 Db 781 VFTSLFALEMLKLVVGPFGYIKNPYNI FGVIVIVISVWEIVGQGGGLSVLRTFLMR 840
 QY 841 VLKVRFLPALQORQLVLMKMDNVATFCMLLMFIFIFSILGMHLCFCKFASERDGTLL 900
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 QY 901 PDRKNDLSLWAIIVTFOILQEDWNKVLVNGMASTSSWAALYFALTMTFGNYVLNLLV 960
 Db 901 PDRKNDLSLWAIIVTFOILQEDWNKVLVNGMASTSSWAALYFALTMTFGNYVLNLLV 960
 QY 961 ALLVEGFOABEISKREDAAGQSCIQLPVDGOGDANKSEPPDFPSLDGDRKKCL 1020
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 QY 1081 HEMKSPSARSPPHSPWGAASWTGRRSRNSLGRAPSLKRSPSGERRSLLSGQESQ 1140
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 QY 1381 RLRTLRPLRVISRAQGLKLVWETLMSLKPIGNIVVICAFFIIFGILGVOLFKGKFFV 1440
 Db 1381 RLRTLRPLRVISRAQGLKLVWETLMSLKPIGNIVVICAFFIIFGILGVOLFKGKFFV 1440

QY 1441 CQGEDTNI TNKSDCAEASVRRVHRKYNFDFNLGALMSLFLVASKDGWVDIMYDGLDAVG 1500
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 QY 1501 VDQOPIMNHNPMWMLLYFISFLIIVAFVLMFVGVVVENPHKCRHQEERREKRL 1560
 Db 1501 VDQOPIMNHNPMWMLLYFISFLIIVAFVLMFVGVVVENPHKCRHQEERREKRL 1560
 QY 1561 RLEKKER-----KQACKPYSDSRFRLLVHHLCTSHVLDLFTIGVIGLNVVWTAME 1613
 Db 1561 RLEKKER-----KQACKPYSDSRFRLLVHHLCTSHVLDLFTIGVIGLNVVWTAME 1613
 QY 1614 HYQOPILDEALKICNYIFTVIFVLESVFKLVAFFGERFFQDRWNQDLDAIVLLSIMGIT 1673
 Db 1614 HYQOPILDEALKICNYIFTVIFVLESVFKLVAFFGERFFQDRWNQDLDAIVLLSIMGIT 1673
 QY 1621 HYQOPILDEALKICNYIFTVIFVLESVFKLVAFFGERFFQDRWNQDLDAIVLLSIMGIP 1680
 Db 1621 HYQOPILDEALKICNYIFTVIFVLESVFKLVAFFGERFFQDRWNQDLDAIVLLSIMGIP 1680
 QY 1674 LEEIEVNASLPINPTIIRIMRVLIARVILKLLKXAGVGRALLDTVMQALPOVGNLGLLFM 1733
 Db 1674 LEEIEVNASLPINPTIIRIMRVLIARVILKLLKXAGVGRALLDTVMQALPOVGNLGLLFM 1733
 QY 1734 LLFFIFAALGVLELFGDLECDETHPCGELGRHATERNFGMAFLTLFRVSTGDNWNGIMKDT 1793
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 QY 1794 LRDCQBSTCYNVTISPIYFVSFVLTQAQVFLNVVIVIAVLMKHLBESNKAEKAELEAEL 1853
 Db 1794 LRDCQBSTCYNVTISPIYFVSFVLTQAQVFLNVVIVIAVLMKHLBESNKAEKAELEAEL 1853
 QY 1854 ELEMKTLSPOHSPGLSGFFLWPGVEGDDSDSPKPGALHPAAHARSASHFSLEHPTMQPH 1913
 Db 1854 ELEMKTLSPOHSPGLSGFFLWPGVEGDDSDSPKPGALHPAAHARSASHFSLEHPTMQPH 1913
 QY 1914 PTELPGLDILTVRKSQSVRTHSLNDSVMCRHGSTAEGPLGHRGWGLPKAQSGLSVLVS 1973
 Db 1914 PTELPGLDILTVRKSQSVRTHSLNDSVMCRHGSTAEGPLGHRGWGLPKAQSGLSVLVS 1973
 QY 1974 QPADTSYILQPKDAPHLLQPHSAPTWTGTPKLPPLPGRSPLAQAPLRQAIRTDLSLVQ 2033
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 QY 2034 GLGSRDILAEVSGSPPLARAYFWGQSTQAQOHSRSHSKI SKHMTTPACPGPEPNW 2093
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 Db 2221 PSPGICLRRRAPSSDKPLASGPPDSMAASPSPKDVLSTGLSSDPADLDP 2273

RESULT 2
 US-09-398-522-52
 ; Sequence 52, Application US/09398522
 ; Patent No. 6783933
 ; GENERAL INFORMATION:
 ; APPLICANT: Issa, Jean-Pierre
 ; TITLE OF INVENTION: CA/CNAIG POLYNUCLEOTIDE POLYPEPTIDE AND
 ; METHODS OF USE THEREFOR
 ; FILE REFERENCE: JHUI1590
 ; CURRENT APPLICATION NUMBER: US/09/398,522
 ; CURRENT FILING DATE: 1999-09-15
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 52
 ; LENGTH: 1207
 ; TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel
US-09-398-522-52

Query Match
Best Local Similarity 53.1%; Score 6315.5; DB 4; Length 1207;
Matches 1207; Conservative 0; Mismatches 0; Indels 23; Gaps 1;

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QY 121 DDFIFAFVAVMVKMVALGFGKCYLGDFTWNLDFIIVAGMLEYSLDQNVFSAVR 180
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QY 241 CFLPENFSLVDLERYQYOTENEDSPFICQPRENMRSCRSVPTLRGDDGGGPPCGL 300
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QY 241 CFLPENFSLVDLERYQYOTENEDSPFICQPRENMRSCRSVPTLRGDDGGGPPCGL 300
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QY 301 DYAYNSSNTTCVNNQYVTCNSAGHNPKGAINFDNIGYAWIAFQVITLEGWVIM 360
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Db |||||
QY 361 YFVMDAHSFYNYFILLIIVGFFMNLCLVVIATQFSETKQESQLMREQVRFLSNA 420
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Db |||||
QY 421 STLASEPGSCYEELLKYLVIYILRKAARLAQVSRAGVRVGLLSPPALPGQETQPS 480
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QY 481 SCRSRRLSVHLVHHHHHHHHYHNGTLAPRASPEIQDRDANGSRRLMLPPSTP 540
Db |||||
QY 481 SCRSRRLSVHLVHHHHHHHHYHNGTLAPRASPEIQDRDANGSRRLMLPPSTP 540
Db |||||
QY 541 ALSGAPPGAESVHSFYHADCHLEPVRQAPPPRSPSEASGRVTGSGKVPVHTSPPE 600
Db |||||
QY 541 ALSGAPPGAESVHSFYHADCHLEPVRQAPPPRSPSEASGRVTGSGKVPVHTSPPE 600
Db |||||
QY 601 TLKEKALVEVAASSGPTLTSNIPPGYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660
Db |||||
QY 601 TLKEKALVEVAASSGPTLTSNIPPGYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660
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QY 661 ACGPSCPCARAGAVEVELADREMPDSEAVYFTQDAQSHDLRPHSRQSLGPPA 720
Db |||||
QY 661 ACGPSCPCARAGAVEVELADREMPDSEAVYFTQDAQSHDLRPHSRQSLGPPA 720
Db |||||
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Db |||||
QY 721 EPSSVLAFWRLICDTFRKIVDSKYFGIMIALVNLVLSMGIEYHEQPELNALEISNI 780
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QY 781 VFTSLFALEMLKLLVYGPFGYIKNPYINFDGVIIVSVWEIVGQGGSLVLRFLMR 840
Db |||||
QY 781 VFTSLFALEMLKLLVYGPFGYIKNPYINFDGVIIVSVWEIVGQGGSLVLRFLMR 840
Db |||||
QY 841 VLKVRFLPALORQVLVLMKTMNDVATFCMLMLFIFISILGMHLFGCKFASERDGT 900
Db |||||
QY 841 VLKVRFLPALORQVLVLMKTMNDVATFCMLMLFIFISILGMHLFGCKFASERDGT 900
Db |||||
QY 901 PDRKNFDSLLMAIVTVFOILTQEDWNKVLVNGMASTSSWAALYFTALMTFGNYVLNLLV 960
Db |||||
QY 901 PDRKNFDSLLMAIVTVFOILTQEDWNKVLVNGMASTSSWAALYFTALMTFGNYVLNLLV 960
Db |||||

QY 961 ALIVEGFOAEISKREDASGQSLQIPLVDSGGDANKSESEPFDFPSLDGDRKKCL 1020
Db |||||
QY 961 ALIVEGFOAEISKREDASGQSLQIPLVDSGGDANKSESEPFDFPSLDGDRKKCL 1020
Db |||||
QY 1021 ALVSLGEHPELRKSLPPLIHTAATPMSLPKSTGTGALGPASRRRTSSSGSAEPGAA 1080
Db |||||
QY 998 ALVSLGEHPELRKSLPPLIHTAATPMSLPKSTGTGALGPASRRRTSSSGSAEPGAA 1057
Db |||||
QY 1081 HEMKSPPSARSPHSPWSAASSWTSRRSRSLGRAPSLKRSPSGERRSLLSGEGQESQ 1140
Db |||||
QY 1058 HEMKSPPSARSPHSPWSAASSWTSRRSRSLGRAPSLKRSPSGERRSLLSGEGQESQ 1117
Db |||||
QY 1141 DEESSEERASPGSDHRRHSGSLERBAKSFDPDITLQVPLHRTASGRGSAESHQDN 1200
Db |||||
QY 1118 DEESSEERASPGSDHRRHSGSLERBAKSFDPDITLQVPLHRTASGRGSAESHQDN 1177
Db |||||
QY 1201 GKSASGRLARALRPDDPPLDGDADDGNNL 1230
Db |||||
QY 1178 GKSASGRLARALRPDDPPLDGDADDGNNL 1207
Db |||||

RESULT 3
US-08-984-709A-50
; Sequence 50, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,709A
; FILING DATE: 02-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 587-5360
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-984-709A-50

Query Match 52.2%; Score 6211; DB 3; Length 2353;
Best Local Similarity 56.6%; Pred. No. 0;
Matches 1365; Conservative 214; Mismatches 523; Indels 310; Gaps 60;
QY 7 GAGAEESQCP-RSPMRLNLSGAGRGPGSGAEKDPGSADEAGLPPYALAPVFFYLS 65

Db	27	GAGSPGAPGREAERSEL-GVSPSESP-AAERGAELGADEBQORVPYALAAVTFFCLG	84	Db	1053	LKMCSLAVTPNGHLEGRGSLSPPLIMCTAATMPPTKSPFFLDAAPSLPDRSSSSSGD	1112
Qy	66	QDSRPRSCWLCRTVCPNPFERISMLVILLNCVTLLGMPRCBEDIAQDSORCRLQAFDDIF	125	Qy	1076	EPGAAHEMKSPPSARSPHSPWGAASWTSRRSRNSLGRAPSLKRSPGSGERRSLISGE	1135
Db	85	QTRPRSCWLCRLVCNPFERISMLVILLNCVTLLGMPRCBEDIAQDSORCRLQAFDDIF	144	Db	1113	PP-LGQKPPASLRSPCAPWGPSCAMSSRRSSWSLGRAPSLKRQGCQGERESLLSGE	1170
Qy	126	AFTAVENWVKVALGIFGKCYLGDWTNRLLDFFVFIAGMLEYSLDLQVFSFVTRVUL	185	Qy	1136	QGSQDEEESSEERASPA-GSDHRRGSLEREAKSSFDPLDPL	1184
Db	145	APFAVENVKVALGIFGKCYLGDWTNRLLDFFVFIAGMLEYSLDLQVFSFVTRVUL	204	Db	1171	GKSTDDDE--AEDGRAAPGPRATPLRAESLDPRPLAPALPPTKCRDRGQVVALPSDF	1228
Qy	186	RPLRANRPSMRILVILLDTLPMGLNVLCCFVFIFIGVGVQVWAGLLNRKCELPE	245	Qy	1185	--RTASRGASASEHQCNGKSASGRALARALRPPDPLDGDADDDEGNLSKGRVRAWIRA	1242
Db	205	RPLRANRPSMRILVILLDTLPMGLNVLCCFVFIFIGVGVQVWAGLLNRKCELDS	264	Db	1229	FLRIDSREDAEALDDSDSCCLRLHKVLEPKP	1268
Qy	246	NFSPLSLVD-LERYQOTENEDSPICQPRENGMRSCSRVP---TLRGDGGGPPCGCLD	301	Qy	1243	RLPACYLERDSWASAYIFPPQSRFELLCHRIITHKMFHDHVLVIFILNCITITAMERPKLDP	1302
Db	265	AFVRNNNLTLFPPYQTEEGENFPICSSRRDNGMQCKSHIPGRREL	318	Db	1269	-----REANALYLFSPQNRFRVSCQVITHKMFHDHVLVIFILNCITITAMERPKLDP	1320
Qy	302	YEAYN-----SSNTTCVNMNYYTNCSEAGHNPFGKAINFDNIGYAWIAIQTIVILE	354	Qy	1303	HSABRIFLTLSNYIFTAVFLAEMTVKVVALGWCCEQAYLSSSNWNLGGLLVLSVIDIL	1362
Db	319	WEATQPAQEGVGAARNACINWQYINVCSDSNPHNGAINFDNIGYAWIAIQTIVILE	378	Db	1321	GSTERVFLSVSNYIFTAIFVAEMMVKVVALGSLGSHAYLOSSWNLGGLLVLSVIDIV	1380
Qy	355	GWVDIMYVMDAHSYNYFIYFILLIIVGSFFMINICLVVIATQFSETKQRESQLMREQV	414	Qy	1363	VSMYSDSTCTKILGMLRVLRLLRTPLRVISRAOGLKLVWETLMSLKPIGNIVVICAF	1422
Db	379	GWVDIMYVMDAHSYNYFIYFILLIIVGSFFMINICLVVIATQFSETKQRESQLMREORA	438	Db	1381	VAMASAGAKILGLVLRVLRLLRTPLRVISRAOGLKLVWETLMSLKPIGNIVVICAF	1440
Qy	415	RFLSNASTLASSEPGSCVEELLYVILIRKAARLAQVRAAGVRLGSLSSAPLGGQ	474	Qy	1423	FIIFGILGVQLFKGKFFVCOGEDTNTNKSDCBASVYRWVRHKYFNPNLGOALMSLVL	1482
Db	439	RHLNSDSTLASSEPGSCVEELLYVILIRKAARLAQVRAAGVRLGSLSSAPLGGQ	498	Db	1441	FIIFGILGVQLFKGKFFVCOGEDTNTNKSDCBASVYRWVRHKYFNPNLGOALMSLVL	1500
Qy	475	ETQPSSSCSRRH--LSVHVLV-HHHHHHHHHYHNGTLPAPRASPEIQDRDANGSREL	532	Qy	1483	ASKQGWDMVDGLDVGVDQOPIMNHNPMMLLYFISLLIVAFVFLNMVGVVYVENPHK	1542
Db	499	--GPHRQRRAGHTASVHVLVYHHHHHHHHYHSHGSPRPPGEPGACD-----TRVL	551	Db	1501	SSKQWNNIMVDGLDVGVDQOPIMNHNPMMLLYFISLLIVAFVFLNMVGVVYVENPHK	1560
Qy	533	MLPPSTPALSCAPGCAESVHSFYHADCHLE--PVRCAOPPRPSPSEASGR--TVGSGKV	589	Qy	1543	CEHQDEEAEARRERREKRLLEKKER-----KAQCKFYSDYSFRLLVHHLCTSHYLD	1596
Db	552	RAGAPSPSPSGRGGPDASVHSIYHADCHIEGPQERAVAAATAAASLALATGLTM	611	Db	1561	CEHQDEEAEARRERREKRLLEKKER-----KAQCKFYSDYSFRLLVHHLCTSHYLD	1620
Qy	590	--HTSP-----PPELTKKALVEVAASGSPPTLSLNPDPGY	629	Qy	1597	LFITGIVGINVVTMAHEHYQQOILDEALKINYITFVIFVLESVKLVAFGRFFQDR	1656
Db	612	NPTTILPSGVGSGKSTSGPKGWAGPPGT-----GGHGLSLNS-----PDY	657	Db	1621	LFITFICVNVITSMHEHYNQKSLDEALKINYITFVIFVLESVKLVAFGRFFQDR	1680
Qy	630	SMHKLLETQSTGACOS-----SKISPCCLKADSGAGGPDSCYCARA--GAGREVELA	681	Qy	1657	WNQDLAIVLLSINGITLLEIEVNASLPLNPTIIRIMVLRIRARVULKLMKMAVGRMALD	1716
Db	658	EKIPHVVGHEGLCAQPHLSGLSVPCPLPSP--PAGTLTCELKSCPCYCTRALEDPPGELS	715	Db	1681	WNQDLAIVLLSINGITLLEIEVNASLPLNPTIIRIMVLRIRARVULKLMKMAVGRMALD	1740
Qy	682	DREMPDSFAVVEFTQDAQHSDLRP-----HSRRQSLGPDABPSSV	725	Qy	1717	TYWQALPQVGNLGLLPMILFFIYFALGVLELFGDETHPCCEGLGRHATFNFGMAFLT	1776
Db	716	GSESGSDGSGVYEFQDVVRHGRWDFTRPPRAITDPFGPGSPQRAQOARAPGPGWM	775	Db	1741	TYWQALPQVGNLGLLPMILFFIYFALGVLELFGDETHPCCEGLGRHATFNFGMAFLT	1800
Qy	726	LAFWRLICDTRFKIVDSKYFGRGIMTALVNTLSMGIEYHEQPEELTNALEISNIVFTSL	785	Qy	1777	LFRVSTGDNWNGIMKDTLRDC-----DOESTCYNTVISPFIYFVSFVLTAQFVLNVNVTAVLM	1833
Db	776	GRLVVTPSGKLRIIVDSKYFSGIMMAILVNTLSMGIEYHEQPEELTNALEISNIVFTSM	835	Db	1801	LFRVSTGDNWNGIMKDTLRDC-----DOESTCYNTVISPFIYFVSFVLTAQFVLNVNVTAVLM	1860
Qy	786	FALEMLIKLVYGPFGVIRKPNYIFDGVIVVISWEIVGQGGGLSVLRFRMLRVULKV	845	Qy	1834	KLHEENKKEAEAEAELELEMLKTLSPQHPSPGLSPFLWPGVEGPDSP--DSPKPGA	1890
Db	836	FALEMLIKLVYGPFGVIRKPNYIFDGVIVVISWEIVGQGGGLSVLRFRMLRVULKV	895	Db	1861	KLHEENKKEAEAEAELELEMLKTLSPQHPSPGLSPFLWPGVEGPDSP--DSPKPGA	1899
Qy	846	RELALOROLVLMKTMNDVATFCLMLFIFIPISILGMHFGCKFASERD--GDTLPDRK	904	Qy	1891	LHPAAHARSASHFSLHPTMQPHFTLPG-----POLLTVRKSGVSRTHSLPNDOSYMRCHG	1946
Db	896	RFULALRQLVVLVKTMDNVATFCTLLMLFIFIPISILGMHFGCKFASERD--GDTLPDRK	955	Db	1900	-----PLQPSGARDAPNLV-ARKVSVSRMLSLPNDOSYMRCHG	1937
Qy	905	NFDSLLWAVTVFOILTQEDKNNKVLVNGMASTSSWAALYFALMTFGNYVFNLLVAILV	964	Qy	1947	STAGEP-----LHROWGLPKAOSGSLVSHSOPADTSYTLQPKDAPHLQPHSA	1997
Db	956	NFDSLLWAVTVFOILTQEDKNNKVLVNGMASTSSWAALYFALMTFGNYVFNLLVAILV	1015	Db	1938	VPASAPHRPLQEVEMETYGAGTP--LGSVASVHSPSPAESCASLQIP-----LAVSSPA	1989
Qy	965	EGFOABELSKEDASQGLSCQLPVDOSGGDANKSESEPPDFSPSLDGD-----GD	1015	Qy	1998	PTWGTIFKLPBPG--RSPLAQRPLRQAAIARTDSLDVQGLGSRREDLL--AEVSGSP--P	2051
Db	1016	EGFOAE-----GDNKSDTDEDKTSVHFEDFKHRELQTE	1052	Db	1990	RSGEPLHALPGRGTARSPLSRLLCRQEAHVHTDSLEK-IDSPRDTLDPAEPGEKTPVRP	2048
Qy	1016	RKCKLALVSLGHEPLRSLAPPLIHTAATPMSLPKSTGLGEALGPASRRSSSGSA	1075	Qy	2052	LARAYSWG--QSSSTQACQHSRSHSKISKMTTPAP--CPGPEPNWKGPPETRSLELDT	2108
Db				Qy	2049	VTQGSLSQSPRSPRPAVTRKHT-FQHCVCVSRPAAPGGE-----EAEASDPADPE	2099

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QY 2109 ELSWISDILLP-----PGQERPP-----SPRDLKCYVSAQSCORRPTSWLDEORHSI 2159
Db 2100 EVSHITSSACPMQPTAEPHGPEASVAGGERDLRLRLYSVDAQGLDKP-CRADEQWRPSA 2158
QY 2160 AVSCLDSGQPHLGTDPNSLGGPLGPGSRPKKLSPPSITIDPP-ESQPRTPPSP-- 2216
Db 2159 ELGSGFPGAKAWGE-----AEP--ALGARKKKMSPPCISVEPDAEDGSGARPSAAEG 2211
QY 2217 -GICLRRAPSSDSK-----DPLASGPPDSMAASPPKDVLSLGLS 2259
Db 2212 GSTTLRRRTSPCEATPHRESLPTGSGAGGDPAAKGERWQA---SCRAHLTVPSFAF 2268
QY 2260 DPADL-----DP 2266
Db 2269 EPLDLGVPSGDP 2280

RESULT 4
US-09-404-650-2
; Sequence 2, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-650-2

Query Match 46.1%; Score 5492.5; DB 3; Length 2175;
Best Local Similarity 51.3%; Pred. No. 0;
Matches 1233; Conservative 214; Mismatches 508; Indels 447; Gaps 55;

QY 31 RCPGSAEKOPGSADSABG-----LPYDALPVVFFYLSQDSRPSRWCRLRTVCNPFERI 86
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QY 87 SMLVILLNCVTLGMFRCEDIACDSORCILQAFDDFIFFAFFAVEMVVMVALGIFOKKC 146
Db 85 SMLVILLNCVTLGMYPQCDMDCLSDRCKILQVDFDFIFFFAMEMVLMKVALGIFGKCC 144
QY 147 YLGDWNRDLFFVIAGMLBYSLDLQNVFSAVRTVRLPLRPLRINRVPMSRILVTLID 206
Db 145 YLGDWNRDLFFVWAGMVEYSLDLQNLINLSAIRTVRVLPPLKALINRVPMSRILVNLID 204
QY 207 TLPMLGNVLLCFEVEFIFGIVGVQLWAGLLNRCHLPENFSLPSVLDLERYQTEDE 266
Db 205 TLPMLGNVLLCFEVEFIFGIIQVQLWAGLLNRCELEENFTIQGDVALPPYQPEEDDE 264
QY 267 SPFICSPQRENGMRSCRSVPTLRLGDCGGPPCGI-----DYEAYNSSNTT---CWNWQ 318
Db 265 MPFICSLGDMGIMGHEIPPLKEQ---GRECCLSKDDVYDFGAGQDLNASGLCVNWR 321
QY 319 YTYNCSAGEHNPFGKAINFDNIGYAMIAFQVITLLEGWVDIMYFVMDAHSFYNYFIYILL 378
Db 322 YYNVCRGTSANPHKGAINDNIGYAMIVFQVITLLEGWEIMYVMDAHSFYNYFIYILL 381
QY 379 IIVGSEFMNLCLVVIATQFSETKQRESOLMBRQVRFLPSNASTLASFSGPSCYBEELK 438
Db 382 IIVGSEFMNLCLVVIATQFSETKQREHRLMLEQRQYLS--SSTVASYAEPPGDCYEEIFQ 440
QY 439 YLVYILRKARLQAQVSRAGVRVGLLSSPAPLGQETQPSSSCSRSHRLSVHHLVHHH 498
Db 441 YVCHILRKAKR-----RALGYQALQSRQALG----- 468
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Db 469 -----PEAPA--PAKPGP-----H 480
QY 559 ADCHLEPVCQAPPPRSPSEASGRVTGSGKVVTVHTSPPTLKEKALVEVAASGPPT 618
Db 481 AK---EPRHYQLCPQHSPLDAPHTL-----VQIPATL----- 511
QY 619 LTSNLPPPGPYSMHKLLETQSTGACQSCSKLSSPCLKADSGACGPDSPCYCAR----- 672
Db 512 -----ASDPASCPCCQHEGRRP 529
QY 673 AGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRRQRSLGSDAPSSVL----- 726
Db 530 SGLGSTD-SGQSGSGSSAGGE--DEADGDGARSEDCASSELKEEEREEQAQAVWL 586
QY 727 --AFWRLICDTFRKIVDSKYFORGIMIALVNTLSMGIEYHEQPELTNALSINIVFTS 784
Db 587 CGDVWRETRAKLRGIVDSKYFNRGIMMALLVNTVSMGIEHHEQPELTNILEICNVFTS 646
QY 785 LFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQCGGLSVLFRFLMRVLKL 844
Db 647 MFALEMLLKLAAGLFDYLRNPYNIFDSIIVISIWEIVGQADGGLSVLFRFLRLVLKL 706
QY 845 VRFLPALQRLVLMKTMNDNVATFCMLMLFIFIPISILGMHLFGCKFASERD-GDTLPDR 903
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QY 964 VEGFQABEISKREDASQSLCQLPVDSCQGDANKSESEDPFFSPS-----LDGD 1013
Db 827 VEGFQAB-----GDANRSYDEDEQSSNTEEFKLOEGLDSS 863
QY 1014 GDRKKCALVSLGEBHELRLKSLPLLIHTAATPMSLPKSTSTGLGALGPASRT----- 1069
Db 864 GDPKLCPIPTNGH-----LDP-----SLPLGGHLGPAGAAGPAPRLSLQPD 906
QY 1070 -----SSGSAEPGAHEMKSPSARSSPHSPWSAASMTSRSSRNSLGRAPSLK 1120
Db 907 PMLVALGSRKSSVMSLGRMSYDQSLSSSRSSYYGPMGRSAAWASRSSWN-----SLK 960
QY 1121 RRSFSGERRLLSGE--GOESODEESSEE--ERASPAGSDH-----RHRG 1162
Db 961 HKPSPAEHESLLSAERGGARVCEVADEGPPRAAPLHTPHAHHHHGHPLAHRHRHR 1020
QY 1163 SLREKAKSPDLPTTLQVPLGHRHTASGR--GSASEHQDCNCKSASGRALARALRPPDPLD 1220
Db 1021 TSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAGHEDCNGRMPSTAKVFTKMGDRGR 1080
QY 1221 GDDADDEGNLSKGERVRAMTRAPLPCYLERSWSAYIFPPQSRFRLLCRRITTHKMFH 1280
Db 1081 GED--EEEDYTLCFRVRKMDVYKPDWCVEVDMSVLYFSPENRFRVLCOITIAHKLFDY 1139
QY 1281 VVLVIFLNCITITAMERPKNIDPHSABRIELTLSNYIFTAVFLAEMTVKVALGWCGBQA 1340
Db 1140 VVLAFLFNCITIALERPQIEAGSTERIFLTSNYIFTAVFVGMETLKVLSGLYFGEA 1199
QY 1341 YLRSSWNLDDGLLVLSIDILVMSVSDSGTILGMLRVLRLLRTPURVLSRAQGLKL 1400
Db 1200 YLRSSWNLDDGLVFNVSIIIDIVVLSASAGAKILGVLRVLRLLRTPURVLSRAQGLKL 1259
QY 1401 VVETLMSLKPICNIVITWCAPFIIFGILGVOLFPGKPFVCOGEDTRNTKSDCAEAS 1460
Db 1260 VVETLMSLKPICNIVITWCAPFIIFGILGVOLFPGKPFVCHLVGVDTRNTKSDCAEAS 1319
QY 1461 RVWRHKYNFNDLGOALMSLFLVLSKDGWVDIMYDGLDVGVDQOQPMHNPWMLLYFISF 1520
Db 1320 RVWVKHYNFNDLGOALMSLFLVLSKDGWVNIMYNGLDVAVDQOQVPTNHNPMWMLLYFISF 1379
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1521 LLIVAFVILNMFVGVVVENFHKCHQHOEEAEARRERKRLRLLEKKRKAQCKPYYSYS 1580
1380 LLIVSFVILNMFVGVVVENFHKCHQHOEEAEARRERKRLRLLEKKRKAQRLPYATYC 1439
1581 RFRLLVHLCTSHYLDLFTITGVIGLVNVTWAMEHYQQPQILDEALKCNVIFTVIFVLES 1640
1440 HTRLLIHSMTCTSHYLDLFTITGVIGLVNVTWAMEHYQQPQILDEALKCNVIFTVIFVLES 1499
1641 VFKLVAQFRFRFODRNQOLDLAILLSIMGITLLEIEFNASLPINPTIIRIMVRLIAR 1700
1500 VKLIVAFGLRFRFODRNQOLDLAILLSIMGITLLEIEFNASLPINPTIIRIMVRLIAR 1559
1701 VLKLLKAVGMRALLDTVMQALPOVGNLGLLPMLLFFIFALGVLELFGDLCEDETHPCGE 1760
1560 VLKLLKAVGMRALLDTVMQALPOVGNLGLLPMLLFFIFALGVLELFGDLCEDETHPCGE 1619
1761 LGRHATFRFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV 1817
1620 MSRHAFFENFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV 1679
1818 LTAQFVLNVVAVLVMKHLFEENKEAKEAEAELELEM-KTLPQPHSLPGSPFLWPG 1876
1680 LTAQFVLNVVAVLVMKHLFEENKEAKEAEAELELEM-KTLPQPHSLPGSPFLWPG 1738
1877 VEGPDSPD-----SPKPGAL-----HPAHA----- 1897
1739 -RGPAGAGGGDEGGLCRRCYSQAQDSLEGELTIIDNLSGSIFFHYSSPAGCKKHDK 1797
1898 -----RSAS-----HFSLEHTMQP-----HPTLPGLDILLTVRKS-- 1929
1798 QEVQLAETAFAFNSDRSSILLGDDLSLEDPTACPPCKDKSGELDPPEPMRVGDLGEC 1857
1930 ---VSRTHSLN-DSYMRHGSTAEGPLHGRWGLPKAQSGLSVSHSQPADTSYLQLP 1985
1858 FPLLSSTAVSPDENFLCENEEIPFPV-RSW-LKHDSSQAPPSPFPDASSPLPMP 1913
1986 KDAPH-----LLOPHSAPTWTGTPKLPDG-----RSLAQRPLRQAIRTSLDVOG 2034
1914 AEFHPAIVASQKGEKGTGTGLPKIALQGSWASLRSRVNCTLLRQATGTSLSLD--- 1970
2035 LGSREDLLAEVSGPPLARAYSFWGOSTQAQCHSRSHSKISKHMTTPPAPCPGFENWG 2094
1971 -----AGPSSAGSLQTTLEDLSLUSPRA-----LGPPAPAGPRAGLS 2012
2095 KGPETRSLELDTLSWISGDLPLPGQOEPPSPDLKXCYVSAOSCORRTSWLDEQ 2154
2013 ---PAARRLSL-----RGRGLFSLRGLRA-----HQ 2036
2155 RHHSIAYCLDSGQPHLGTDPN---LGGPLGGPSRPPKLSPPSIT---IDPPESQ 2208
2037 RSHSGGS-TSPGCTHDSMDPSDEGRGGAGGAGGSEHSETLSSLSLTSFCPPP--- 2092
2209 GPRTPSPGICLRRAPESSDS---KDLASGPPDSMAASPPSKKDLVLSLGLSSDPADL 2264
2093 ---PPAPGLTPARKFSTSSLAAPGRPHAAALHGLARSFSAAD-----RSKDPGR 2143
2265 DP 2266
2144 AP 2145
RESULT 5
US-09-935-541-2
; Sequence 2, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGovern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23

PRIOR APPLICATION NUMBER: 09/404,650
PRIOR FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2175
TYPE: PRN
ORGANISM: Homo sapiens
US-09-935-541-2

Query Match 45.1%; Score 5492.5; DB 4; Length 2175;
Best Local Similarity 51.3%; Pred. No. 0;
Matches 1233; Conservative 214; Mismatches 508; Indels 447; Gaps 55;

QY 31 RPGSGSAEKDPSADSEAEAG-----LPYPALAPVVFYFYLQSQRSPRSWGLRTVCNPNWPERI 86
DB 25 QGFRSPSSPPGLEPLDGDAPHPHDLAPIAFFCLRTQTTSPRNWCIMKVCNPFECV 84
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DB 85 SMLVILLNCVILGMPCEDDMDCLSDRCKILQVDFDIFIFFAMEMVLKVALGIFGKCC 144
QY 147 YLGDFTWNRLLDPTVIAGLMLEYSLDQNVSFSAVRTVRVLRPLRAINRVPSMRILVLLD 206
DB 145 YLGDFTWNRLLDPTVIWAGWEVSLDQNLNSAIRTVRVLRLPLKAINRVPSMRILVLLD 204
QY 207 TLPMLGNVLLLCFFVFFIFGVGVOLWAGLLNRNCFELPENFSLPLVDLERYVOTENEDE 266
DB 205 TLPMLGNVLLLCFFVFFIFGVGVOLWAGLLNRNCFELPENFTIQGVVALFPYYPQEDDE 264
QY 267 SPFICSQPRENGMRSCRSVPTLRGGGGGPPCGL-----DYEAYNSSNTT--CYNMNO 318
DB 265 MPFICSLSDGNGIMGCHIEPPIKEQ---GRECLSKDDVYDFGAGQDLNAGSLCYNMNR 321
QY 319 YVYVNCAGEHNPFGKAINFDNIGYAMIAIFQVITLEGWVDIMYFVMDAHSFYNYFIYILL 378
DB 322 YVYVNCAGEHNPFGKAINFDNIGYAMIAIFQVITLEGWVEIMYVMDAHSFYNYFIYILL 381
QY 379 IIVGSFPMINCLVVIATQFSETKQRESQLMRQVRFLSNASTLASFSFSGCYBELLK 438
DB 382 IIVGSFPMINCLVVIATQFSETKQREHRLMLRQRYLS--SSTVASYAPGDCYBEIFQ 440
QY 439 YLVYILKRAARLAQVSRAGVGLLSSPAPLGGQGTQPSSSCSRSHRLSVHHLVHHH 498
DB 441 YVCHILKRAK-----RALGLYQALQSRQALG----- 468
QY 499 HHHHHVHLNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPAGSASVHSFYH 558
DB 469 -----PEAPA--PAKPGP-----H 480
QY 559 ADCHLEPVRQAPPPSPSEASGRVTGSKYVTVVHTSPPPETLKEKALVEVAASSGPPT 618
DB 481 AK---EPHYQLCFQHSPLDATPHTL-----VQPIPATL----- 511
QY 619 LTSNIPPGPYSSMEKLELTQSTGACQSSCKISSPCLKADSGACGPPSCPYCAR----- 672
DB 512 -----ASDPASCPCCQEDGRPP 529
QY 673 AGAGEVELADREMPDSDSEAVYEFQDAHQHSDLRDPSRRORSRSGDPAEPSVL----- 726
DB 530 SGLGSTD-SGQEGSGSGSSAGGE--DEADGDGARSSEDGASSELGKEEEDQADGAVML 586
QY 727 --AFWRLLCDTFRKIVDSKYFGRGIMAILVNTLSMGTEYHEOPELTNALRISNIVFTS 784
DB 587 CGDVWRETRAKLRGIVDSKYFNIRGIMAILVNTSMGTEHHEQPELTNILEICNVVFTS 646
QY 785 LFALEMLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQGGSLVLRFRMLRVKL 844
DB 647 MFALMILKLAARGLFDYRPNYINFDISIIVISWEIVGQADGSLVLRFRMLRVKL 706
QY 845 VRFLPALORQLVLMKTMNVATFCMLMLFIFISILGMHFGCKFASERD-GDTLPDR 903
DB 707 VRFMPALRQLVLMKTMNVATFCMLMLFIFISILGMHFGCKFASERD-GDTLPDR 766

QY	267	SPFICSPRENGMRSRVPTLRGDDGGGPPCGL-----DYEAYNSSNTT--CVNWNQ	318	Db	1140	VWLAFLNLCITIALERPOEAGSTERIFUTSVNYIFTAIFVGMTLKVVSGLYFGEQA	1199
Db	265	MPFICSLSGDNGMGCHIEPLKEQ--GRECCLSKDDVYDFGAGRODLNAGLVCVNWR	321	QY	1341	YLRSSWNVLDGLVLIIVSIDILVMSVSDSGTKILGMLRLVRLLELTPLRLPRVISRAQGLKL	1400
QY	319	YYTNCAGEHPFGAINFDNIGYAWIAI FOVITILEGWNVDIMYFMDAHSFYNYFILL	378	Db	1200	YLRSSWNVLDGLVLIIVSIDILVMSVSDSGTKILGMLRLVRLLELTPLRLPRVISRAQGLKL	1259
Db	322	YYNVCRTGSANPHGAINFDNIGYAWIAI FOVITILEGWNVDIMYFMDAHSFYNYFILL	381	QY	1401	VWETLMSLKEPIGNIVVICCAFFIIFGILGVOLFKGPFVFCQGEDTRNITKNSDCABASY	1460
QY	379	LIIVGFFMINCLVVIATQFSETKQREORVRELSNASTLASFSFGSCYEEELK	438	Db	1360	VWETLMSLKEPIGNIVVICCAFFIIFGILGVOLFKGPFVFCQGEDTRNITKNSDCABASY	1319
Db	382	LIIVGFFMINCLVVIATQFSETKQREORVRELSNASTLASFSFGSCYEEELK	440	QY	1461	RWVRHKYNFDMGOALMSLFLVASKDQGVDMYDGLDAGVDQOPIMHNHFWMLLYFISF	1520
QY	439	YLVILRKARRLAQSRAAGVVRVGLLSAPLGGQETQPSSSCSRSHRLSVHHLVHH	498	Db	1320	RWVRHKYNFDMGOALMSLFLVASKDQGVDMYDGLDAGVDQOPIMHNHFWMLLYFISF	1379
Db	441	YVCHILRAXR-----RALGLYQALQSRQALG-----	468	QY	1521	LLIVAFFVLNMFVGVVVENFHKCHQHOBEERREXRLRLEKRRKRAQCKPYYSYS	1580
QY	499	HHHHHHYHLNGTLPAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYH	558	Db	1380	LLIVAFFVLNMFVGVVVENFHKCHQHOBEERREXRLRLEKRRKRAQCKPYYSYS	1439
Db	469	-----PEAPA--PAKEGP-----H	480	QY	1581	RFRLVHLCTSHYLDLFTITGVIGLVNVTMAHEHYQQOILDEALKI CNYITFTVIFVLES	1640
QY	559	ADCHLEPVRQCAPPSPSEASGRIVGSKVYPTVHTSPPTLKEKALVEVAASGPPT	618	Db	1440	HTRLIHSMTCTSHYLDLFTITGVIGLVNVTMAHEHYQQOILDEALKI CNYITFTVIFVLES	1499
Db	481	AX--EPRHYQLCPQHSPLDAPHTL-----VQIPATL-----	511	QY	1641	VPKUVAFFRRFQDRWNQDLAIIVLSIMGITLEEIEVNASLNPINPTIIRMRVLIAR	1700
QY	619	LTSINIPGPYSMMKILLETQSGACQSSCKISSPCLKADSGACGDCPCYCAR-----	672	Db	1500	VKLVAFLGRFFKDRWNQDLAIIVLSIMGITLEEIEVNASLNPINPTIIRMRVLIAR	1559
Db	512	-----ASDPASCPCQHEHGRPP-----	529	QY	1701	VKLKLMKMAVGRALLDVTVMQALPOVGNLGLLPMLLFFIPAAALGVLFGLDETHPCBG	1760
QY	673	AGAGEVELADREMPDSSEAVVEFTQDAQHSDLRDPHSRRQRSLGPDARFSSVL-----	726	Db	1560	VKLKLMKMAVGRALLDVTVMQALPOVGNLGLLPMLLFFIPAAALGVLFGLDETHPCBG	1619
Db	530	SGLGSTD--SGQEGSGSGSAGGE--DEADGDGARSSEDCASSSELGKEEBEESQADGAVML	586	QY	1761	LGRHATFRNFGMAFTLPRVSTGDNWNGIMKOTLDDC--DOESTCYNV--ISPIYFVSFV	1817
QY	727	--AFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEBLTHALEISNIVFTS	784	Db	1620	MSRHATFRNFGMAFTLPRVSTGDNWNGIMKOTLDDC--DOESTCYNV--ISPIYFVSFV	1679
Db	587	CGDWEETRKLGRIVDSKYFNKGIMAILVNTLSMGIEYHEQPEBLTHALEISNIVFTS	646	QY	1818	LTAQFVLNVAIVLIMKLEESNKAKEAEAEAELEEM--KTLSPQHPSPGSPPLWPG	1876
QY	785	LFPALEMLLKVTVPGFYIKPNYINIDGIVLVSWEIYVQOQGLSVLRTPLRMVLKL	844	Db	1680	LTAQFVLNVAIVLIMKLEESNKAKEAEAEAELEEM--KTLSPQHPSPGSPPLWPG	1738
Db	647	MFPALEMLLKVTVPGFYIKPNYINIDGIVLVSWEIYVQOQGLSVLRTPLRMVLKL	706	QY	1877	VEGPD-----SP-----DSPKPGALH--	1892
QY	845	VRELPALQRLVLMKMDNVAFVFCMLLMFIFISILGMHFLGCKPFASERD--GDTLPDR	903	Db	1739	RGPGGAGGGDTEGGLCRRCYSPAQENLWLDVSLIIDSLEGELTIIDNLSGSIFFHY	1797
Db	707	VREMPALRRLQVLMKMDNVAFVFCMLLMFIFISILGMHFLGCKPFASERD--GDTLPDR	766	QY	1893	RGPGGAGGGDTEGGLCRRCYSPAQENLWLDVSLIIDSLEGELTIIDNLSGSIFFHY	1918
QY	904	KNFDSLLWAIIVFQILTOBDMNKVLVNGMASTSSWAAALYFIALMTPGNVVLNLAAIL	963	Db	1798	SSPAGCKCHDKQEVQVLAETAEAFSLNSDRSSSILIGDILSLEDPTACPPGRKDSKGLD	1857
Db	767	KNFDSLLWAIIVFQILTOBDMNKVLVNGMASTSSWAAALYFIALMTPGNVVLNLAAIL	826	QY	1919	GPOLLTVRKSG-----VSRTHSLPN--DSVMCRHGSTAEGPLGHRGWSLQSGSVLSVH	1972
QY	964	VEGFAQEEISKREDASQLSCIQLPVDQSGDANKSESEDPFSPS-----LDGD	1013	Db	1858	PPFPMRVDLGECEFFPLSSTAVSPDENFCEMBEETPFNV--RSM--LKHDSQAAPPSP	1913
Db	827	VEGFAQEEISKREDASQLSCIQLPVDQSGDANKSESEDPFSPS-----LDGD	863	QY	1973	SQADTSYIILQPKDAPH-----LQPHSAPTWTGIPKLPDPG-----RSLAQRPLRR	2021
QY	1014	GDRKKCLALVSLGHPBLRSLPLLIHTAATPMSLPKSTSTGLGHALGPASRRT-----	1069	Db	1914	FSPDASPLPMPAEFFHPAVSASQKGEKGTGTGLPKIALQGSWASLSPRVNCTLLR	1973
Db	864	GDPKLCIPMTPNH-----LDP-----SLPLGHLGPAGAAGPAPRLSLQPD	906	QY	2022	QAARTDSLVOGLGSRREDLLAEVSGSPPLAARAYSFWGSSSTOAOQHSRSHSKIXHMT	2081
QY	1070	-----SSSGAEPGAHEMKSPSPASRSPHSPWASASSWTSRSSRNSLGRASLX	1120	Db	1974	QATGSDTSLD-----ASESSAGSLQTTLEDLSLTUSDSPRA-----IG	2012
Db	907	PMLVALGSRKSSVMSLGRMSYDQSLSSRSYTGPMGRSAAMASRRSSWN-----SLK	960	QY	2082	PPAPCPGPEPNWKGKPPETRSSLSLEDTLWISGDLPLPGQEBEPFPRDIKKCYSVRAQ	2141
QY	1121	RRSPSGERSLISGE--GOESODEESSEE--ERASPAQSDH-----RRHG	1162	Db	2013	PPAPCPGPEPNWKGKPPETRSSLSLEDTLWISGDLPLPGQEBEPFPRDIKKCYSVRAQ	2047
Db	961	HKPPSAEHESLSAERGGGARVCEVADEGPPRAAPLHTPHAHIIHGHPLAHRHHR	1020	QY	2142	SCORRPTSWLDEQRHRSIAVSCLDGSGQPHLGTDPN-----LGGQPLGPGSRPKKLSP	2198
QY	1163	SLEREAKSFDLPOTLQVGLHRTASGR--GSASEHQCNCNKSASGRILARLDRDDPLD	1220	Db	2048	-----HQRSHSGGS--TSPGCTHDSMDPSDEEGRGAGGAGGAGSEHETLSSL	2095
Db	1021	TLSLDRSVDLAELVPAVGAHPRAAWRAAGPAPGHEDCNGRMFSAIAKDVFTKMGDRGR	1080	QY	2199	SIT---IDPPESQGPRTFPPSGICLRRAPSSDS-----KOPLASGPPDMSMAASPKKDV	2251
QY	1221	GDDADDEGNLSKGERVRAWIRAPLACVLERDSWASYIFPPQSRPLAHLIHTHMFTH	1280	Db	2096	SLTSLFCFPP-----PPAPGLTFAKRSSTSSLAAPGRPHAAALAHGLARSWARD--	2148
Db	1081	GED--BEEDYTLCTFRVRKMDIVYKPDWCVEVDNSVFLFSPENRFRVLICQIIIAKJFY	1139	QY	2252	LSLSGLSDRADLDP	2266
QY	1281	VVLVIFLNCITIAERPKIDPHSAERIFLTLNYSIFTAVFLAEMTVKVVALGWCFCGSA	1340				

Db	2149	-----RSKDPGGRAP 2158	
RESULT 7			
US-09-935-541-4			
; Sequence 4, Application US/09935541			
; Patent No. 6589787			
; GENERAL INFORMATION:			
; APPLICANT: Dietrich, Paul S.			
; APPLICANT: McGivern, Joseph G.			
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;			
; FILE REFERENCE: R0043B-REG sequence listing			
; CURRENT APPLICATION NUMBER: US/09/935,541			
; PRIOR FILING DATE: 2001-08-23			
; PRIOR APPLICATION NUMBER: 09/404,650			
; PRIOR FILING DATE: 1999-09-23			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 4			
; LENGTH: 2188			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-935-541-4			
Query Match 46.1%; Score 5484; DB 4; Length 2188;			
Best Local Similarity 51.1%; Pred. No. 0;			
Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;			
Qy	31	RPGSGSAEKDGSADSEAG-----LPYPALAPVVFYLSQDSRPSWCLRTVCNPFERI 86	
Db	25	QPGFSPSSPPGEEPLDGDADPHVPHDLAPIAFFCLRTTSPRNWCIMKVCNPFECV 84	
Qy	87	SMVLILLNCVTLGMFRPCEDIACDSORCKILQAPDDETFAPFAVEMVVMVAGLFGKCC 146	
Db	85	SMVLILLNCVTLGMVQPCDDMDCLSDCKILQVDDFIFFAMEMVLMVAGLFGKCC 144	
Qy	147	YLGDTWRLDFFVIAGLMVSLDQNVSFSAVRVRLRLRAINRVPSRIILVTLID 206	
Db	145	YLGDTWRLDFFVIWAGVVEYSLDQNLINLSAIRTVRVRLKAINRVPSRIILVTLID 204	
Qy	207	TLPLMGNVLLCFVFEFTFGVQLWAGLNRFCFIPENSLPLVDLERYOTENEDE 266	
Db	205	TLPLMGNVLLCFVFEFTFGVQLWAGLNRFCFLEENFTIQDVALPPIYQDEEDE 264	
Qy	267	SPFICSQPRENGMRSRCSVPTLRDGGGPPCGL-----DYEAYNSSNTT--CVANNQ 318	
Db	265	MPFICSLSGDNGIMGCHIEIPLKEQ---GRECCLSKDDVDYDFGAGRODLNASGLCVNNR 321	
Qy	319	YVNCVCSAGEHNPFGKAINFNIGNIYAWIAIFQVITLEGWVDIMYFVMDAHSFYNIYFILL 378	
Db	322	YVNCVCSAGEHNPFGKAINFNIGNIYAWIAIFQVITLEGWVEIMYVMDAHSFYNIYFILL 381	
Qy	379	IIVGSEFMNLCVLVATQFSEKQESQMLRQRVRLFNASTLASFPSPGSCYBELLK 438	
Db	382	IIVGSEFMNLCVLVATQFSEKQESQMLRQRVRLFNASTLASFPSPGSCYBELLK 440	
Qy	439	YLVIILKARLRQAQVSRAGVRVGLLSAPALGGQGTQPSSCSRSHRLSVHHLVHHH 498	
Db	441	YVCHILRKAKR-----RALGLVQAQSRQAUG----- 468	
Qy	499	HHHHHHVHLNGTLRAPRASPEIQDRDANGSRRLMLPPPTPALSGAPPGAESVHSFYH 558	
Db	469	-----PEAPA--PAKGP-----H 480	
Qy	559	ADCHLPPVRCQAPPSPSEASRTVSGKVPTVHTSPPTLKEKALVEVAASGPPT 618	
Db	481	AK--BPRHYQLCPQSPDLATPHL-----VQPIPAL----- 511	
Qy	619	LTSNLNPPGPPYSMMHKLLETQSTGAQCSCKISSPCGLKADSGCGPDSCEYCAR----- 672	
Db	512	-----ASDPASCPCCQHDGRRP 529	
Qy	673	AGAGEVELADREMPDSDSEAVYFTQDAQHSRLDRPHSRQRSLGPADEPSSYL----- 726	
Db	530	SGLGSTD--SQEGSGSGSSAGGE--DEADGDGARSSEDGASSSELKEEEEEEQADGAVML 586	
Qy	727	--AFWELICDTPRKIVDSKYFGSGMIALVNTLSMGIYHPOBELTVALEISNVTFTS 784	
Db	587	CGDVWRETRAKLRGIVDSKYFNRMALVNTVSMGIHHEQPEBELTILNCVFTS 646	
Qy	785	LPFALEMLKLIVYGPFGYIKNPNYINFDGVIIVISVWEIVGQGGGLSVLTRLMRVLK 844	
Db	647	MEALEMLKLAAFGGLFDYLRNPNYINFDIIVISVWEIVGQGGGLSVLTRLMRVLK 706	
Qy	845	VRELPALQRLVLMKMDNVATFCMLLMFIFISILGMHILFGCKFASERD--GDTLPDR 903	
Db	707	VREMPALRRQLVLMKMDNVATFCMLLMFIFISILGMHILFGCKFSLRTDGTVPDR 766	
Qy	904	KNFDSLLWAIIVTFQILLTQEDMKNVLYNGMASTSSKAAALFYALMTFGNYVLPNLLVAIL 963	
Db	767	KNFDSLLWAIIVTFQILLTQEDMKNVLYNGMASTSPWASLYFVALMTFGNYVLPNLLVAIL 826	
Qy	964	VEGFOAEIRISKREDASGQLSCIQLPVDQGGDANKSEPPDFSPS-----LDGD 1013	
Db	827	VEGFOAE-----GDANRSYSDSDQSSNIIEFQKQLQGLDGS 863	
Qy	1014	GDRKKCLALVSLGHEPRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRT---- 1069	
Db	864	GDPKLCIPIMTPNGH-----LDP-----SLPLGHLGPAAGAAGAPAPRLSLQPD 906	
Qy	1070	-----SSSGSAEPGAAHEMKSPPSARSPHSPSAASSWTSRRSRSLGRAPSLK 1120	
Db	907	PMVALGSRKSVMSLGRMSYDQRLSSRSYSGPWGRSAAMASRSMWN-----SLK 960	
Qy	1121	RRSPGERRSLSGE--GOESQDEEESBEE--ERASPAQSDH-----RRHG 1162	
Db	961	HKPSEAEHSLSAERGARGARCEVADEGPRAAPLHTPAHHIHHGPHLAHRHRRH 1020	
Qy	1163	SLREAKSSPDLPTLQVPGHRTASGR--GSASEHODCKGKSASGLARALRDPDPLD 1220	
Db	1021	TLSDNDSDVDLAEVPAVGAHPRAAAGAPAGHEDCNGRMPSIAKVFTKMGDRGR 1080	
Qy	1221	GDDADDGSLKSGRVRARLPAACVLRDSASVIFPQSFRLCHRIITHKMFHD 1280	
Db	1081	GED--BEIDYTLCFVRKMDIVTKPDWCEVREDSVYLFSPENRFRVLCQTIHAKLF 1139	
Qy	1281	VVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVLAEMTVKVALGWCFOEA 1340	
Db	1140	VLAFLPNCITIALBRPQIEAGSTERIFLTVSNYIFTAIFVGMETLKVSLGLYFGEQA 1199	
Qy	1341	YLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMRLVRLRLTLRPLRVIISRAQGLK 1400	
Db	1200	YLRSSWNVLDGLLVLSVIDIVVSLASAGAKILGLVRLRLTLRPLRVIISRAQGLK 1259	
Qy	1401	VVETLMSLLKPIGNIVVICCAFFIIFGILGVQFKGFFVCGEDTNTINKSDCAEAS 1460	
Db	1260	VVETLMSLLKPIGNIVVICCAFFIIFGILGVQFKGFFVCGEDTNTINKSDCAEAS 1319	
Qy	1461	RWRHKNYFNDNLQALMSLVFLASKDQWVDIMYDGLDAVGDQOQPMNHNPMMLLVFISF 1520	
Db	1320	RWVHKNYFNDNLQALMSLVFLASKDQWVIMYDGLDAVGDQOQPMNHNPMMLLVFISF 1379	
Qy	1521	LLIIVAEFLVMFVGVVVENFHCRQHQEBEAREERREKRLRLLEKXKRAQCKPYYS 1580	
Db	1380	LLIIVAEFLVMFVGVVVENFHCRQHQEBEAREERREKRLRLLEKXKRAQCKPYYS 1439	
Qy	1581	REFRLVHLLCTSHYLDLFTITVGLNVVTMAHEVQOQPIIDLEALKICNYIFTVIFVLS 1640	
Db	1440	HTRLLHSMCTSHYLDLFTITVGLNVVTMAHEVQOQPIIDLEALKICNYIFTVIFVLS 1499	
Qy	1641	VFKLVAFGFRFQDRWNQDLAIIVLLSIMGITLBEIEVNASLPIPTIIRMRVLRAR 1700	
Db	1500	VFKLVAFGFRFQDRWNQDLAIIVLLSIMGITLBEIEVNASLPIPTIIRMRVLRAR 1559	
Qy	1701	VFKLVAFGFRFQDRWNQDLAIIVLLSIMGITLBEIEVNASLPIPTIIRMRVLRAR 1760	

Db	1560	VLKLMATGRRALLDVTQVLPQVGNLGLFLLFFIYAALGWFELFKLVNDENPCG	1619	Db	19	GITEQPPRPPPPPPGLEBFELEGTDVPHDPDAPVAFCLRTTSPRNWCIKVCNPNW	78
Qy	1761	LGRHATFNCFMFLTLFRVSTGDNWNGIMKDTLRDC--DOBSTCVNTV--ISPIYFVSFV	1817	Qy	83	PERISMLVILNCVTLTGMFERCEDIACDSORCIRLOAFDDIFAFFAFVEMVVKVWLGIF	142
Db	1620	MSRHATFNCFMFLTLFQVSTGDNWNGIMKDTLRDCTHDSRCLSSIQFVSFLYVSFV	1679	Db	79	FECVSMVILNCVTLTGMFYQCDMECLSDCKILQVDFDIFIFFAFVEMVVKVWLGIF	138
Qy	1818	LTAQFVLNVVVIAMVLMKHEESNKEABEAELEALEM--KTLSQPHSPLGSPFLWPG	1876	Qy	143	GKKCYLGDWNRDLFFIYIAGMLYSLDLQNVFSASVTVTVLRLPRAINRVPSMRLVY	202
Db	1680	LTAQFVLNVVVIAMVLMKHEESNKEABEAELEALEM--KTLSQPHSPLGSPFLWPG	1738	Db	139	GKKCYLGDWNRDLFFIYIAGMLYSLDLQNVFSASVTVTVLRLPRAINRVPSMRLVY	198
Qy	1877	VEGPD-----SP-----DGPKCALH--	1892	Qy	203	LLDTLPMGLNVLLCFVFFIFGIYVGMAGLNRCELPENFSLPLSDVLEBYOTE	262
Db	1739	RGPGAGGGDTEGLCCRCYCSPAQENMLDVSLLIKDSLEGELTIIDNLGSGIFHHY	1797	Db	199	LLDTLPMGLNVLLCFVFFIFGIYVGMAGLNRCELPENFSLPLSDVLEBYOTE	258
Qy	1893	RAA-----HARSAS-----HFSLEHPTMQP-----HPTLTP	1918	Qy	263	NEDSPETCSOPRENGMSSCRSVPTLRGDDGGGPPCGL-----DYEAYNSSNTT--CV	314
Db	1798	SPAGCKKHDKQEVQVLAETAFSLNGDRSSILLGDDLSLEDTACPPGGRKDSKGLD	1857	Db	259	EDDEPFICSTGDNINGMGCHIEIPPLKSEQ--GRECCLSKODVDYDFGAGRQDLNAGLCV	315
Qy	1919	GPDLITVRKSG-----VSTHSLPN--DSYMRHGSTAGPLGRGWGLPKAOSGVSLSVH	1972	Qy	315	NWNYTNTCSAGEHNPFGKAINFNDIGNYAVTAIFQVITLEGWDTMYFMDAHSFNFTY	374
Db	1858	PEPMRVGDLGECFFPLSSTAVSPDPENFLCEMEEIPFNVP--RSW--LKHDSOAPPSP	1913	Db	316	NWNYTNTCSAGEHNPFGKAINFNDIGNYAVTAIFQVITLEGWDTMYFMDAHSFNFTY	375
Qy	1973	SQADTSYILQPKDAPH-----LLQHSAPTWTGTPKLPPLPG-----RSLAQRPLRR	2021	Qy	375	FILLIIVGSFFMINICLVVIATQFSETKOBSQLEORVRELSNASTLASFSEPCSYE	434
Db	1914	FSPDASSPLPMAEFHFAVASOKGPKGTGTGLPKIALOGSWASLSRVRNCTLLR	1973	Db	376	FILLIIVGSFFMINICLVVIATQFSETKOBSQLEORVRELSNASTLASFSEPCSYE	434
Qy	2022	QAIRTSDLVQGLSREDLLAEVSGPSPPLARAYSFQGSSTQAQOHSRSHSKIMT	2081	Qy	435	ELKLYLVITLRAARLQAQVRAAGVVRVGLLSSPAPLGGQETQPSSSCSRRHRSVHL	494
Db	1974	QATGSDTSLD-----ASPSSSAGSLQTTLEDSTLSDSPRA-----LG	2012	Db	435	EIVQVCHILRAKARALGLYQALQNR-----	461
Qy	2082	PPAPCPGPNKGGPPTRSSLELDTLSWISGDLPLPGQEEPPSPDLKKCYVEAQ	2141	Qy	495	VHHHHHHHHYHLGNGTLRAAPASPEIQDRDANGSRRLMLPPSPALSGAPGGAESVH	554
Db	2013	PPAPCPGPNKGGPPTRSSLELDTLSWISGDLPLPGQEEPPSPDLKKCYVEAQ	2047	Db	462	-----RQMG-----PGTFA--PAKGP-----	477
Qy	2142	SCORRTSMLEDRHRSIAVCLSDSGSQHLGTDPSN--LGGQPLGGGSRPKKLSP	2198	Qy	555	SFVHADCHLEPVRCQAPPSPSEASGRVTVGSKVPTVHTSPPTLKEKALVEVAASS	614
Db	2048	-----HQRSHSSGGS--TSPGCTHDSMDPSDEBGRGAGGGAGSEHSETLSSL	2095	Db	478	---HAK---EPHCKLCPRHSLD-----PTHTLVQP-----	504
Qy	2199	SIT---IDPPESQGRTPSPFGICLRRRAPSDS---KDPLASGPPDMSNAASPSPKOV	2251	Qy	615	GPPTLTSLNIPPGPYSSMHKLETTQGTGACQSSCKISSPCLKADSGACGDSQPCYCAR--	672
Db	2096	SLTSLCFFP-----PPAPGLTPARKFSTSSLAAPGRPHAAALAHGLARSFSAAD--	2148	Db	505	-----ISAILASD-----PSSCPHCOHEA	523
Qy	2252	LSLSGLSSDPADLDP 2266		Qy	673	---AGAGEVELADREMPDSDSEAVYFTODAHSDLRDPHSRRQSLGPDAPSSVLA--	727
Db	2149	-----RSKOPPGRAP 2158		Db	524	GRPEGLGSTD--SGQEGSGSGSAEAFANGDG---LQSEDDGVSDLGKBEQEDGAAR	578
RESULT 8				Qy	728	---FWRLICDTRFKIVDSKYFCRGIMIALVNTLSMGIEYHEQPELITNALSINIVFT	783
US-09-404-650-5				Db	579	LCGDVWRETRKKLGIIVDSKYFNRGIMIALVNTLSMGIEYHEQPELITNALSINIVFT	638
; Sequence 5, Application US/09404650				Qy	784	SLEFALEMLKLVLVGPFGYIKNPYINIPDGVIVVISVWEIVGQGGGLSVLRTFLMRVLK	843
; Patent No. 6309858				Db	639	SFALEMLKLVLVGPFGYIKNPYINIPDGVIVVISVWEIVGQGGGLSVLRTFLMRVLK	698
; GENERAL INFORMATION:				Qy	844	LVRPLPALQOLVLMKTMNDVATFCMLLMFIFIPFISILGMHFGCKFASERD--GDTLPD	902
; APPLICANT: Dietrich, Paul S.				Db	699	LVRPLPALQOLVLMKTMNDVATFCMLLMFIFIPFISILGMHFGCKFASERD--GDTLPD	758
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;				Qy	903	RKNFDSLMLWALTQVQILLTOEDMNKVLNGWMASTSSWAALYFIATMFGNVLNLLVAI	962
; FILE REFERENCE: R0043B-REG sequence listing				Db	759	RKNFDSLMLWALTQVQILLTOEDMNKVLNGWMASTSSWAALYFIATMFGNVLNLLVAI	818
; CURRENT APPLICATION NUMBER: US/09/404,650				Qy	963	LVEGFQAEIISKREDASQSLQIOLPVDSQGGDANKSESEDPFSPS-----LDG	1012
; CURRENT FILING DATE: 1999-09-23				Db	819	LVEGFQAEIISKREDASQSLQIOLPVDSQGGDANKSESEDPFSPS-----LDG	855
; NUMBER OF SEQ ID NOS: 12				Qy	1013	DGDRKKCLALVSLGHEPRLKSLPLLIHTAATPMSLPKSTSTGLGELGPA--SRRTSS	1071
; SOFTWARE: Patentin ver. 2.0				Db	856	SRDLKLCPIPTPNH-----LDP-----SLP-----LGNHGLPAGTMGTAP	892
; SEQ ID NO 5				Qy	1072	SGSABPG-----AAHEMKSPPSARSSPHSPWASASSWTSSRRSRL 1113	
; LENGTH: 1835				Db			
; TYPE: PRT							
; ORGANISM: Rattus sp.							
US-09-404-650-5							
Query Match 45.1%; Score 5366; DB 3; Length 1835;							
Best Local Similarity 56.8%; Pred.No. 0;							
Matches 1138; Conservative 183; Mismatches 346; Indels 336; Gaps 38;							
Qy 27 GAGGRPGSABEKDFGSADSEAG-----LPYALAPVVFYFYLSDSRPSWCLRTVCNPNW 82							

Db 893 RLSLQPDVPLVALDSKSSVMSLGRMSYDORSLSSSRSSYYGPWGRSGTWASRRSSWN-- 950
QY 1114 GRAPSLKRSPSGERRSLSSGEGESQDER-ESSEBE---RASPAGSDH----- 1158
Db 951 ----SLKHPPSAEHESSLLSGEGGCVRACEGAREAPTRAPLAPHANHAHGHPHLA 1006
QY 1159 ----RHGSLERAKSFDDLPTLVQVGLHRTAS--GRGSASEHOCNGKSGASGLARAL 1212
Db 1007 HHRHRRHRTLSLDTROSDVLGELVPVVGAGHRAAWRAGAGAPGHEDCNGRMPNIAKDVVT 1066
QY 1213 RPDPPDLODDADDEGNLSKGRVRAWIRAPLACVLERDSWYAFPPQSPRLLCHRI 1272
Db 1067 KMDRRDRDCE-EEEDYTLCTFRVRKMDIVYKPDWCCEVEDSWVLFSPEKFRILCQRI 1125
QY 1273 ITHKMFHVHVLVIIFLNCITIAMERKIDPHSAERIFLTLNSVIFTAVFLAEMTVKVAL 1332
Db 1126 IAHKLFYVVLAFIFLNCITIALERPOIEAGSTERIFLTVSVYIFTAIFVGEWTKVVS 1185
QY 1333 GWCFCGEQAYLRSSWNLVGLLVLISVIDILVMSVDSGKILGMLRVLRLTLRLPLRVI 1392
Db 1186 GLYFGEQAYLRSSWNLVGLVFLVFSIIDIVWSVAGGAKILGLVRLVRLTLRLPLRVI 1245
QY 1393 SRAQGLKLVETLMSLXPIGNIVVICCAFFIIFGILGVOLPKGFVFCQEDTNTNK 1452
Db 1246 SRAPGLKLVETLMSLXPIGNIVVICCAFFIIFGILGVOLPKGFVFCQEDTNTNR 1305
QY 1453 SDCBAASVVRHVKYNFNLGQALMSLFLVLSKDGWVIDIMYDGLDAVGVDQOPIMHNPW 1512
Db 1306 SDCVAANVRVHHKYNFNLGQALMSLFLVLSKDGWVIMYNGLDVAVDQOPVTHNPW 1365
QY 1513 MLYFISLLVAVFVLMFVGVVVENPHKCRQHOEEERREKRLRLEKRRKQAC 1572
Db 1366 MLYFISLLVAVFVLMFVGVVVENPHKCRQHOEEERREKRLRLEKRRKQAC 1425
QY 1573 KPYSDYSRFRLLVHLLCTSHYLDLFTGVIGLVNVTMAMEHYOQPOLDEALKICNVIF 1632
Db 1426 LPYATYCTPELLHSMCTSHYLDLFTGVIGLVNVTMAMEHYOQPOLDEALKICNVIF 1485
QY 1633 TVIFVLSVFKLVAFGRFRFRQDRWNQDLAIVLISMGITLEEIVNASLPINPTIIRI 1692
Db 1486 TVFVLEAVLKVAFGLRRFPKDRWNQDLAIVLISMGITLEEIVNASLPINPTIIRI 1545
QY 1693 MRVRIARVLKLMVGMRAALLDTVMQALPOVGNLGLLFFIFAALGVLEFGDLEC 1752
Db 1546 MRVRIARVLKLMVGMRAALLDTVMQALPOVGNLGLLFFIFAALGVLEFGDLEC 1605
QY 1753 DETHPCGLGRHATFRNFGMAFLTLFRVSTCDNNGIMKTDLRDC-DOESTCVNTV--IS 1809
Db 1606 NDENPCGMSRHATFRNFGMAFLTLFRVSTCDNNGIMKTDLRDCDTHDERTCLSSLOFVS 1665
QY 1810 PIYFVSFLVTAQVFLVNVVIAVLMKHLLEESNKEAKEAEAELELELM-KTLPSPQHSPL 1868
Db 1666 PIYFVSFLVTAQVFLVNVVIAVLMKHLDDSNKEAQEDAEMDAIELEMAHGLGPCP 1721
QY 1869 GSPFLWPGVEGDPSPSPKPGALHPAAHARSASHFSLEHTTMOHPHTELPGLLTV-- 1925
Db 1722 -----GPCPG-----PCPCPCPCPCAGPRLTSSPG 1747
QY 1926 ---RKSGVSRTHSLPNDSYMCRH 1945
Db 1748 APCGGSGAGAGG-DTESHLCRH 1769

RESULT 9

US-09-935-541-5
; Sequence 5, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1835
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-09-935-541-5

Query Match 45.1%; Score 5366; DB 4; Length 1835;
Best Local Similarity 56.8%; Pred. No. 0;
Matches 1138; Conservative 183; Mismatches 346; Indels 336; Gaps 38;
QY 27 GAGCGPRGPGSAEKDPSGADSEAG---LPPALAPVVPFYLSQDSRPSWCLRTVCNPM 82
Db 19 GITEQGPSPSPSPGEEPLEGNTDVPVHDLAPVAFCLRTQTSRPNWCIMVCNPM 78
QY 83 FERISMLVILLNCVTLGMFRPCEDIACDSQRCLIQAFDDFIAPFAVEMVMKVALGIF 142
Db 79 FECVSMVILLNCVTLGMVQPCDDMECLSDRCKILQVDDFIFFAMVLMKVALGIF 138
QY 143 GKCYLIGDTWRLDFFVIAGMLEYSLDLQNVFSAVRTRVLRPLRINRVPSPRIIVT 202
Db 139 GKCYLIGDTWRLDFFVIAGMWVEYSLDLQNLINLSAIRTVRVLRPLKAINRVPSPRIIVN 198
QY 203 LLLDTLPMGNVLLCCFFVFIIGVQVGLWAGLNRCLFIPENSLPLSDVLERYOTE 262
Db 199 LLLDTLPMGNVLLCCFFVFIIGVQVGLWAGLNRCLFIPENSLPLSDVLERYOTE 258
QY 263 NEDSPFICSPRENGMRSCRSVPTLRDGGGGPPCGL-----DYEAVNSSNTT--CV 314
Db 259 EDDMPFICSLTGDNGIMGCHEIPLKEQ---GRECCLSKDDVDFGAGRODLNAGLVC 315
QY 315 NNNQYVNCSSAGENPKGAINFDNIGYAMTAIFQVITLEGWVDIMVMDAHSFYNTY 374
Db 316 NNNRYVNCRTGNANPHKGAINFNIGYAGIVIFQVITLEGWVEIMYVMDAHSFYNTY 375
QY 375 FILLIIVGSFMINCLAVIATOPSETKQESQIMREORVFLSNASTLASFSFGSCYE 434
Db 376 FILLIIVGSFMINCLAVIATOPSETKQREHLMLEQORYL--SSTVASYAEPGDCYE 434
QY 435 ELLKYLVIILKARLAQVSRAGVRVGLLSPAPLGGQETOPSSSCSRSHRLSVHLL 494
Db 435 EIFYVCHILKAKRAGLYQALQNR----- 461
QY 495 VHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPFSTPALSGAPGGAESVH 554
Db 462 -----RQAMG-----PGTFA--PAKPGP----- 477
QY 555 SFYHADCHLEPVRCQAPPSPSPSEASGRVTGSKVYVHTSPPTLKEKALVEVAASS 614
Db 478 ---HAK---EPHCKLCPRHSPLD-----PTPHTLVQP----- 504
QY 615 GPPTLSLNIIPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSCACGDCPCYCAR-- 672
Db 505 -----ISAILASD-----PSSCPHQHEA 523
QY 673 ----AGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRRQSLGDPDAPSSVLA- 727
Db 524 GRPSPGLGSTD-SGQEGSGSGSAEANGDG---LQSSDGVSSDLGKEEQEQAAR 578
QY 728 ----FWRLICDTPRKIVDSKYFCRGITMIALIVNTLSMGIEYHEQPEELNALEISNIVFT 783
Db 579 LCGDVMRETRKKLGRIVDSKYFNRMGIMAILVNTVSMGIEHHEQPEELNILEICNVFT 638
QY 784 SLFALEMLKLIVYGPFGYIKNPYINFDGVIIVISWEIVGQGGGLSVLRTFLMRVLK 843
Db 639 SMFALEMLKLAAGLFDYLRPNYINFSIIVLSIWEIVGQGGGLSVLRTFLMRVLK 698
QY 844 LVRFPLAQRLVLMKTDNVNATFCMLLMFLIFIFSLGMHLFGCKEASERD-GDTLPD 902

Db 1722 -----GCPFG-----PCPCPCPCAGRLPTSSPG 1747

Qy 1926 ---RKSGVSRTHSLPNDSYMCRH 1945

Db 1748 APGRSGGAGG-DTSHLCRH 1769

RESULT 10

US-09-268-163-4

; Sequence 4, Application US/09268163B

; Patent No. 6353091

; GENERAL INFORMATION:

; APPLICANT: Lipscombe, Diane

; APPLICANT: Schorge, Stephanie

; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF

; FILE REFERENCE: B1055/7000

; CURRENT APPLICATION NUMBER: US/09/268,163B

; CURRENT FILING DATE: 1999-03-12

; EARLIER APPLICATION NUMBER: US 60/077,901

; EARLIER FILING DATE: 1998-03-13

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 2343

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-268-163-4

Query Match 14.7%; Score 1750.5; DB 3; Length 2343;

Best Local Similarity 24.2%; Pred. No. 2.4e-133;

Matches 639; Conservative 363; Mismatches 827; Indels 815; Gaps 84;

Qy 27 GAGGPGGSAEKDPSGADSEAGLFPYPALAPVVF-----FYLSDSRP 70

Db 25 GAGGAGGPGGLOPQGVLYKQSIQARATWALYNPIPVKQNCFTWNSLFFVSDNVV 84

Qy 71 RSWCLTVCNPNFERISMLVILLNCVTLGMFRPCEDIACDSRCRILQAPDD---FIFAF 127

Db 85 RKYAKRITTEPPPEYMLATITIANCIVLAL---EQHLPDGDKTPMSERLDDTEPFI 140

Qy 128 FAVEMVVMKVALG-IFGKCYIGDGTWNRLDFFIVIAMLEYS---LDLQNVSFSAVTVR 183

Db 141 FCEAGIKIITAGFVFKHKSYLENGWNVDMFVVVLGILATAGTDFDLR-----TLRAVR 195

Qy 184 VLRLPLRAIRVPSMRLLVTLTDLTLMGLNVLLCTFFVFIIGVIGVQLWAGLLNRCLF 243

Db 196 VLRLPLKIVSGIPSLQVVLKSIKAMVPLLOIGLLFFAILMFAIGLEFTYMGKPHKACF- 254

Qy 244 PENFSLPLVDLERYQYOTENEDESPFCISQPRENGMRSRCSVPVTLRGDGGGPPCGLDYE 303

Db 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273

Qy 304 AYNSSNTTCVNNQVYNTCSAGEHNPFKGAINFNDNIGYAMIAIFQVITLEGWVDIMYFV 363

Db 274 ARLCGTEC---REYWP-----GENFGITNEDNILFAITLVFOCITWEGWTDILYNT 323

Qy 364 MD-AHSFYNFYFILLIIVGFFMINCLVVIATQFSETKQES-----QLMSEQRVRF 416

Db 324 NDAAGTWNMLYFPLIIIGSFFMLNLVLGSLGEFAKERERVENRRAFLKRRQQQTE- 382

Qy 417 LSNASTLASPEPSCVEELKLYLVITLKAARLAQVSRAGVVRGILLSSPAPLGGQET 476

Db 383 -----RELNGYLEWIFKAEVMLAEEDRNA-----EEK 410

Qy 477 QPSSSSCRSHRLSLVHHHHHHHHHHHNGTLRAPRASPEIQDRDANGSRRLMPP 536

Db 411 SPLDLVKRAATYKSRNDLIH-----AEEGEDRFAD----- 440

Qy 537 PSTPALSGAPPGAESVHSFYHADCHLEPVRQAPPPSPSEASRTVSGKVYPTVHTS 596

Db 441 ----- 440

Qy 597 PPFETLKEKALVEVAASSGPPTLTSLNIPPGFYSSMHKLLTQSTGACQSSCKLSSPCLK 656

Db 699 LVREMPALRQLVLMKMDNVATFCMLLLMFIFFISILGHIIFGCKFSRLTDGDIVPD 758

Qy 903 RKNFDSLWALVTYFQILTOEDMKNLYNGMASTSSWAALYFIALMTFNGVYVFNLLVAI 962

Db 759 RKNFDSLWALVTYFQILTOEDMKNLYNGMASTTPWASLYFVALMTFNGVYVFNLLVAI 818

Qy 963 LVEGFQAREISKREDASQSLCIQLPVDSQGDANKSESDPFFSPS-----LDG 1012

Db 819 LVEGFQAE-----GDANRSCSDQSSNLEEFDKLPEGLDN 855

Qy 1013 DGRKKKUALVSLGHPBLKSLPLLIHTAATPMSPKSTSTGLGALGPA-SRRTSS 1071

Db 856 SRDLKLCIPMTENGH-----LDP-----LGHLGPGAGTGTAP 892

Qy 1072 SGSAEPG-----AAHEMSPSPSARSHPWSAASWTSRRSRNSL 1113

Db 893 RLSLQDPVLVLDKRSKSVMSLGRMSYDQSLSSRSYYGFWGRSGTWAASRRSSWN-- 950

Qy 1114 GRAPSLKRRSPGERRSLLSGEQBSQDEE-BSSBEE---RASPAGSDH----- 1158

Db 951 ----SLKHKPPSAEHESLLSGEGGSCVRACEGAREEAPRTAPLHAPHAAHGHPLA 1006

Qy 1159 ----RHRGSLREAKSSFLPDTLQVPLGHTAS--GRGSASEHODCNCKSASGLRAL 1212

Db 1007 HRHRHRRRTLSLTDSDVLDGELVPVVGHAHRAAMKAGQAQPCHEDCNRMENIAKDVFT 1066

Qy 1213 RDPDPELDGDDADDEGNLSKGRVRAIRAPACYLERSDSAYIFPPQSRFLRLCHRI 1272

Db 1067 KMDRRDRGED-EEEDYTLCFVRKVIDYKEDWCVEWEDSVLFFSPENKFRILCQTI 1125

Qy 1273 ITHKMFHDVVLVIIFLNCITIAMERKIDPHSAERIFLILSNVIFTAVFLAEMTVKVAL 1332

Db 1126 IAHKLFYVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNVIFTAIFVGMTLKVWSL 1185

Qy 1333 GWCFGEQAYLRSSWNLGLVLISVIDILVSVSDSGTKILGLMLRVLRLLRLRLRVI 1392

Db 1186 GLYFGEQAYLRSSWNLGLVLFVFSIIDIVVSVASAGAKILGLVLRLLRLRLRVI 1245

Qy 1393 SRAQGLKLVVETLMSSLKPIGNIVVICAPFIIFGILGVLFKGFVCOGEDTRNITNK 1452

Db 1246 SRAPGLKLVVETLISLKPIGNIVLICAPFIIFGILGVLFKGFVCHVLGVDTRNITNR 1305

Qy 1453 SDCAEASVWRVHKYFNFDNIQALMSLFLVASKDQWVDIMYDGLDAGVVDQOPLMHNPW 1512

Db 1306 SDCAVANYRWVHKYFNFDNIQALMSLFLVASKDQWVIMYNGLDVAVDQOQPVNINPW 1365

Qy 1513 MLLYFISFLATVAFVFLNMFVGVVFNHFKRQHOEEERARRRERLEKRRKRAQC 1572

Db 1366 MLLYFISFLATVAFVFLNMFVGVVFNHFKRQHOEEERARRRERLEKRRKRAQR 1425

Qy 1573 KPYYSDSYRFRLLVHHLCTSHYLDLFTGVIGLVNVTMAMEHYQOQOILDEALKI 1632

Db 1426 LPYATYCPTELLIHSCTSHYLDLFTFIICLVNVTMSLEHYNQPTSLTALYKCYMF 1485

Qy 1633 TVIFVLSVFKLVAFGFRFPQDRWNQDLDAIVLLSINGITLERIEVNASIPNPTIIRI 1692

Db 1486 TTVFVLEAVLKVAFGLRFRFPDRWNQDLDAIVLLSVMGVTLEEBINAALPNTIIRI 1545

Qy 1693 MRVRIARVLLKXMGVMBALLDTVMQALQVGNLGLFLLMFLFFIAALGVLFGLDEC 1752

Db 1546 MRVRIARVLLKXMGVMBALLDTVMQALQVGNLGLFLLMFLFFIAALGVLFGLKVC 1605

Qy 1753 DETHPCEGLGRHATPRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DOESTCYNTV--IS 1809

Db 1606 NDENPECGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCDTHDERTCLSSLOQVS 1665

Qy 1810 PIYFVSFVLTAQFVLNVVIAVLMKHLSESNKEAEAELEAELEM-KTLLSPQPHSPL 1868

Db 1666 PIYFVSFVLTAQFVLNVVIAVLMKHLDDSNKEAQEDAEADAEIELEMAHGLGFCP- 1721

Qy 1869 GSPFLWPGVEGPDSPDSPKPGALHAAHARSASHFSLEBHTMQPHFTLPGLDITV--- 1925

441 : : : : :
 457 : : : : :LCAVGSPEAR 450
 451 : : : : :ADSGACGPDSCPYCARAGAVEVELADREMPDSDSEAVYEFTQDAQSHDLDPHSRQORSL 716
 473 : : : : :ASLKSCKTSSSYFR-----KEKMF-----
 717 : : : : :GPDAPSSVLAFWRLICDTRKIVSKYFGRGIMIALVNTLSMGIEYHEQPELTNALE 776
 474 : : : : :FIRRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRLLITLY 515
 777 : : : : :ISNIVTSLFALEMLKLLVYGFYKPNYINFDGVIIVISWEIVGQ-----QGGGLS 831
 516 : : : : :PREFVLGLFLEMSLMKTGLGRSFRSFCNCFDGVIVGSFVYVWAAIKPGSSFGIS 575
 832 : : : : :VLRTRFLMRVLKLVRFALPQRLVLMKTMONVATFCMLLFIPIFISLGMHFLGCKF 891
 576 : : : : :VLRALRLRIFKVKYSSLRNLVSVLSNMSKISILFELLFIVFVALLGMQLFGGQF 635
 892 : : : : :ASERDGDITLDRKNDLWAIWTVFQILTOEDMKNVLYNGM-----ASTSSWAALYFTA 946
 636 : : : : :NFQDETPT-----TNFDTFPAALITVQILTGEDNVMVHYGIESQGVSKGMFESSFYFIV 691
 947 : : : : :LMTFGNYLVNLLVALLVEGF-QABEISK-----REDASQ-----LSCIQ 986
 692 : : : : :LTLFGNYLLNVLALVONLANAQBELTKOBEEMEEAANQKALQAKAEVAVSPMSAAN 751
 987 : : : : :LPVDSQGGDANKSESEPDPFSPSLDGDGRKCLALVSLGE-----HPELRK 1033
 752 : : : : :ISIAAROQNSAKARVWQASQALQNLRLASCEALYSEMDEPEELRATTHLRPDWMT 811
 1034 : : : : :SILLPLIITHAATMSLP-----KSTSTGLGHALGPASR-----RTSSSG----- 1073
 812 : : : : :HLDRPLVVELRGDARGVGGKARPEAAABEGVDPRRHRHRDKONTPAAGDQDRAEA 871
 1074 : : : : :SABEGA-----AHEMKSPSPARS-----SPH-----SPWSAASW 1103
 872 : : : : :PKAESGEGAREPRPHRSKSKAAGPPEARSEGRGPGEGRRHRRGSPPEAARE 931
 1104 : : : : :TSR-RSSRNSIGRAPSKRRSPSERRSLLEGQESODEBESSE-----ERASP- 1153
 932 : : : : :PRRRAURH-----QDPSKACAGAKERRARHRGGRPRAGPREAESGEEPARRRHAKQA 988
 1154 : : : : :-----AGSDHRRGSLEREAKSSFDLPDITLQVPLGHRASRG 1191
 989 : : : : :HEAVEKETTEKATEKEAEIVADKEKELRNHQPREPHCDLETSGTVTVGMHMLTPTCL 1048
 1192 : : : : :SASHQDCNGKSASGLARALRPDP-----PLDGDADDEGNI-----SKGE 1234
 1049 : : : : :QKVEEQEDADQNVTVMGSOQPPDNTIVHPVMLTGPLGEATVPVPSGNDVLESQAEK 1108
 1235 : : : : :R-----VRARIRALPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVIF 1287
 1109 : : : : :KEYEADVMESGRPIVPYS-----SMFLSTNLRLRPFCHYIVTMVTFYFVVILVIA 1161
 1288 : : : : :LCITITAMERPKDPSAERIFLTSNIYIFTAVFLAEMTVKVALGCMFGEQAYLRSSWN 1347
 1162 : : : : :LSSIALAEDP-VRTDPSRNNALKYDIETGFTFEMWIKMIDGLLLHPGAYFRDLWN 1220
 1348 : : : : :VLDGLVLISVIDI-LVSMYSDSGTKLGMRLVRLRLTLRPLRVISRAOGLKLVVETLM 1406
 1221 : : : : :ILDPIVUSGALVAFARSSVFGSGKGDINTIKSLRVLRLRPLKTRKLPKKAEDCVV 1280
 1407 : : : : :SSUKPIGNIVVICCAFFIIFGILGVOLFKGKFFVQCE-----DTRN-----ITNKSDCAE 1458
 1281 : : : : :NSLKNVLNILLVYMLEMFIKFAVIAVQLFKGFCYCTDSEKELERDCRGQVLDYEKEVEA 1340
 1459 : : : : :SYR-WYRHKYFNENLQALMSLFLVASKGDWIMYDGLDVGVDQOQPINHNPMLLYF 1517
 1341 : : : : :QPRQWKYDFHYDNVNLWALLTLFTVSTGEGWPMVLKXSDATVEEGPSPGYRMEISIFY 1400
 1518 : : : : :ISGFLIVAFVFLNMFGVVVENPHKCRQHQEBEAREERREKRLRLRLEKKRKA-----QC 1572

1401 : : : : :VVYFVFPFFFNIFVALLIITF-----CEQGDKWSE-----CSLEKNERACIDFAISA 1450
 1573 : : : : :KPY--YSDYSR--FRLLVHHLCTSHYLDLFIITGIVGLNVVTWAMEHYQQOILDEALKIC 1628
 1451 : : : : :KPLTRYMPQNRQSFQKTVFVSPPEFYFIMAMIALNIVLNMKFYDAPYELEMLKCL 1510
 1629 : : : : :NLIFTVIFVLESVKLVAERFRFQDRWNQDLALVLSIMGITLEEI-EVNASLFINP 1687
 1511 : : : : :NIVFTSMFMECVKLTIAFGLVNFYDANVDFVTVLGSITDILVTEAETN-----NF 1565
 1688 : : : : :TIIRMRVLRIRARVLKLLKMAVCMRALLDTVMQALPOVGNLGLLMLFIIFALGVELF 1747
 1566 : : : : :INLSFLRFRARLIKLRQGTIRILLMTFVQSFKALPYVCLLIAMLFYIALLIGQMF 1625
 1748 : : : : :GLECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOTLRD--CDQE--SIC 1803
 1626 : : : : :GNIALDDD--TSINRHNFRFTLOALMLLFRSATGEAMHEIMLSCLSNQACDEQANATE 1682
 1804 : : : : :YNTVISPIYFVSFVLTAQFVLNVVIVLUM-----KHLBE----- 1838
 1693 : : : : :CGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHLHDEFIRVWAEYDP 1742
 1839 : : : : :----- 1838
 1743 : : : : :AACGRISYNDMPEMLKMSPPGLGKKCPARVAYKRLVMMNPISNEDMTVHTSTLMAL 1802
 1839 : : : : :-----SNKEAKEBAEAELEMLKTLSPQPHSPGLSPFLWPGVGGPDPSP 1886
 1803 : : : : :IRTALEIKLAPAGTKHQCDALRKEISVVWANL-POKTDLVLP-----PHKPEM 1853
 1887 : : : : :KPGALHPA-----AHARSASHFSLEHPTM-----QPHPTLPGPD 1921
 1854 : : : : :TVGKYAALMTIDFYKONKTTDQMQAPGGLSQMGFVSLFHLPLKATLEOTOPAVLRGAR 1913
 1922 : : : : :LLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGCLPKAQSGLSVLSVHSQPADTSYI 1981
 1914 : : : : :VFLRQKSTSLN-----GGAIONQESGIKESV-----SWG 1944
 1982 : : : : :LQLPKDAPHLLQP-----HSAPTWTGTPKLPPLPPGSRPLAQRLRQAIR-----TDS 2029
 1945 : : : : :TQRTQDAPHEARPPLERGHSTEI-----PVGSRGALAVDVQMQSITRGRGPGEPQG 1996
 2030 : : : : :LDVQGLSGREDLLAEVSGP--SPPLARAYSFVWQSSQTAQHSRSHSKISKHMTTPAPC 2086
 1997 : : : : :LESQRAASMPRLAAETQPVTDASPMKRST-----STLAQRPRTGLCST---TPDRPP 2047
 2087 : : : : :PG-----PEPNWKGPPETRRSLELDTLSWTSGLLPPGQEEPPSP 2129
 2048 : : : : :PSQASSHHHHRCHRRDRKORSLEKGP--SLSAMDMGAPSSAVGGLPPG--EGTGC 2102
 2130 : : : : :RDLKKCVSVEAQSCORR-PTSWLDEQRRHSIAVSCLDG-----SOPHLG 2173
 2103 : : : : :RRERERRQRRGRGSOERQPSSSSEKQRF--YSCDRFGGREGPPKPKPSLSSHTPTAG 2159
 2174 : : : : :TDP-----SNLGGQPL-----GGQSRPKKKLSP-PSITI-----DPPESQ 2209
 2160 : : : : :QEPGPHQSGSVNGSPLLSTSGASTFGRGRQLPQTLTPRPSITYTKTANSSPIHFAG 2219
 2210 : : : : :PRT--PP-SPG-----ICLRREAPSDSKDPLASGPPDSMAASPCKKDVLSGL 2257
 2220 : : : : :AQTSLPAPFGRSLRGLSEHNALLQORDPLS--OPLAPG-----SRI 2258
 2258 : : : : :SSDP 2261
 2259 : : : : :GSDP 2262

RESULT 11

US-08-713-118-2

; Sequence 2, Application US/08713118

; Patent No. 6040436

; GENERAL INFORMATION:

; APPLICANT: Franco, Rodrigo

APPLICANT: Sun Chen, Ai Ru
 APPLICANT: Suet, David J.
 TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
 TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173-4799
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/713,118
 FILING DATE: 16-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mata, Elizabeth W.
 REGISTRATION NUMBER: 38,236
 REFERENCE/DOCKET NUMBER: ACC96-01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2337 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-713-118-2

Query Match 14.7%; Score 1749; DB 3; Length 2337;
 Best Local Similarity 24.3%; Pred. No. 3.1e-133;
 Matches 645; Conservative 359; Mismatches 812; Indels 820; Gaps 86;
 14 GQPRSFRLNDLSGAGRPGGSAEKDPGSADSEAEGLYPALAPVVF-----61
 13 GPGGGERARG-GGAGGAGGPGGLQGQGVLYKQSIARATMALYNIPVKQNCFTV 71
 62 ----FVLSQDSRPSWCLRTVCPNWPFRISMVLINCVLGMFPCDIACSQRCL 117
 72 NRSIFVFESEDNVVRKYAKRITWPPPEYMLATIANCIVAL-----EQHLPDGDKTPMS 127
 118 QAFDD----FIFAFVEMVVMVALG-IFGKKCVLGDITWNRDLDFIIVAGMLEYSS---LD 170
 128 ERLDDTBPYFIGFCFAGIKIIALGFVFKGSLRNGWVMDVFWVLTGILATAGTDFD 187
 171 LQNVFSFSAVRVRLRLRAINRVPMSRLVTLLLDLPLMGNVLLLCFFVFFIFGIVGV 230
 188 LR-----TLRAVRVRLPLKLVSGIPSLQVILKIMKAMVPLQIGLLFFAILFAIIGL 242
 231 QLWAGLLNRCLFENFSLPLSVDLERYQYQTEDEDESPFICSQPRENGMRCRSPVILRG 290
 243 EYMGKPHKACF-----FNSTDAE-----PV---263
 291 DGGGPGPGLDYAEVNSSNTTCVNNQYTNCSAGEHNPKGAINFNIGNYAMIAIFQV 350
 264 ---GDFPGCKAPARLCEGDTCC---REYWP-----GNFGITNFNAILFAITVFC 310
 351 ITLEGWIMVFMVD-AHSFYNYFIILLIIVGSPFMNLCVIVATQFSETKQRES---406
 311 ITMEGWTDLTYNTDAAGTNWLYFIPLIIIGSPFMNLCVIVATQFSETKQRES---370
 407 ---QLMRQVRVFLNASTLASFSPGSCYBELLYVILKARRLAQAQVRAAGVRVG 463
 371 APLKLRQOQIE-----RELNGYLEWIFKAEEMVLAEDRNA-----407
 464 LLSSPAPLGQGTQPSSCSRSHRLSLVHLLVHHHHHHHHVHLGNGTLRAPRASPEIQD 523

408 -----BEKSPDLVLRRAATKSRNDLIH-----AERGED 436
 524 RDANGSRRLMLPPSPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPSPSEASGRT 583
 437 RFAD-----440
 584 VSGKVPVHTSPPTLKEKALVEVAASGPPTLSLNTPPGPYSMMHKLLETQSTGA 643
 441 -----440
 644 COSCKISPCPKADSGAGCPDSCPCYCARAGAGEVELADREMPDSDSEAVVEFTQAOHS 703
 441 ---LCAVGPFPARASLKSCKTESYFRR-----KEKMF-----473
 704 DLDRPHSRQRSLGPDAPSPSLAFWRLICDTFRKIVDSKYFGRGIMTIALNTVNTSMGIE 763
 474 -----FIRMVKAQSPYVWVLCVVALNTLCVAMV 502
 764 VHEQPEELTNALISNIVFTSLFALEMLKLLVYGPFGYKIPYNIIDGVIVIVISVETV 823
 503 HYNQPRRLTTLYFAEFVFLGLFTEMGLKMYGLGERSYFRSFCNCFDGVIVGVSEV 562
 824 GQ-----QGGLSVLRTFLMEVLKLVFLPALQRLVLMKMDNVATFCMLLMFIFI 878
 563 WAAIKPGSGFISVLRAULRLRIFKVKYSSRLNVLWSLNSMKSIISLLFLFLFIV 622
 879 FSLGMHLFGCKFASERDGTLPDRKNFDSLWALVITVFQILTQEDWNKVLNMG-----933
 623 FALLGMQLFGGQNFQDETPT---TNFTFPAALITVFOILTGEDWNAVYHGIESQGG 678
 934 ASTSSWAALFYIALMTFGNYVLFNLLVAILVEGF-OAEELSK-----REDASGO-----981
 679 VSKGPFSSFYFVLTFLFGNYTLINVLAVLAVNLANAQLTKDEEEMEAANOKLALQKA 738
 982 -----LSCITQLPVDVDSQGGDANKSEBPPDPSLDGDKKCKLALVS-----1024
 739 KEVAEYSPMSAANISIAARQONSAKARSVWEQASQRLONLRASCEALYSEMDPEERLR 798
 1025 ---LGEHPERKSLPLPPIIHTAATPMSLP-----KSTSTGLGEALGPASR-----1067
 799 FATTRIRRDPMKTHLDRPLVVLGRDARGVGKARPEAAEAPEGVDPPRRHRHRDKD 858
 1068 RTSSSG-----SAPPGA-----AHMKSPPSARS-----SPH-----1094
 859 KTPAAGQDRAEAPKAESGEPGAREPRPHRSKSEAAAGPEARSERGPGPEGGRH 918
 1095 ---SPWSAASSWTSR-RSSRNSLGRAPSLKRRSPSGERSLLSGEQESQDEEESSEE-1148
 919 HRRGSPPEAERBFRHRAHRH---QDPSKECAGAKGERRARHRRGGPRAGPREAESGE 975
 1149 -----ERASP-----AGSDHHRGSLEREAKESSFDLPDITL 1178
 976 ARHRAHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPHRECDLETSGTV 1035
 1179 QVPGHLHTAGRGSAHEQDCNGKSGASGRILARALRDPD-----PLDGDADD 1226
 1036 TVGPMHTLPSTCLQKVEEQEDADNQRNVTMGQPPDNTIVHIVPMLTGLPEATVTP 1095
 1227 EGNL-----SKGER-----VRAWIRARLPACYLERSDSWISYIFPQSRFLICHLIT 1274
 1096 SGNVDLSQAGKKEVEADVMRSGPRPIVPS-----SMFCLSPINLLRRFCHYITV 1148
 1275 HKMFHDVVLVIFINCTIAMERPKIDPHSAERFLILSNYIFTAVFLAENTVAVVAGW 1334
 1149 MRYFEVLLVIVIALSSIALAAEDP-VRTDPSRNALKYLDYIFTGVFTFEMVIKMDLGL 1207
 1335 CFGQAYLRSSWNVLDGLLVISVIDILVSMV-SDSGTKILGMLRLLRLTLRPLRVIS 1393
 1208 LLHPGAYFRDLWNILD-----FIVSGALVAFAGSKGKDINTIKSLVLRPLKTIK 1263
 1394 RAQGLKLVETIMSLKPIGNIVVICCAFFIIFGLGVOLFPGKFFVCOGE-----DTR 1447

Db	1264	RUPKLVKAVDFCVVNSLKNVNLNLLIYVLMFMETFAVIAVQLFKGKFFYCTDSKELDR	1320
QY	1448	N---ITNKSDEAASVSR-WVRHKYFNFDNLGOALMSLFLVSLASXGQWVDIMYDGLDAVGVDQ	1504
Db	1324	GOVLDYKEEVEAQPQWKXDFHYDNVLMALLTFTVSTCEGFWMLKHSVDATYEEQG	1383
QY	1505	PIMNHNPMMLLYIFSLFLIVAFFVLNMFVGVVNFHFKCRHQHQEERBARREERLRLE	1564
Db	1384	PSPGVYRMELSIYVYVVFVFFVFIALLIITF-----OQGDKWSE-----CSLE	1433
QY	1565	KKRKA-----QCKPY---YSYSR--FRLVHHLLCTSHYLDLFTIGVGLNVVTMAHEHY	1615
Db	1434	KNERACIDPAISAKPLTYMPQNQSFQYKTFVWSPPEFYFMALINTLVVLMKFY	1493
QY	1616	QOPQILDALKICNVIFVIFVLESVEKLVAFGRFQDEWQOLDIAIVLLSIMGITLE	1675
Db	1494	DAPYEYELWKLNIIVFTSMSECVLKIIAFGVNLYFRDANWVDFVTVLGSITILVT	1553
QY	1676	EIEVNASLPINPTIIRIMRVLRIRVLKLVQVGMRAALLDTVMQALPQVGNLGLLFML	1735
Db	1554	ETANNF---IN---LSFLRLFRAARLIKLRQGYTIRILLWTFVQSFKALPYVCLLIAML	1607
QY	1736	FFIFAAALGVELFGDCEDETHPCBGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLR	1795
Db	1608	FFIYAILGQWFGGIALDDD---TSINRHNFTFLQALMLLFRSATGEAWHEIMLSCLS	1664
QY	1796	D---CDQE---STCYNTVISPIFYVFSVLTAQFVLNVVVIAM-----KHL	1836
Db	1665	NOACDEQANATECSDFAFYFVFSIFLCSFLMLNLFVAVIMDNFEYLRTRDSILGPHEL	1724
QY	1837	EE-----1838	
Db	1725	DEFIRVMAEYDPAACGRISYNDMFEMLKHMSPLPLGKKCPARVAYKLRVMMPISNED	1784
QY	1839	-----SNKEAKEAEAELEMEKTLTSPHSPGSPFLW	1874
Db	1785	MTVHTSTLMALIRTALEIKLAPAGTKHQCDAEKREISVYWANL-PQKTLDLLVP---	1840
QY	1875	PGVEGPDSPSPKPGALHPA-----AHARSASHFSLEHPTM---	1910
Db	1841	-----PHKPEMTVGKYIAALMIFDFYKQNTTRDQMQAPGSLQMGVSLFHLKATL	1895
QY	1911	-QPHPTLPGPDLITVRKSGVSRTHSLPNDSYMCRHGSTAEGPLHGRWGLPKAOGSVL	1969
Db	1896	EQTQPAVLRCARVFLRQKSTSLN-----GGAIQNQGSGIKE	1933
QY	1970	SVHSQPADTSYIILPKDAPHLLQ-----HSAPTWTGTIPKLPFGRSFLAQRPLRQAA	2024
Db	1934	SV-----SWGTRQTQDAPHEARPLRERGHSTEI-----PVGRSALAVDQMQSI	1978
QY	2025	IR-----TDSLDVOGLSREDLLAEVSGP---SPPLARAYSPWGQSGSTQHQHRSHS	2074
Db	1979	TRRGPDGEQPQLESQGRASMPRLAAETQPVTDASPMKRST-----STLAQPRGTHL	2032
QY	2075	KISKHMTTPAPCPG-----PEPNWKGKPPETRSSELDLTSLWISGDL	2117
Db	2033	CST---TPDRPPPSQASSHHHHRCHRRDRXQRSLEKGP---SUSADMGAPSAVGP	2086
QY	2118	LPQGGQEEPPSFDLKKYVSAQSQRR-PTSLWDEQRHRSIAVSLDSG-----	2167
Db	2087	LPQG---EGPTGCRERRERQERSQOERQPPSSSEKQRF---YSCDRFGREPPKPKP	2141
QY	2168	-----SQPHLGTDP-----SNLGGQPL-----GGQSRPKKKLSP-PSITI	2202
Db	2142	SUSHTFTPTAQEPDHPHGGSGSVNGSPLLSTGASTFGRGRRQLPQTLTPRPSITY	2201
QY	2203	-----DPPESQGPRT---PP-SPG-----ICLRRRAPSSDSKODPLASGPPDSMAASP	2245
Db	2202	KTANSSPIHFAQAQISLPAFSGRLSRGSLSEHALLQRDPLUS-----QPLAPG-----	2249
QY	2246	SPKQVLSLSGLSGSDP	2261
Db	2250	-----SRIGSDP	2256

Db 264 ---GDFPCGKEAPARLCBGDETC---REYWP-----GNFGITNFDNILLFALLTVFQC 310
QY 351 ITLEGWDIMFYVMD-AHSFYFNFIYILLITVGSFFMINCLVIAIATQFSTKORES--- 406
Db 311 ITMEGWTDILYNTDAAGTNWLYFIPIIIGSFMLNLVLGSLGSFAKERERVENRR 370
QY 407 ---QLMRQRVRFSLNASTLASFSBPGCYBELLKYLVIYLKARRLAQAQVRAAGVRVG 463
Db 371 AFLKLRQOIE-----RELNGYLEWIFKAEVLMJAEEDRNA----- 407
QY 464 LSSPAPLGGQETOPSSSCSRSHRLSVHLLVHHHHHHHHYHLGNGTLRAPRASFEIQD 523
Db 408 -----BEKSLDVLKRAATKSRNDLIH-----AEEGED 436
QY 524 RDANGSRRLMLPPSTPALSGAPGABSVHSFYHADCHLEVRCOAPPPSPSEASORT 583
Db 437 RFAD----- 440
QY 584 VSGSKVYPTVHTSPPELTKEXALVEVAASSGPTLITSLNIPPGYSSMHKLETTQSTGA 643
Db 441 ----- 440
QY 644 COSSCKISPLKADSGACGDBSCPYCARAGAGEVELADREMPDSDSEAVYFTQDAQHS 703
Db 441 ---LCAVGSPPARASLSKGTSESSYFR-----KENMFR----- 473
QY 704 DLRDHSRRQRSLGDAEPSSVLAFWRLICDTRKIVDSKYGRGIMIALVNTLSMGIE 763
Db 474 -----FTRMVKQAQSFYVWVLCVVALNTLCVAMV 502
QY 764 YHQPELTNALEISNIVTSIFALEMLKLLVYGPYIKPNYINIFDGVIVVISVMEIV 823
Db 503 HYNQPRRLATLTYFAEFYGLGFLTEMSLKMVGLGPRSYFRSFCNDFGVIVGSVPEV 562
QY 824 GO-----QGGSLVRLTEFLMRVLKVRPALQOLVLMKTMNDVNATFCMLLFIPI 878
Db 563 WAAIKGSSFGISVLRAELRLRFKYKYWSSLENLVLSLMSKSIISLFLLELFIIV 622
QY 879 FSLGMHLFCCKPASERBDGTLPRKNFDSLMAVTVFOILLQOEDWNKYLNGM----- 933
Db 623 FALLGWLFGGQFNQDETPT---TNFDTFPAAILTVFOILGEDWNAVMYHIGISQGG 678
QY 934 ASTSSWALYFIAMTFGNVYVNLVALLAVEGF-QAEEISK-----REDASGO----- 981
Db 679 VSKGMFSSFYFVILTFGNVTLNVLAIADNLANAQELTKDREMEERANQKIALOKA 738
QY 982 -----LSCIOLEVDSDGANKSSEPDFFSPSLDGDGDRKKICALVS----- 1024
Db 739 KEVAEUSPMGAANISIAARQONSAKARSVWEQASQLRLQNLRASCEALYSEMDPEERLR 798
QY 1025 ---LGBHPELKSLLPLIHTAATPMSLP-----KSTSTGLGEALGPASR----- 1067
Db 799 FATTHRRRPMKTHLDPLVVELGRDGAQVGVGKARPEAAEPGVDPFRHHRHRDKD 858
QY 1068 RTSSSG-----SAEPGA-----AHEMKSPSPARS-----SPH----- 1094
Db 859 KTPAAGQDRAEAPKASGEPGARERRPRHRSKELAGPEARSEGRGFGEGGRH 918
QY 1095 ---SPWSASSWTSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGQSDQDESSSE- 1148
Db 919 HRRGSPAEARERRPRHRAHH---QDPSKECAGAKERRARRHGGPRAGPREAESGSEP 975
QY 1149 -----ERASP-----AGSDHHRGSLREAEKSSDPLDPTL 1178
Db 976 ARHRAHKAQAHAWEKETEKEATEKEAEIWEADKEKELRNHQPREHCDDLTSGIV 1035
QY 1179 QYFGHRTASGRGSAHEQDCNGKSASGLARALRPDOP-----PLDGDADD 1226
Db 1036 TVGPMHTLPTSTCLQKVEQPEDADNQRNVTMGSPQDPDNTIVH.PVMLTGFLGEATVVE 1095
QY 1227 EGNL-----SKGER-----VRAMIRALPACYLERSWSYIIFPQSRFLLCHRIIT 1274
Db 1096 SGNVLESQAEGKKEVEADVMRSGPRPIVPS-----SMFCLSPNLLRFFCHYIIVT 1148

QY 1275 HKMEDHVVLVLIIFANCIITIAMERPKIDPHSABRIFLISNVIITAVFLAEMTVKVALGM 1334
Db 1149 MRYEVLVIVIALSSIALAAEDP-VRTDSPRNALKYLDYIFTGVTFEVIKIDJLGL 1207
QY 1335 CFGQOAVLRSSWNLVLDGLLVLSVIDIIVSMV-SDSGTKILGMLRVLRLTLPLRVRIS 1393
Db 1208 LLHFGAYFRDLWNLTLD---FIVVSGALVAFAPSGSGKDNITKSLVLRVLRPLKTIK 1263
QY 1394 RAQGLKLVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCOGE-----DTR 1447
Db 1264 RLPKLKAVFDCVNSLKNVNLILVYMLFMFIFAVIAVOLFEGKFFYCTDESKELERDCR 1323
QY 1448 N--ITNKSDCBAASYR-WVRHKYNPDNLGOALMSLFLVASKDWDIMYDGLDAGVDQO 1504
Db 1324 GOYLDYEEVEAQAQRQWKYDHYDNVLMALLTLFTVSTGEGWPMVLKHSVDAYEBOG 1383
QY 1505 PIMNENPMWLLYFISFLIVAFVFNMFVVVVENFHKRCQHOBEERREKRIRRIE 1564
Db 1384 PSPGYRMSLSFYVYVVFVFPFFVNIIFALLIITF-----OEQGDKMSE---CSLE 1433
QY 1565 KKRRKA-----QCKEY--YSDYSR--FRLLVHHLCTSHYLDLFTITGVGLNVVTWAMEHY 1615
Db 1434 KNERACIDPAISAKPLTRYPNQNRQSFQYKTWTFVVPPEFYFIMAMIALNTVWLMKFEY 1493
QY 1616 QOQFQILDEALKTCNIVTFVLESVFKLVAFRRFQDRMNQDLDAIVLISIMGITLE 1675
Db 1494 DAPIYELMKCLINIVFTSMESMECVLKIAPGVNLVFRDANWVDFVTVLGSITDILVT 1553
QY 1676 EIEVNASLPIINIIIRIHEVLAIRVLKLLKMAVGMRALLDTVMQALPQVGNLGLFMLL 1735
Db 1554 EIANNF---IN---JSLFLFRARLIKLLRQYTRILLWTWFVQSFKALPYVCLLIAML 1607
QY 1736 FFIYALIGMQVFNIALDDD---TSINRHNFRFTLQALMLLPRSATGEAWHEIMLSCLS 1664
Db 1796 D--CDQE--STCVNVTWISPIYFVSFVLTAQVFLVNVVIAVLM-----KHL 1836
QY 1665 NQACDEQANATECGSDFAVYFYFSLFCFLNLNFVAIMONFVIMONFEYLRDSSILGPHHL 1724
Db 1837 EE----- 1838
QY 1725 DEFIRVMAEYDPAACGRISYNDMFEMKMSPLGLGKKCPARVAYKELVRMNPISNED 1784
Db 1839 -----SNKBAKEEAELAELEBLEMTKLSQPQHSPLGSPFLW 1874
QY 1785 MTHVFTSLMALIARTALEIKLAPAGTKHQHOCDAELKEISVWVANL-PQKTLDLLVP--- 1840
Db 1875 PGVEGPDSPSPKPGALHPA-----AHARSASHFSLEHTW--- 1910
QY 1841 -----PHKPDWTVGKYAALMIFDFYQNKTTDQMQAPGGLSQMGVSLFHPILKATL 1895
QY 1911 QHPTTELDPDILLTVKRSVSRTHSLPNDSYMCRHGSTAEGPLGHRGWLGPKAQSGSVL 1969
Db 1896 EQTOPAVLRGARVFLRQKSTSLN-----GGAIONQESGIKE 1933
QY 1970 SVHSOPADTSYILQPKDAPHELLQ-----HSAPTWGTIPKLPPLPPSRPLAQRPLRQAA 2024
Db 1934 SV-----SWGTRQTDAPHEARPLERGHSTEI-----FVGRSGALAVDVQWQSI 1978
QY 2025 IR-----TDSLVQVGLGSRDILLAEVSGP---SPPLARAYSFWGQSSTOQOQHSRHS 2074
Db 1979 TRRGDPGRPPGLSQRGAASMPRLAETQVTDASPMKRSI-----STIAQPRGHHL 2032
QY 2075 KISKHMTPEAPCG-----PEPNWKGPPETRSSLELDELTELWISGDL 2117
Db 2033 CST---TPDRPPPSQASHHHHCHRRERDRKQSRLEKGP---SLSDMDGAPSAVGP 2086
QY 2118 LPPGQEBPPGRDOKCYSAVEASCQR--PTSMLEQORHSIAVCLDSG----- 2167
Db 2087 LPPG--EGTGCRRERRRQSRSRQRRQPSSSSEKQRF---YSCDRFGREPPKPKP 2141

QY 2168 -----SOPHIGTDP-----SNLGGQPL-----GGPGSRPKKKLSP-PSITI 2202
Db 2142 SLSSHPTSPAGQPHGPHGPGSGVNGSPLSTSGASTPGGRRQLPQTPLTPRPSITY 2201
QY 2203 -----DPESQGPRT--PP-SPG-----ICLRRAPSSDSKDLASGPDPSMAASP 2245
Db 2202 KTANSPIHAGAQTSIPSPGRLSRGLSEHALLQDPLS---QLAPG----- 2249
QY 2246 SPKKVLSLGLSSDP 2261
Db 2250 -----SRIGSDP 2256

RESULT 13

US-08-455-543A-47
; Sequence 47, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062

; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-455-543A-47

Query Match 14.7%; Score 1748.5; DB 1; Length 2339;
Best Local Similarity 24.2%; Pred. No. 3.4e-133;
Matches 641; Conservative 359; Mismatches 825; Indels 819; Gaps 85;
QY 27 GAGGRPGGSAEKDPSADSEAGLFPYPALAPVVF-----FVLSQDSRP 70
Db 25 GAGGAGGPGGLQPGQVLYKQTAQRARTWALYNPIPVKONCFVNRSLFVSEDNVV 84
QY 71 RSWCLRTVCNPFERISMLVILLNVCVTLMFRPCEDIACDSQRCRILQAFDD---FIPAF 127
Db 85 RYAKRITETWPPFENMILATIIANCIVLAL---EQHLPDGDKTPMSERLDDTEPFYIGI 140
QY 128 FAVEMVMVMVALG-IFGKCYLGDWTNRLDFFIVTAGMLEYS---LDLQNVFSFSAVTVR 183
Db 141 FCFEAGIKIIALGTFVHKGSYLRLNGWNVDMFVVVLTGLATAGTDFDLR-----TLRAVR 195
QY 184 VLRPLRAINRVPSMRILVTLLDITLMLGNVLLLCFFVFFIFGIVGVOLWAGLLNRNCF 243
Db 196 VLRPLKLVSGIPSLQVVLKSIKAMVPLQLGLLFFAILMFAIIGLSEFYMGKFKHACF- 254
QY 244 PENFSLPLSVDLERYQTEDEDESPFICSPRENGMRSRCSVPTLRGGGGPPCGLDYE 303
Db 255 -----PNSTDAE-----PV-----GDPPCGKEAP 273
QY 304 AYNSSNTTCVNMNYYTNCAGHNPKGAINPDNIGYAMIAIFQVITLGGWDMIVTV 363
Db 274 ARLCGDETC---REYWP-----GNFGITNFDNLFALTVPQCITMEGWTDLVNT 323
QY 364 MD-AHSFYNFYIFILLIIVGSGFFMINCLVVIATQFSETKORES-----CLMEQVRVF 416
Db 324 NDAAGTWNWLYFIPLLIIGSFFMLNLVGLVSEFAKERVENRRAFLRLRQQQIE- 382
QY 417 LSNASTLASPSEPGSCYEELKLYVYILRKAARLAQVRAAGVRVGLLSSPAPLGGQT 476
Db 383 -----RELNGYLEWIFKAEVVMLEEDRNA-----EEK 410
QY 477 QPSSSCSRSHRLSVHLLVHHHHHHHHHHLNGTILRAPRASPEIQORDANGSRMLPP 536
Db 411 SPLDLKRAATKKSRNDLIH-----AEEGEDRFAD----- 440
QY 537 PSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPSPSEASGRVTSKGVYPTVHTS 596
Db 441 ----- 440
QY 597 PPETILKEKALVEAASSGPPTLTSLNIPPGYSSMHKLELTQSTGACSSCKISSPCLX 656
Db 441 -----LCVAGSPPAR 450
QY 657 ADGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSUDLRPHSRQRSL 716
Db 451 ASLKSQKTESSEYFR-----KENMFRF----- 473
QY 717 GPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIALVNTLSMGIEYHEQPELTNALE 776
Db 474 -----FIRMVVRQSFYVWVLCVVALNTLCVAMVHNPQRRLTTLTY 515
QY 777 ISNIVFTSLFALEMLKLIVGPGFYKNPYNIFDGVIVVISVWEIVGQ-----QGGGLS 831
Db 516 FAEFVFLGLFLTEMSLKMVGLGFSYSSFFCFDGVIVGVSVFVWMAIKPGSSFGIS 575
QY 832 VLRTERLMEVLKVRFLPALQVILVLMKTMONVATFCMLMLFIFISILGMHLFGCKF 891
Db 576 VLRLRLRIFKVTKYWSSLRNLVSVLSNMSKSIISLLFLFLFIWFWALLQMLFGGQF 635

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QY 1804 YNTVISYFVSFVLTAQFVLVNVVIAVLM-----KHLEE----- 1838
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QY 1839 ----- 1838
Db 1739 AACGRISYNDMFEMLKHMSPLGLGKCPARVAYKELVRNMPISNEDMTVHTSTLMAL 1798
QY 1839 ----- 1838
Db 1799 IRTALEIKIAPAGTKHQCDALKEISVWVANL-PQKTLDLLVP-----PKPDEM 1849
QY 1887 KEGALHPA-----AHARSASHESLEHPTM-----QPHTELPQPD 1921
Db 1850 TVGKYAALMIFDFYKQNKTRTDQMQAPGGLSQMGVSLFHLPLKATLEQTPAVLRGAR 1909
QY 1922 LLTVKSGVSTHSLPNDSYNCRHGSTAEGPLGHRGWLGPKAQSGSVLSVHSQPADTSYI 1981
Db 1910 VFLRQKSTSLN-----GGAIQNGESGIKESV-----SWG 1940
QY 1982 LQLPKADAPHLQ-----HSAPTWTGTPKLPPLPGSRPLAORPLRQAAR-----TDS 2029
Db 1941 TQRTQAPHEARPLERGHSTEI-----PVGRSGALAVDVQMOSITRRGPDGEPQ 1992
QY 2030 LDVQGLGSRDLLAEVSGP---SPPLARAYSFWSQSTOAOQHSHSHKISXHMTPPAPC 2086
Db 1993 LSSQGRAASMPRLAAETQVTDASPMKRSI-----STUAQPRGTHLCST---TPDRPP 2043
QY 2087 PG-----PETNWKGPPTETRSSLELDTLSWISGDLPLPGQEPDPPSP 2129
Db 2044 PQASSHHHHRCHRRDRKQSRLEGP---SLSADMGAPSSAVGGLPPG---EGTGC 2098
QY 2130 RDLKCYCYEAQSCORR-PTSMLEDEORRHSHIAVCLDSG-----SOPHLG 2173
Db 2099 RREERRRQGRSGRQERRQPSSSSEKQRF---YSCDRFGGREGPPKPSLSHPTSETAG 2155
QY 2174 TDP-----SNLGGQPL-----GGPSRPPKKLSP-PSITI-----DPSESQ 2209
Db 2156 QEPGPHQSGSVNGSPLLSTGASTFGRRQLQTPLTPSPSYTYKTANSPIHFAG 2215
QY 2210 PRT--PP-SPG-----ICLRRRAPSDDSKDPLASGPPDSMAASPSKKOVLISGL 2257
Db 2216 AQTSLPAFSPRLSGRLSEHNALLQDPLS---QPLAPG-----SRI 2254
QY 2258 SSDP 2261
Db 2255 GSDP 2258

RESULT 14
US-08-223-305C-47
; Sequence 47, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESS: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/223,305C
/ FILING DATE: April 4, 1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/868,354
/ FILING DATE: April 10, 1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/745,206
/ FILING DATE: 15-AUG-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/620,250
/ FILING DATE: 30-NOV-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/482,384
/ FILING DATE: 20-FEB-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/603,751
/ FILING DATE: 04-APR-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US89/01408
/ FILING DATE: 04-APR-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/176,899
/ FILING DATE: 04-APR-1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seidman, Stephanie L.
/ REGISTRATION NUMBER: 33,779
/ REFERENCE/DOCKET NUMBER: 52516 (P519739)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619)238-0999
/ TELEFAX: (619)238-0062
/ INFORMATION FOR SEQ ID NO: 47:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2339 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-08-223-305C-47

Query March 14.7%; Score 1748.5; DB 2; Length 2339;
Best Local Similarity 24.2%; Pred.No.3.4e-133;
Matches 641; Conservative 359; Mismatches 825; Indels 819; Gaps 85;

QY 27 GAGRGPGGSAEKDPGSADSEAGLPALAPVVF-----FYLSDSRP 70
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Db 25 GAGGAGGPGGGLQPGORVLYKQIAORATMALYNFIPVKQNCFTVNRSLFVPSDDNVV 84
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QY 71 RSWCLRTVCNFWFERISMLVILLNCVTILGMFRPCEDIACDSQRCRIIQAADD---FIFAF 127
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Db 85 RKYAKRITWPPFPENMILATIANCIVIAL-----EQHLPDQKTPMERLDDTPEYFIGI 140
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 128 FAYEMVVVMVALG-IFKCKCYLGTWNRLDPFFIVIAGMLEYS---LDLQNVSFSAVRTVR 183
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 141 FCFEAGIKIIALGFVFHKGSLRNGWNVDFVVVLTGILATAGTDFDLR-----TLRAVR 195
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 184 VLRLPLRAINVPMSRIILVTLTLLTMLGNVLLLCFPVFIPIGVGVQLWAGLLRNRCLF 243
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 196 VLRLPLKLVSGIFSLQVVKLSIMKAMVELLQIGLLFFAILMFAIIGLEFYMGKFKACF- 254
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 244 PENFSLPLSVDLERYVQTENEDESPFICSPRENGMRSCRSVPTLRGDCGGGPGCLDYE 303
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 304 AYNSSNTTCVNNQYNTNCAGHNPFKGAINFDNIGYAMIAIFQVITLEGWVDIMYFV 363
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 274 ARLCGSDTEC---REYWP-----GNFGITNFDNLLFALLTVFQCIWEGWTDILYNT 323
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QY 364 MD-AHSFYNFIFILLIIVGSPFMINLCLVVIATQSETKQRES-----QLMREQRVRF 416
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 Db 441 -----LCAVGSPFAR 450
 QY 657 ADSGACGPDSCPCYCARAGAVELEADREMPDSDSEAVYETQQAQSHDURDPSRRQRL 716
 Db 451 ASLSKSTESSYFR-----KERXFR----- 473
 QY 717 GPDAEPSSVLAFWRLICDTRKIVDSKYFORGIMIALVNTLSMGLEYHEOPEELTNAL 776
 Db 474 -----FIRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRLLTTL 515
 QY 777 ISNIYFTSLFALMLKLIVYGFYKPNYNIFDGVIVVISWEIVGQ-----QGGGLS 831
 Db 516 FAEPVFLGLFTEMSLKMXYGLGPRSYFRSFCNFDFGVIVGVFEVVMAAIKPGSSFGLS 575
 QY 832 VLRTFLRMVLKLVFLPALQOLVLMKTMNVATFCMLLMFLPIFISILGHMHFGCKP 891
 Db 576 VLRLRLRLIFKTKWSSRLNLVSLNSKMSIISLLFLFLFIVFVALLQMLFGGQF 635
 QY 892 ASERDGLTLPDRKFNDSLLWITVTFQILTQEDWNKVLNGM-----ASTSSWAALYFTA 946
 Db 636 NFQDETPT-----TNEDTPAALTTFQILTGEDWNAVMYHGIESQGVSKGMFFSYFIV 691
 QY 947 LMTFGYVLFNLLVAILVEGF-QABEISK-----REDASQ-----LSCIQ 986
 Db 692 LTLFGNYTLNVLFLAIVADNLANAQELTKDEBEMEEMANOKLQAKAEVABVSFMSAAN 751
 QY 987 LPVDSQGDANKSESEDPFSPSLDGDGRKCLALVSLGE-----HPELRK 1033
 Db 752 ISIAARQONSARVWEQASQLRNLASCEALYSEMDPEERLRFATTHLRPDMDKT 811
 QY 1034 SLLPLLIHTAATMSLP-----KSTSTGLGALGPASR-----RTSSG----- 1073
 Db 812 HLDPLVELGDRGARGPVGKARPEAAEAGEVDPFRHHRHDKOKTPAAGQODRAEA 871
 QY 1074 -----SAPGA-----AHEMKSPPSARS-----SPH-----SPMSAASSW 1103
 Db 872 PKASSGFGAREERPRHRSHSKEAAGPPEARSEGRGPGEGGRHRRGSPPEAARE 931
 QY 1104 TSR-RSSRNSLGRAPSLKRRSPSERRSLLSGEQESODEESSEB-----ERASP- 1153
 Db 932 PRHRAHRH-----QDPSKECAGAKARHRGGRPRAGREAESGEEPAARRHARHKAQA 988
 QY 1154 -----AGSDHRHRSLEAKSSFDLPDTLOVPLGHRITASGRG 1191
 Db 989 HEAVEKETTEKEATEKEAIVEADKEKELRNHQPREPHCDLETSGTVVGPMTLPTCL 1048
 QY 1192 SASEHQCNKGSASGRILARLPDDP-----PLDGDADDDEGNL-----SKGE 1234
 Db 1049 QKVEEQPEDADNQRNVTRMGSPDPDPNTIVHI PVMLTGPLGEATVPFSGNVLDLESQAEK 1108
 QY 1235 R-----VRAWIRARLPACVLERDSAVIFPQSRFRLLCHRIITHKMFHDHVLVIF 1287
 Db 1109 KEVEADDVMSGRPIVPS-----SMFCLSETNLLRRFCHYIVTMRYFEVVLVIA 1161
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 Db 1162 LSSIALAAEDP-VRTDSPRNALKYLDYIFGTTFEMVIMKMDLGLLHPGAYFRDLWN 1220
 QY 1348 VLDGLVLISVIDILVSMV-SDSGTKILGMLRVLRLRLTLPRLVISAQGLKLVAVETLM 1406
 Db 1221 ILD-----FIVVSGALVAFSGSGKDINTIKSLRVLRLVRLPLKTIKRLPKLXAVDCV 1276
 QY 1407 SSLKIGNIVICCAFIIFGILGVQLFKGKFFVCOGE-----DTRN-----ITNKSQCAEA 1458
 Db 1277 NSLKNVILIVYMLFMFIFAVTAVQLFKGKFFYCTDESKELERDCRGQVLDYKEEVEA 1336
 QY 1459 SYR-WVRHKYNFONLGOALMSFLVASKQGVIMYDGLDAGVQDQOPMHNWMLLYF 1517
 Db 1337 QPQWKKYDHYDNVLWALLTFTVSTGEGWPMVLKHSVDATYEEQGPSGVAMELSIFY 1396

QY 1518 ISPLLIVAFVFLNMFVGVVVVENPHKCRQHQEERREARRRERLRLLEKKRKA-----QC 1572
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 QY 1573 KPY--YSDYSR--FRLLVHHLCTSHYLDLFTIGVIGLVNVTWMAHEHYQOQILDEALKIC 1628
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 Db 1507 NIVFTSMFMECVKLIIFAGVLNYPFRDANNVDFVTVLGSITDLVTEAETN-----NF 1561
 QY 1688 TIIRIMVLRIRARVLKLLKMAVGMALLDTVMQALPQVGNLGLLMLFFIFAALGVLELF 1747
 Db 1562 INLSLRFLRAARLLKLLRQGGYTIIRILLWTFQSKALFVYVCLLAMLFFVAILGMQVF 1621
 QY 1748 GLECDETHPCBGLGRHATFRNFGMAFTLFRVSTGDWNGIMKOTLRD--CDOE--STC 1803
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 QY 1887 KPGALHPA-----AHARSASHPSLEHPTM-----QPHTELPGD 1921
 Db 1850 TVGKYAALMTFDFYKQNTTRDQMQAPGGLSQMGVSLFHPKATLEQTOQPAVLROAR 1909
 QY 1922 LLTVRKSVSTHSLPNDNSMCRHGSTAEGPLGHRGWLGLPKAQSGSVLSVHSQFADTSYI 1981
 Db 1910 VFLQKSTSLSN-----GGAIQNESGIKESV-----SWG 1940
 QY 1982 LQLPKDAPHLLQP-----HSAPTWTGTIPKPPPGESPLAQBPPLRQAIR-----TDS 2029
 Db 1941 TQTQDAPHEARPPLEGRHSTEI-----PVRSGALAVDVMQMSITRGRGDPGEFQPG 1992
 QY 2030 LDVGLGSRREDLLAEVSGP---SPPLARAYSFWQSQSTQAQOHSRSHSKIKHMTTPAPC 2086
 Db 1993 LESQGRAASMPRLAAETQPVTDASPMKRSI-----STLAQRPGRGTHLCST---TPDRPP 2043
 QY 2087 PG-----PEPNWKGKPPETRSLELDTELSTWISGDLPLPGQOEPPSP 2129
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 QY 2174 TDP-----SNLGGQPL-----GGPSRPRKKLSP-PSITI-----DPBESQ 2209
 Db 2156 QEPGPHPGSGSVNGSPLLSTSCASTGRRRQLPQTLTPRPSITYKTANSPIHFAG 2215
 QY 2210 PRT--PP-SPG-----ICLRRAPSDSKDPLASGPPDSMAASPSPKDVLISGL 2257
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 Db 2255 GSDP 2258

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 Job time : 77.3132 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:32:41 ; Search time 178.672 Seconds
(without alignments)
4491.206 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEDGAGAEESGQPRSPM.....PKKVLISLGLSSDPADLDP 2266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	ID	Description
1	11815.5	99.3	2377	17	US-10-757-262-16	Sequence 16, Appl
2	11758.5	98.8	2243	16	US-10-408-765A-625	Sequence 625, App
3	11111	93.3	2374	10	US-09-383-894-2	Sequence 2, Appl
4	11111	93.3	2425	10	US-09-383-894-4	Sequence 4, Appl
5	6212	52.2	2353	16	US-10-408-765A-1128	Sequence 1128, Ap
6	5492.5	46.1	2175	9	US-09-935-541-2	Sequence 2, Appl
7	5492.5	46.1	2175	14	US-10-425-800-2	Sequence 2, Appl
8	5484	46.1	2188	9	US-09-935-541-4	Sequence 4, Appl
9	5484	46.1	2188	14	US-10-425-800-4	Sequence 4, Appl
10	5366	45.1	1835	9	US-09-935-541-5	Sequence 5, Appl
11	5366	45.1	1835	14	US-10-425-800-5	Sequence 5, Appl
12	3959.5	33.3	1853	9	US-09-030-482B-19	Sequence 19, Appl
13	3564.5	29.9	1657	14	US-10-369-493-6836	Sequence 6836, Ap

14	1753	14.7	2264	15	US-10-627-370-2	Sequence 2, Appl
15	1750.5	14.7	2343	13	US-10-033-026-4	Sequence 4, Appl
16	1748.5	14.7	2339	15	US-10-375-253-12	Sequence 12, Appl
17	1746.5	14.7	2339	13	US-10-033-026-6	Sequence 6, Appl
18	1746.5	14.7	2339	17	US-10-736-883-32	Sequence 32, Appl
19	1743	14.6	2237	15	US-10-375-253-14	Sequence 14, Appl
20	1741	14.6	2237	13	US-10-033-026-8	Sequence 8, Appl
21	1741	14.6	2237	17	US-10-736-883-34	Sequence 34, Appl
22	1740.5	14.6	2333	17	US-10-736-883-38	Sequence 38, Appl
23	1732.5	14.6	2327	17	US-10-736-883-38	Sequence 38, Appl
24	1729.5	14.5	2331	17	US-10-736-883-44	Sequence 44, Appl
25	1722	14.5	2336	13	US-10-033-026-10	Sequence 10, Appl
26	1722	14.5	2336	17	US-10-736-883-30	Sequence 30, Appl
27	1714	14.4	2288	17	US-10-736-883-40	Sequence 40, Appl
28	1710	14.4	2339	17	US-10-736-883-42	Sequence 42, Appl
29	1673.5	14.1	1745	15	US-10-627-370-4	Sequence 4, Appl
30	1667	14.0	2313	16	US-10-322-696-178	Sequence 178, App
31	1665	14.0	2270	15	US-10-375-253-40	Sequence 40, Appl
32	1663.5	14.0	2251	15	US-10-375-253-38	Sequence 38, Appl
33	1659	13.9	2270	16	US-10-322-696-176	Sequence 176, App
34	1657.5	13.9	2251	16	US-10-322-696-84	Sequence 84, Appl
35	1632	13.7	1873	13	US-10-029-413A-22	Sequence 22, Appl
36	1625.5	13.7	1748	16	US-10-408-765A-1968	Sequence 1968, Ap
37	1619.5	13.6	1984	10	US-09-457-571-10	Sequence 10, Appl
38	1615.5	13.6	1989	10	US-09-457-571-12	Sequence 12, Appl
39	1602	13.5	2016	16	US-10-632-342-2	Sequence 2, Appl
40	1602	13.5	2510	15	US-10-375-253-34	Sequence 34, Appl
41	1598.5	13.4	2015	16	US-10-632-342-6	Sequence 6, Appl
42	1597.5	13.4	2157	16	US-10-467-491-2	Sequence 2, Appl
43	1596.5	13.4	2151	16	US-10-467-491-4	Sequence 4, Appl
44	1594	13.4	2016	15	US-10-632-342-4	Sequence 4, Appl
45	1591	13.4	1854	13	US-10-029-413A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-757-262-16
; Sequence 16, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MPI03-007PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156

; PRIOR FILING DATE: 2003-07-30
 ; PRIOR APPLICATION NUMBER: US 60/499,594
 ; PRIOR FILING DATE: 2003-09-02
 ; PRIOR APPLICATION NUMBER: US 60/506,332
 ; PRIOR FILING DATE: 2003-09-26
 ; NUMBER OF SEQ ID NOS: 136
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 2377
 ; TYPE: PR2
 ; ORGANISM: Homo sapiens
 ; US-10-757-262-16

Query Match 99.3%; Score 11815.5; DB 17; Length 2377;
 Best Local Similarity 95.2%; Pred. No. 0;
 Matches 2264; Conservative 1; Mismatches 1; Indels 111; Gaps 2;

QY	1	MDEEDGAGAESGQPRSMRLNDLSGAGRPGSAEKDPGSAADSEAGLPPALAPV	60
DB	1	MDEEDGAGAESGQPRSMRLNDLSGAGRPGSAEKDPGSAADSEAGLPPALAPV	60
QY	61	EFVLSQDSRPNWCLRTVCPNPERISMLVILNCVTLGMFRPCEDIACDSQRCRILQAF	120
DB	61	EFVLSQDSRPNWCLRTVCPNPERISMLVILNCVTLGMFRPCEDIACDSQRCRILQAF	120
QY	121	DDFIFAFFAVEMVVMVALGIFGKKCYLGDWNRDLFFIVIAQMLEYSIDLQVSESAYR	180
DB	121	DDFIFAFFAVEMVVMVALGIFGKKCYLGDWNRDLFFIVIAQMLEYSIDLQVSESAYR	180
QY	181	TVRVLRLPRAINVPMSRIILVTLTLMGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240
DB	181	TVRVLRLPRAINVPMSRIILVTLTLMGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240
QY	241	CFLPENFSLPLSDVLEERYOTENEDSPFFICSPRENGMESCRCVPTLRGDGGGPPCGL	300
DB	241	CFLPENFSLPLSDVLEERYOTENEDSPFFICSPRENGMESCRCVPTLRGDGGGPPCGL	300
QY	301	DYBAYNSSNTTCVNMQYVNTCSAGBNPFKGAINDNIGYAWIAFQVITILEGWVDIM	360
DB	301	DYBAYNSSNTTCVNMQYVNTCSAGBNPFKGAINDNIGYAWIAFQVITILEGWVDIM	360
QY	361	YFVMDAHSFYNYFIILLIIVGSPFMNLCVLIATQFSETKQRESQLMREQVRFLSNA	420
DB	361	YFVMDAHSFYNYFIILLIIVGSPFMNLCVLIATQFSETKQRESQLMREQVRFLSNA	420
QY	421	STLASFSEPGSCYBELLKYLVIILKKAARLAQVSRAGVRVGLLSSPAPLGGQETQPS	480
DB	421	STLASFSEPGSCYBELLKYLVIILKKAARLAQVSRAGVRVGLLSSPAPLGGQETQPS	480
QY	481	SCSSSHRRLSVHLLVHHHHHHHHVHLNGTLRAPRASPEITODRDANGSRRLMLPPSTP	540
DB	481	SCSSSHRRLSVHLLVHHHHHHHHVHLNGTLRAPRASPEITODRDANGSRRLMLPPSTP	540
QY	541	ALSGAPPGGASVHSFYHADCHLEPVRCAAPPPSPSEASGRITVSGKVYPTVHTSPPE	600
DB	541	ALSGAPPGGASVHSFYHADCHLEPVRCAAPPPSPSEASGRITVSGKVYPTVHTSPPE	600
QY	601	TLKEKALVEVAASSGPPTLTSINIPPGPYSSMHKLETTQSTGACQSSCKISSPCLKADSG	660
DB	601	TLKEKALVEVAASSGPPTLTSINIPPGPYSSMHKLETTQSTGACQSSCKISSPCLKADSG	660
QY	661	ACGPDSCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQSHSLDRPHSRQRSLGPD	720
DB	661	ACGPDSCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQSHSLDRPHSRQRSLGPD	720
QY	721	EPSSVLAERLLCDTFRKIVDSKYFGRGIMAILVNTLSMGLEYHEQPEELTNALEISNI	780
DB	721	EPSSVLAERLLCDTFRKIVDSKYFGRGIMAILVNTLSMGLEYHEQPEELTNALEISNI	780
QY	781	VFTSLFALEMLKLLVYGPFGYKPNYINFDGVIVVISWEIVGQCGGLSVLRTFLMR	840
DB	781	VFTSLFALEMLKLLVYGPFGYKPNYINFDGVIVVISWEIVGQCGGLSVLRTFLMR	840

QY	841	VKLVRFLPALQRLVLMKTMNDNVATFCMLMLFIPIFISILGMHLFCCKEASERDGTLL	900
DB	841	VKLVRFLPALQRLVLMKTMNDNVATFCMLMLFIPIFISILGMHLFCCKEASERDGTLL	900
QY	901	PDRKNFDSLLWAIIVTVFOILTQEDWNKVLXNGMASTSSWAALYFIALMTFGNYVLFNLIV	960
DB	901	PDRKNFDSLLWAIIVTVFOILTQEDWNKVLXNGMASTSSWAALYFIALMTFGNYVLFNLIV	960
QY	961	AIIVEGFOAEISKREDASGQLSCIQLPVDSDGGDANKSESPDFPSLDGDRKKCL	1020
DB	961	AIIVEGFOAEISKREDASGQLSCIQLPVDSDGGDANKSESPDFPSLDGDRKKCL	1020
QY	1021	ALVSLGEHPELRKSLPPLIITHAATPMSLPKSTSTGLGEALGPASRRSSSGSAEGAA	1080
DB	1021	ALVSLGEHPELRKSLPPLIITHAATPMSLPKSTSTGLGEALGPASRRSSSGSAEGAA	1080
QY	1081	HEMKSPPSARSPSPHSPWASNAASWTSSRSRNSLGRAPSLKRRSPGSEERSLSLSEGEQESQ	1140
DB	1081	HEMKSPPSARSPSPHSPWASNAASWTSSRSRNSLGRAPSLKRRSPGSEERSLSLSEGEQESQ	1140
QY	1141	DEESESSEERASGPDGHRHRSLEREAKSSFDLPDLQVPGHLRTASGRGSAEHQDCN	1200
DB	1141	DEESESSEERASGPDGHRHRSLEREAKSSFDLPDLQVPGHLRTASGRGSAEHQDCN	1200
QY	1201	GKSASGLRALARPDDPPDLGDDADDEGNLSKGERVRAMIRARLPACYLERSWSAYIFP	1260
DB	1201	GKSASGLRALARPDDPPDLGDDADDEGNLSKGERVRAMIRARLPACYLERSWSAYIFP	1260
QY	1261	POSREFLLCHRIITHKQFDHVVLIIFLNCITITAMERP KIDPHSAERIFLTSNYIFTAV	1320
DB	1261	POSREFLLCHRIITHKQFDHVVLIIFLNCITITAMERP KIDPHSAERIFLTSNYIFTAV	1320
QY	1321	FLAEMTVKVVVALGWCQEAYLSSWNVDLGLVLIISVIDILVSMVSDSGTKILGMLRVL	1380
DB	1321	FLAEMTVKVVVALGWCQEAYLSSWNVDLGLVLIISVIDILVSMVSDSGTKILGMLRVL	1380
QY	1381	RLRLTLRPLRVISRAQGLKLIVETIMSSLKPIGNIVVICAFPIIFGILGVQLFKGKFFV	1440
DB	1381	RLRLTLRPLRVISRAQGLKLIVETIMSSLKPIGNIVVICAFPIIFGILGVQLFKGKFFV	1440
QY	1441	COGEDTNTINKSDCAEASVYRWVHKYFNFDNLQALMSLFLVASKDQWVDIMYDGLDVG	1500
DB	1441	COGEDTNTINKSDCAEASVYRWVHKYFNFDNLQALMSLFLVASKDQWVDIMYDGLDVG	1500
QY	1501	VDQOPIMNHNPMMLLYFISELLIVAFVLMNVGVVVENFHKCRQHOEEBEEARRERKRL	1560
DB	1501	VDQOPIMNHNPMMLLYFISELLIVAFVLMNVGVVVENFHKCRQHOEEBEEARRERKRL	1560
QY	1561	RLLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTGV	1620
DB	1561	RLLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTGV	1620
QY	1603	IGLVNVTWAMEHYOQOQILDEALKICNVITFVLESVFKLVAFGRFRFPQDRWNQDL	1662
DB	1621	IGLVNVTWAMEHYOQOQILDEALKICNVITFVLESVFKLVAFGRFRFPQDRWNQDL	1680
QY	1663	AIIVLLSINGITLIEIEVNASLPINPTIIRINVRIRARVLKLLKXAVGNRALLDTVMQAL	1722
DB	1681	AIIVLLSINGITLIEIEVNASLPINPTIIRINVRIRARVLKLLKXAVGNRALLDTVMQAL	1740
QY	1723	POVGNLGLLFFLFFIIPALGVLELFGDLECDDETHPCGELGRHATFRNFGMAFLTLFRVST	1782
DB	1741	POVGNLGLLFFLFFIIPALGVLELFGDLECDDETHPCGELGRHATFRNFGMAFLTLFRVST	1800
QY	1783	GDNNNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVNVIATVLMKHEESNKE	1842
DB	1801	GDNNNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVNVIATVLMKHEESNKE	1860
QY	1843	AKEEAELEAELEMKTLSPQHPSPGSPFLWPVGEGPDSPKPGALHAAHARSASH	1902
DB	1861	AKEEAELEAELEMKTLSPQHPSPGSPFLWPVGEGPDSPKPGALHAAHARSASH	1920
QY	1903	PSLEHT-----	1909

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Db 1921 FSLEHPTDQLFDTTISLLTQGSLEWELKLMDELACGPGQPSAFPSAPSLGSDPQIPLAE 1980
Qy 1910 -----MQPHETELPGPDLITVRKSG 1929
Db 1981 MEALSLTSEIVSEPCSLALTDLSLPDDMHITLLLSALESNMQPHETELPGPDLITVRKSG 2040
Qy 1930 VSRTHSLPNDYSYMRHGSTAEGPLGHRGWLGPKAQSGSVLSVHSPADTSYILOLPKADP 1989
Db 2041 VSRTHSLPNDYSYMRHGSTAEGPLGHRGWLGPKAQSGSVLSVHSPADTSYILOLPKADP 2100
Qy 1990 HLLQHSAPTWTGIIKLPPLPGRSPLAQRPLRQAAIRTDSDVOGLGSRDILAEVSGPS 2049
Db 2101 HLLQHSAPTWTGIIKLPPLPGRSPLAQRPLRQAAIRTDSDVOGLGSRDILAEVSGPS 2160
Qy 2050 PPLARAYFWGQSSQTAQOQHSRSHKISKHMTTPAPCPGPRNWKGPETRSSLELDE 2109
Db 2161 PPLARAYFWGQSSQTAQOQHSRSHKISKHMTTPAPCPGPRNWKGPETRSSLELDE 2220
Qy 2110 LSWISGDLPLPGGQBEPPSPRLDKCYVSAQSCQRRPTSWLDEQRHSIAVSCLDGSQ 2169
Db 2221 LSWISGDLPLPGGQBEPPSPRLDKCYVSAQSCQRRPTSWLDEQRHSIAVSCLDGSQ 2280
Qy 2170 PHLGTDPSNLGGQPLGGGSRPKKLSPPSITIDPPESQGRTPPSPGICLRRRAPSDS 2229
Db 2281 PHLGTDPSNLGGQPLGGGSRPKKLSPPSITIDPPESQGRTPPSPGICLRRRAPSDS 2340
Qy 2230 KDPLASGPPDPSMAASPSPKDVLISLGLSSDPADLDP 2266
Db 2341 KDPLASGPPDPSMAASPSPKDVLISLGLSSDPADLDP 2377
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RESULT 2

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US-10-408-765A-625
; Sequence 625, Application US/10408765A
; Publication No US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 625
; LENGTH: 2243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-625
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Query Match 98.9%; Score 11758.5; DB 16; Length 2243;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 1; Indels 23; Gaps 1;

Qy 1 MDEEDGAGAEESGQPRSFMRNLDSGAGGRPGPSAEKDPGSADEAGLPPALAPVV 60
Db 1 MDEEDGAGAEESGQPRSFMRNLDSGAGGRPGPSAEKDPGSADEAGLPPALAPVV 60
Qy 61 FFYLSQDSRSPRCLRTVCNPNWFERISMLVILNCVTLMFRPCDIACSQRILQAF 120
Db 61 FFYLSQDSRSPRCLRTVCNPNWFERISMLVILNCVTLMFRPCDIACSQRILQAF 120
Qy 121 DDFIFAFFAVEMVVKVALGIFGKKCYLGDWNRLODFIVIAQMLYSIDLQNVFSAVR 180
Db 121 DDFIFAFFAVEMVVKVALGIFGKKCYLGDWNRLODFIVIAQMLYSIDLQNVFSAVR 180
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Qy 181 TVRVLRPRAINRVPMSRILVTLTLLDTPMLGNVLLLCFFVFFIIFGIIVGVQVWAGLLRNR 240
Db 181 TVRVLRPRAINRVPMSRILVTLTLLDTPMLGNVLLLCFFVFFIIFGIIVGVQVWAGLLRNR 240
Qy 241 CFLPENFSLPLSVDLERYQTEENEDSPFIQSPRENGMRSCRSVPTLRGCGGPPCCGL 300
Db 241 CFLPENFSLPLSVDLERYQTEENEDSPFIQSPRENGMRSCRSVPTLRGCGGPPCCGL 300
Qy 301 DYEAYNSSNTTCVNNQYNYNCASAGHNPKFAGNFDNIGYAWIAIFQVITLEGWVDIM 360
Db 301 DYEAYNSSNTTCVNNQYNYNCASAGHNPKFAGNFDNIGYAWIAIFQVITLEGWVDIM 360
Qy 361 YFVMDAHFYFIYFILLIIVGSPFMNLCVWITATQSETKQRESQLMRQVRVFLNA 420
Db 361 YFVMDAHFYFIYFILLIIVGSPFMNLCVWITATQSETKQRESQLMRQVRVFLNA 420
Qy 421 STLASFSPGSCYBELLYVILRKAARRLAQVRAAGVRVGLLSSPAPLGQGTQSS 480
Db 421 STLASFSPGSCYBELLYVILRKAARRLAQVRAAGVRVGLLSSPAPLGQGTQSS 480
Qy 481 SCSSRHRLSLVHLLVHHHHHHHHHHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db 481 SCSSRHRLSLVHLLVHHHHHHHHHHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
Qy 541 ALSGAPPGCAESVHSFYHADCHLEPVRCAOPPPSPSEASGRTVSGKVTYVHTSPPE 600
Db 541 ALSGAPPGCAESVHSFYHADCHLEPVRCAOPPPSPSEASGRTVSGKVTYVHTSPPE 600
Qy 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660
Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660
Qy 661 ACGPDCPYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRQRSLGPD 720
Db 661 ACGPDCPYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRQRSLGPD 720
Qy 721 EPSSVLAFWRILICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780
Db 721 EPSSVLAFWRILICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780
Qy 781 VFTSLFALEMLLKLVLVYGPFGYIKNPYINIDGVTWISVWEIVGQGGSLVLTFRMLR 840
Db 781 VFTSLFALEMLLKLVLVYGPFGYIKNPYINIDGVTWISVWEIVGQGGSLVLTFRMLR 840
Qy 841 VLKLVRLPALQRLVLMKTMONVATFCMLLMFIFIFSILGMHLFGCKFASERDGTLL 900
Db 841 VLKLVRLPALQRLVLMKTMONVATFCMLLMFIFIFSILGMHLFGCKFASERDGTLL 900
Qy 901 PDRKNFDSLWALVTVFQILTOEDMKNKLYNGMASTSSWAALYFIALMTGNVLFNLIV 960
Db 901 PDRKNFDSLWALVTVFQILTOEDMKNKLYNGMASTSSWAALYFIALMTGNVLFNLIV 960
Qy 961 AILVEGFQAEISKREDASQGLSCIQLPVDSCQGDANKSESEPOFFSPSLDGDGDKKCL 1020
Db 961 AILVEGFQAE-----GDANKSESEPOFFSPSLDGDGDKKCL 997
Qy 1021 ALVSLGEHPELRKSLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAPGAA 1080
Db 998 ALVSLGEHPELRKSLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAPGAA 1057
Qy 1081 HEMKSPSPASRSPSPSWSAASWTSRRSRNSLGRAPSLKRRSPGSRERSLLSGEGQESQ 1140
Db 1058 HEMKSPSPASRSPSPSWSAASWTSRRSRNSLGRAPSLKRRSPGSRERSLLSGEGQESQ 1117
Qy 1141 DEEESSEERAPAGSDHHRHRSLEAKSSFDLPDLTVPGIHRTASGRGSAEHODCN 1200
Db 1118 DEEESSEERAPAGSDHHRHRSLEAKSSFDLPDLTVPGIHRTASGRGSAEHODCN 1177
Qy 1201 GKSASGLARALRPDPPLDGDADDDEGNLSKGERVRAMIRARLPACYLERSWSAYIFP 1260
Db 1178 GKSASGLARALRPDPPLDGDADDDEGNLSKGERVRAMIRARLPACYLERSWSAYIFP 1237
Qy 1261 POSRFLLCRRIITHKMFHDHVVVLIIFLNCITIAMER?KIDPHSABRIFLTLNSYIFTAV 1320
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1238 POSRRLCHRIITHKMDHVVULVILFNCITIAMERKIDPHSARIFLISNVIFAV 1297
1321 FLAEMTVKVALGWCFCQAYLRSSWVLDGLLVLSVIDILVMSVSGTKILGMLRVL 1380
1298 FLAEMTVKVALGWCFCQAYLRSSWVLDGLLVLSVIDILVMSVSGTKILGMLRVL 1357
1381 RLLETRRLRVLSRAQGLKLVVETLMSLKPIGNIWIICCAFFIIFGILGVLFGKGFV 1440
1358 RLLETRRLRVLSRAQGLKLVVETLMSLKPIGNIWIICCAFFIIFGILGVLFGKGFV 1417
1441 COGEDTRNITNKSDCAEASRYVRKYNFNDLGOALMSLFLVLSKDGWVDIMYDGLDVG 1500
1418 COGEDTRNITNKSDCAEASRYVRKYNFNDLGOALMSLFLVLSKDGWVDIMYDGLDVG 1477
1501 VDQOPIMNHPWMLLYFISFLIIVAFVLMVFGVVVNFHRCRQHEEEERARRREKRL 1560
1478 VDQOPIMNHPWMLLYFISFLIIVAFVLMVFGVVVNFHRCRQHEEEERARRREKRL 1537
1561 RLLEKRRKAQCKPYSDYSRRLVHLLCTSHYLDLFTVGLNVVTMAHEHYQOPOI 1620
1538 RLLEKRRKAQCKPYSDYSRRLVHLLCTSHYLDLFTVGLNVVTMAHEHYQOPOI 1597
1621 LDEALKICNYITFVIFVLESVKLVAFGFRFFQDRWNQDLAIIVLLSIMGITLBEIEVN 1680
1598 LDEALKICNYITFVIFVLESVKLVAFGFRFFQDRWNQDLAIIVLLSIMGITLBEIEVN 1657
1681 ASLPINPFTIIRMRVLRIRARVILKLVAVGMRALDVTVMQALPOVGNLGLPMLFFIFA 1740
1658 ASLPINPFTIIRMRVLRIRARVILKLVAVGMRALDVTVMQALPOVGNLGLPMLFFIFA 1717
1741 ALGVLELFGDLEDETHPCGLGHATFRNFGMAFLTLFRVSTGDNNGIMKOTLRDQOE 1800
1718 ALGVLELFGDLEDETHPCGLGHATFRNFGMAFLTLFRVSTGDNNGIMKOTLRDQOE 1777
1801 STCYNTVISPYPVSVFLTAQFVLNVVIAVLMKHEESKEAEAELESEMKTLL 1860
1778 STCYNTVISPYPVSVFLTAQFVLNVVIAVLMKHEESKEAEAELESEMKTLL 1837
1861 SPQFHSPLGSPFLWPGVEGSDPSKPGALHPAAHARSASHFSLEHPTMQPHTLPGP 1920
1838 SPQFHSPLGSPFLWPGVEGSDPSKPGALHPAAHARSASHFSLEHPTMQPHTLPGP 1897
1921 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWI:PKACSGSVLSVHSPADTSY 1980
1898 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWI:PKACSGSVLSVHSPADTSY 1957
1981 ILQLPKDAHLLQPHSAPTWTGTPKLPPLPGRSPLAQRLRRQAAIRTDSDVQGLGSRD 2040
1958 ILQLPKDAHLLQPHSAPTWTGTPKLPPLPGRSPLAQRLRRQAAIRTDSDVQGLGSRD 2017
2041 LLAEVSGSPPLARAYSFWQGSSTQAQOHSRSHSKISKXMTTPAPCPGPFENWKGPPET 2100
2018 LLAEVSGSPPLARAYSFWQGSSTQAQOHSRSHSKISKXMTTPAPCPGPFENWKGPPET 2077
2101 RSSLELDELTSWISGDLPLPGQOEPPSPDLKKCYVEAQSCORRTSMWDEORRHSIA 2160
2078 RSSLELDELTSWISGDLPLPGQOEPPSPDLKKCYVEAQSCORRTSMWDEORRHSIA 2137
2161 VSCLDGSGPHLGTDPNGLGQPLGPGSRPKKLSPPSITIDPPESQGRTPPSPGICL 2220
2138 VSCLDGSGPHLGTDPNGLGQPLGPGSRPKKLSPPSITIDPPESQGRTPPSPGICL 2197
2221 RRRAPSSDSKDPPLASGPPDSMAASPSPKDVLSLSGLSSPADLDP 2266
2198 RRRAPSSDSKDPPLASGPPDSMAASPSPKDVLSLSGLSSPADLDP 2243

RESULT 3
US-09-383-894-2
; Sequence 2, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:

; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2374
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-383-894-2

Query Match 93.3%; Score 11111; DB 10; Length 2374;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;

QY 1 MDEEDGAGAESGQPRSFMRNDLSGAGRPGSGAEKDPGSADSEAEGLPYPALAPV 60
Db 1 MDEEDGAGAESGQPRSFMRNDLSGAGRPGSGAEKDPGSADSEAEGLPYPALAPV 60
QY 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTILGKFRPCEDIAQSORCRLQAF 120
Db 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTILGKFRPCEDIAQSORCRLQAF 120
QY 121 DDFIAPFAFVAVVVKVVALGIFGKCYLGTWNRDLDFRIVAGMLBYSIDLQVNSFSVR 180
Db 121 DDFIAPFAFVAVVVKVVALGIFGKCYLGTWNRDLDFRIVAGMLBYSIDLQVNSFSVR 180
QY 181 TVRVLRPLRAINRVPMSRILVTLTDLTLPMLGNVLLLCFFVFFIFGIVGVQWAGLLRNR 240
Db 181 TVRVLRPLRAINRVPMSRILVTLTDLTLPMLGNVLLLCFFVFFIFGIVGVQWAGLLRNR 240
QY 241 CFLPENFSLPLSDVLEERYQTNEDSPFICSOPTRENGMRSCRSVPTLRGDGGGGPPCGL 300
Db 241 CFLPENFSLPLSDVLEERYQTNEDSPFICSOPTRENGMRSCRSVPTLRGDGGGGPPCGL 300
QY 301 DYEAYNSSNTTCVNNQVYTCNSAGEHNPFGKAINFDNIGYAWIAIFOVITLEGWVDIM 360
Db 301 DYEAYNSSNTTCVNNQVYTCNSAGEHNPFGKAINFDNIGYAWIAIFOVITLEGWVDIM 360
QY 361 YFVMDAHSFYNTFYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
Db 361 YFVMDAHSFYNTFYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
QY 421 STLASFSEPGSCYBEELLKYLIVYILRKAARLAQVSRAGVRLGLLSPAPLGGQETQPS 480
Db 421 STLASFSEPGSCYBEELLKYLIVYILRKAARLAQVSRAGVRLGLLSPAPLGGQETQPS 480
QY 481 SCRSRHRRLSVHLLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db 481 SCRSRHRRLSVHLLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCAQPPRPSSEASGRVVGSKVPTVHTSPPE 600
Db 541 TPSGGPPRGAESVHSFYHADCHLEPVRCAQPPRPSSEASGRVVGSKVPTVHTSPPE 600
QY 601 TLKEKALVVEAASGPPTLTSLNIPPGPYSMHKLLETQSTGACOSSCKISSPCLKADSG 660
Db 601 ILKDKALVEVAPSPGPTLTSPNIPPGPYSMHKLLETQSTGACOSSCKISSPCLKADSG 660
QY 661 ACPGDSQPCYCARAGAGVELADREMPDSDSEAVVEFTQDAQHSDLRDPHS-RRORSILGPD 719
Db 661 ACPGDSQPCYCARAGAGVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRORSILGPD 720
QY 720 AEPSSVLAFWRLICDTFRKIVDSKYFORGIMAILVNTLSMGIEYHQPBEELTALALSN 779
Db 721 AEPSSVLAFWRLICDTFRKIVDSKYFORGIMAILVNTLSMGIEYHQPBEELTALALSN 780

QY 780 IVFTSLFALEMLKLVYGFYKPNYNI FDGVIIVISWEIVGQGGSLVLRTRLM 839
DB 781 IVFTSLFALEMLKLVYGFYKPNYNI FDGVIIVISWEIVGQGGSLVLRTRLM 840
QY 840 RVKLVRFLPALQOLVLMKMDNVATFCMLLMFLFIFISILGMHLFCKPASERBDGDT 899
DB 841 RVKLVRFLPALQOLVLMKMDNVATFCMLLMFLFIFISILGMHLFCKPASERBDGDT 900
QY 900 LPDRKNFDSLLWAI VTVFOILLTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLENLL 959
DB 901 LPDRKNFDSLLWAI VTVFOILLTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLENLL 960
QY 960 VAILVEGFOABEISKREASGOLSCIQLPVDSQGGDANKSESEPFDFPSLGDGDRKCK 1019
DB 961 VAILVEGFOABEIGKREASGOLSCIQLPVDSQGGDANKSESEPFDFPSVGDGDRKCK 1020
QY 1020 LALVLSIGHEPELRSKLLPPLIITHTAATPMSLPKSTSTGLGEALGPASRRTSSGSAEPGA 1079
DB 1021 LALVLSIGHEPELRSKLLPPLIITHTAATPMSLPKSTSTGLGEALGPASRRTSSGSAEPGA 1080
QY 1080 A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGOE 1138
DB 1081 AHHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGOE 1140
QY 1139 SODEEESSEERASPAAGSHRHRGSLEREAKSSFDLPDTLQVPGHLRTASGRGSAEHQD 1198
DB 1141 SODEEESSEERASPAAGSHRHRGSLEREAKSSFDLPDTLQVPGHLRTASGRGSAEHQD 1200
QY 1199 CNGKSASGLARALPDPDPDGDADDGEGNLSKGERVRAMIRALPACYLERDSWSAYI 1258
DB 1201 CNGKSASGLARALPDPDPDGDADDGEGNLSKGERIQAWVRSLPACCRERDSWSAYI 1260
QY 1259 FPQOSRFLLCRRITTHKMFQHVWLVIIIFLCITTIAMERPKIDPHSAERIFLTLSNYIFT 1318
DB 1261 FPQOSRFLLCRRITTHKMFQHVWLVIIIFLCITTIAMERPKIDPHSAERIFLTLSNYIFT 1320
QY 1319 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLDDLVLISVIDILVMSVSDSGTKILGMLR 1378
DB 1321 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLDDLVLISVIDILVMSVSDSGTKILGMLR 1380
QY 1379 VLRLRLTLPRLVRSRAGGLKLVETLMSLKPIONIVVICAPFIIPGILGVOLFCKGF 1438
DB 1381 VLRLRLTLPRLVRSRAGGLKLVETLMSLKPIONIVVICAPFIIPGILGVOLFCKGF 1440
QY 1439 FVCGQEDTRNITNKSDCAEASYRWRHKYNDNLGOALMSFLVLSKDGWDIMYDGLDA 1498
DB 1441 FVCGQEDTRNITNKSDCAEASYRWRHKYNDNLGOALMSFLVLSKDGWDIMYDGLDA 1500
QY 1499 VGVDQOPIIMNHPWMLLYFISFLIIVAFFVLNMFVGVVVENFHKRQHQBEEAEARRBEK 1558
DB 1501 VGVDQOPIIMNHPWMLLYFISFLIIVAFFVLNMFVGVVVENFHKRQHQBEEAEARRBEK 1560
QY 1559 RLRLLEKKRR-----KAQCKPYYSYDSYRFRLLVHLCTSHYLDLFT 1600
DB 1561 RLRLLEKKRRMLDDVIASSGSSAASAEQAQCKPYYSYDSYRFRLLVHLCTSHYLDLFT 1620
QY 1601 GVIGLNVVTWAMEHYQOQILDEALKICNYITFTVIFVLESVKLVAFGRFRFFODRNQOL 1660
DB 1621 GVIGLNVVTWAMEHYQOQILDEALKICNYITFTVIFVLESVKLVAFGRFRFFODRNQOL 1680
QY 1661 DLAIIVLSIGMITLEEVNLSAPINPTIIRIMVRLRIARVLKLLKXAVGMRALLDIVMQ 1720
DB 1681 DLAIIVLSIGMITLEEVNLSAPINPTIIRIMVRLRIARVLKLLKXAVGMRALLDIVMQ 1740
QY 1721 ALPOVGNLGLLMLFFIFAALGVLELFGDLECDETHCEGLGRHATFRNFGMAFLTIFRV 1780
DB 1741 ALPOVGNLGLLMLFFIFAALGVLELFGDLECDETHCEGLGRHATFRNFGMAFLTIFRV 1800
QY 1781 STGDNWNGIMKDTLRDCDQBSTCVNTVISPIYFVSFVLTAQFVLNVVIVIAVLMKHLEESN 1840
DB 1801 STGDNWNGIMKDTLRDCDQBSTCVNTVISPIYFVSFVLTAQFVLNVVIVIAVLMKHLEESN 1860
QY 1841 KEAKEAEAELEMEKTLSPQHSPLGSPFLWPGVEGPDSPSPKPGALHPAAHARS 1900

DB 1861 KEAKEAEAELEMEKTLSPQHSPLGSPFLWPGVEGPDSPSPKPGALHPAAHARS 1920
QY 1901 SHFSLEHPTMQPHPTLP---GPDLLTVRKSGSVSRTHSLPNDSYMCRHSGSTAEGPLGHRG 1957
DB 1921 SGFSLEHPTMQPHPTLP---GPDLLTVRKSGSVSRTHSLPNDSYMCRHSGSTAEGPLGHRG 1980
QY 1958 WGLPKAQSGLSVLSVHSQPADTSYIIQLPKDAPHILOPHSAPTWTGTPKLPPGGRSPLAQR 2017
DB 1981 WGLPKAQSGLSVLSVHSQPADTSYIIQLPKDAPHILOPHSAPTWTGTPKLPPGGRSPLAQR 2040
QY 2018 PLRROAAARTDLSLDVQGLGSRDLAEVSGSPPLARAYSWFGQSQSTQAQOHRSHSKTS 2077
DB 2041 PLRROAAARTDLSLDVQGLGSRDLAEVSGSPPLARAYSWFGQSQSTQAQOHRSHSKTS 2100
QY 2078 KHMTPAPCPGPEPNWKGPPETRSLSLELDTLSWISGDLPLPPGQGEPPSPSRDLKKCVS 2137
DB 2101 KHIRLPAPCPGLEPSWAKDPETRSLSLELDTLSWISGDLPLPPGQGEPPSPSRDLKKCVS 2159
QY 2138 VEAQSCQRRTSWLDQORRHISIAVSCLDGSGOPHLGTPDSMLGGQPLGGPSRPPKCLSP 2197
DB 2160 VETOSCRERRPGSWLDQORRHISIAVSCLDGSGOPHLGTPDSMLGGQPLGGPSRPPKCLSP 2219
QY 2198 PSITIDPPESQOPRTPPSPGICLRRERAPSSDSKOPLASGPPDSMAASPKKDVLSLGL 2257
DB 2220 PSISIDPPESQOPRTPPSPGICLRRERAPSSDSKOPLASGPPDSMAASPKKDVLSLGL 2279
QY 2258 SSDPADLDP 2266
DB 2280 SSDPTDMDP 2288
RESULT 4
US-09-383-894-4
; Sequence 4, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383.894
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2425
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-383-894-4
Query Match 93.3%; Score 11111; DB 10; Length 2425;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;
QY 1 MDEEDGAGAEESGQPRSFMRNLNLSGAGRPGPSAEKDPGSADSEAEGLPYPALAPV 60
DB 52 MDEEDGAGAEESGQPRSFMRNLNLSGAGRPGPSAEKDPGSADSEAEGLPYPALAPV 111
QY 61 FFYLSQDSRPSRCLRTVCNPFERISMLVILNCVTLGMFRPCEDTACDSQRCLIQAF 120
DB 112 FFYLSQDSRPSRCLRTVCNPFERISMLVILNCVTLGMFRPCEDTACDSQRCLIQAF 171
QY 121 DDFIFAFVAVVVMKVALGIFGKKCYLGTWRNLPFFIVIAQMLEVSLDLQNVFSAVR 180
DB 172 DDFIFAFVAVVVMKVALGIFGKKCYLGTWRNLPFFIVIAQMLEVSLDLQNVFSAVR 231
QY 181 TVRVLRLPRLAINRVPMSRILVTLTLLDTPMLGNVLLLCFFVFIFGIVGVQWAGLLRNR 240
DB 232 TVRVLRLPRLAINRVPMSRILVTLTLLDTPMLGNVLLLCFFVFIFGIVGVQWAGLLRNR 291

QY	241	CFLPENFSLPLSVDLERYQYOTENEDESPFI	CSQPRENGMRSRCSRYPTLRDGGGPPCGL	300
Db	292	CFLPENFSLPLSVDLERYQYOTENEDESPFI	CSQPRENGMRSRCSRYPTLRGEGGPPCGL	351
QY	301	DYEAVNSNTTCVWNQYNTNC	SAGEHNPFGAINFNDIGNYAWIAI	FOVITLEGWVIM 360
Db	352	DYETVNSNTTCVWNQYNTNC	SAGEHNPFGAINFNDIGNYAWIAI	FOVITLEGWVIM 411
QY	361	YFVMDAHSFYNFYIFILLI	IVGSFFMINCLVVIATQFSETKORSQMLREORVFLSNA	420
Db	412	YFVMDAHSFYNFYIFILLI	IVGSFFMINCLVVIATQFSETKORSQMLREORVFLSNA	471
QY	421	STLASFPSCYBELLKYL	VILKAAARLAQVRAAQRVGLISSPAPLGQSTQPS	480
Db	472	STLASFPSCYBELLKYL	VILKAAARLAQVRAAQRVGLISSPAPLGQSTQPS	531
QY	481	SCSRSHRLSVHHLVHHHHHHH	YHGLNGTLRAPRASPEIQORDANGSRRLMLPPPSTP	540
Db	532	SCSRSHRLSVHHLVHHHHHHH	YHGLNGTLRVPRASPEIQORDANGSRRLMLPPPSTP	591
QY	541	ALSGAPPGAGSVHGFYHAD	CHLEPVRCQAPPPRSPSEASGRTVSGKYIPTVHTSPPE	600
Db	592	TPSGGPPRGAESVHSFYHAD	CHLEPVRCQAPPPRSPSEASGRTVSGKYIPTVHTSPPE	651
QY	601	TLKEALVFAASSGPPTL	TSNIPGPYSSMHKLETTOSTGACQSSCKISSPCLKADSG	660
Db	652	ILKDALVFAVSPGPPTL	TSPNIPGPYSSMHKLETTOSTGACHSCKISSPCLKADSG	711
QY	661	ACGPDSPCYACAGAGEV	ELADREMPDSSEAVYFTQDAQSHDLDPHS-RRQSLGPD	719
Db	712	ACGPDSPCYACAGAGEV	ELADREMPDSSEAVYFTQDAQSHDLDPHSRRQRSLGPD	771
QY	720	APPSSVLAFLRLICDTR	KIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISN	779
Db	772	APPSSVLAFLRLICDTR	KIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISN	831
QY	780	IVFTSLFALEMLIKL	VYGFYKPNYINFDGVIVISWELVGOOGGSLSVLRTFLM	839
Db	832	IVFTSLFALEMLIKL	VYGFYKPNYINFDGVIVISWELVGOOGGSLSVLRTFLM	891
QY	840	RVLKLVRELPALQRL	VLMKTMNDVATFCMLLMLEIFIFISILGMHFGCKFASERDGT	899
Db	892	RVLKLVRELPALQRL	VLMKTMNDVATFCMLLMLEIFIFISILGMHFGCKFASERDGT	951
QY	900	LPDRKNFDSLWAIV	TVFQILLTOEDWNKVLINGMASTSSWAALYFIALMTFGNYVFNLL	959
Db	952	LPDRKNFDSLWAIV	TVFQILLTOEDWNKVLINGMASTSSWAALYFIALMTFGNYVFNLL	1011
QY	960	VAILVEGFOAEI	SKREDASQJLQVDSOGGDANKSESPDFPSPLDGDGRKKC	1019
Db	1012	VAILVEGFOAEI	SKREDASQJLQVDSOGGDANKSESPDFPSPLDGDGRKKR	1071
QY	1020	LALVSLGEHP	ELRKSLLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAPPGA	1079
Db	1072	LALVSLGEHP	ELRKSLLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAPPGA	1131
QY	1080	A-HEMKSPPARS	PHSPWAAASWTSRRSRNSLGRAPSLKRRSPGERRSILSCGQE	1138
Db	1132	AHEMKSPPARS	PHSPWAAASWTSRRSRNSLGRAPSLKRRSPGERRSILSCGQE	1191
QY	1139	SQDEESSERFAS	PAGSDHRRHGLSLEAKSFDPDTPQLVQGLHRTASGRGSASEHQD	1198
Db	1192	SQDEESSERFAS	PAGSDHRRHGLSLEAKSFDPDTPQLVQGLHRTASGRGSASEHQD	1251
QY	1199	CNGKSASGR	LARLPDPPDLGDADDDEGNLSKGERVRAWIRARLPACYLERSWSAYI	1258
Db	1252	CNGKSASGR	LARLPDPPDLGDADDDEGNLSKGERIQAQVWRSLPACCRERSWSAYI	1311
QY	1259	FPQSRFELLCHRIITH	KMDHVVIIIFNCITIAMERPKIDPHSAERIFLTLNSYIFT	1318
Db	1312	FPQSRFELLCHRIITH	KMDHVVIIIFNCITIAMERPKIDPHSAERIFLTLNSYIFT	1371

QY	1319	AVFLAEMTVK	VVALGWCFCGEQAYLRSSWNVL	DGLLVLSIVDILVMSVSDSGTKILGMLR 1378	
Db	1372	AVFLAEMTVK	VVALGWCFCGEQAYLRSSWNVL	DGLLVLSIVDILVMSVSDSGTKILGMLR 1431	
QY	1379	VLRLETRLP	LRVLSRAQGLKLVVETLMSS	LKPIGNIIVVICAPFIIFGLIGVOLFKGKF 1438	
Db	1432	VLRLETRLP	LRVLSRAQGLKLVVETLMSS	LKPIGNIIVVICAPFIIFGLIGVOLFKGKF 1491	
QY	1439	FVQCQEDTRN	ITNKSDCAEASVVRVHRKYNF	DNLGQALMSLFLVASKDGVIMYDGLDA 1498	
Db	1492	FVQCQEDTRN	ITNKSDCAEASVVRVHRKYNF	DNLGQALMSLFLVASKDGVIMYDGLDA 1551	
QY	1499	VGVDOQP	IMNHNPMMLYFISLLIVAF	VMFVGVVVENPHKCRQOESEAREEREK 1558	
Db	1552	VGVDOQP	IMNHNPMMLYFISLLIVAF	VMFVGVVVENPHKCRQOESEAREEREK 1611	
QY	1559	RURLEKKRR	-----	---KAQCKPYYSYRFRLLVHHLCTSHYLDLFTT 1600	
Db	1612	RURLEKKRR	IMLDDVIASSGSSASAEAO	CKPYYSYRFRLLVHHLCTSHYLDLFTT 1671	
QY	1601	GVIGLVNVT	MAHEHYQOQOILDEALKI	CNYIETVIFVLESVFKLVAFGRFRFQDRWNQJ 1660	
Db	1672	GVIGLVNVT	MAHEHYQOQOILDEALKI	CNYIETVIFVLESVFKLVAFGRFRFQDRWNQJ 1731	
QY	1661	DLAIVLLS	TMGITLBEIEVNASL	PNPTIIRMRVLRIRARVLKLMAYGMALDVTMQ 1720	
Db	1732	DLAIVLLS	TMGITLBEIEVNASL	PNPTIIRMRVLRIRARVLKLMAYGMALDVTMQ 1791	
QY	1721	ALPOVGNL	GLLFWLFFIFAALGV	LEFGLEDETHPCBGLGRHATFRNFGNAFLTFRV 1780	
Db	1792	ALPOVGNL	GLLFWLFFIFAALGV	LEFGLEDETHPCBGLGRHATFRNFGNAFLTFRV 1851	
QY	1781	STGDNWNG	IMKOTLRDCDOEST	CYNTVISPFIYFVSFVLTAQFVLNVNVI	AVLMKHEESN 1840
Db	1852	STGDNWNG	IMKOTLRDCDOEST	CYNTVISPFIYFVSFVLTAQFVLNVNVI	AVLMKHEESN 1911
QY	1841	KEAKEAE	LEAELEEMKTLSPQ	HSPLGSPFIMPGVEGVNSPDSKPGAPHTTAHIGAA 1900	
Db	1912	KEAKEAE	LEAELEEMKTLSPQ	HSPLGSPFIMPGVEGVNSPDSKPGAPHTTAHIGAA 1971	
QY	1901	SHFSLEHPT	MQPHTPLP---	GPDLTVRKSGVSRTHSLPNDSYMCRHGSTARGPLGHRG 1957	
Db	1972	SGFSLEHPT	QVPHPEVVP	PLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTARSJLGHRC 2031	
QY	1958	WGLPKAQ	SGSVLSVHSQPADTSY	ILQPKDAPHLQPHSAPTWTGTIPKUPPPGRSPLAQ 2017	
Db	2032	WGLPKAQ	SGSVLSVHSQPADTSY	ILQPKDAPHLQPHSAPTWTGTIPKUPPPGRSPLAQ 2091	
QY	2018	PLRRQAA	IRTDSDLVQGLS	REDLLAEBVSGSPPLARAYFWQSSSTQAQOHSRSHKIS 2077	
Db	2092	PLRRQAA	IRTDSDLVQGLS	REDLLAEBVSGSPPLARAYFWQSSSTQAQOHSRSHKIS 2151	
QY	2078	KMTTPAP	CPGPPNMGKPPETR	SSLELDTLSWISGDLPLPGQOEPEPPSDRLKKCY 2137	
Db	2152	KHRLPAP	CPLGSPWAKOP	PETRSSLELDTLSWISGDLPLPGQOEPEPPSDRLKKCY 2210	
QY	2138	VEAQSC	QRRRTSWLDQR	RHSIAVSCLDGSGPHLGTDPNLQOQPLGGPGSRPKKLSP 2197	
Db	2211	VEAQSC	QRRRTSWLDQR	RHSIAVSCLDGSGPHLGTDPNLQOQPLGGPGSRPKKLSP 2270	
QY	2198	PSITIDP	PPSQGRTPPS	PGICLRRAPSDSDKPLASGPPDWSAASPSPKKVLISLGL 2257	
Db	2271	PSISIDP	PPSQGRTPPS	PGICLRRAPSDSDKPLASGPPDWSAASPSPKKVLISLGL 2330	
QY	2258	SSDPAD	LDP 2266		
Db	2331	SSDPTD	MDP 2339		

RESULT 5
US-10-408-765A-1128
; Sequence 1128, Application US/10408765A
; Publication No. US20040101874A1


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; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1128
; LENGTH: 2353
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-1128

Query Match      52.2%; Score 6212; DB 16; Length 2353;
Best Local Similarity 56.7%; Pred. No. 0;
Matches 1366; Conservative 214; Mismatches 525; Indels 304; Gaps 61;

QY      7 GAGAEESGQP-RSPWRLNDLSGAGRGPGGSAEKDPGSADSEAEGLPYPALAPVVFVLS 65
Db      27 GASPEFGAPGREARSEL-GVSEFSP-NAERGAELGADEQRVPYALAAATVFFCLG 84
QY      66 QDSPPRSWCLTVCPNPFERISMLVILNCVTLGMRPCEDIACDSORCRILQAFDDFIF 125
Db      85 QTTTPRSWCLRLVCPNPFERISMLVILNCVTLGMRPCEDIACDSORCRILQAFDDFIF 144
QY      126 AFFRAVEMVVMVALGIGKCKYLGDWTNRDLDPFTVIAGMLEYSLDLQNVFSAVRTVRVL 185
Db      145 AFFRAVEMVVMVALGIGKCKYLGDWTNRDLDPFTVIAGMLEYSLDLQNVFSAVRTVRVL 204
QY      186 RPLRAINRVPMSRLILVLLDTPMLGNVLLLCFFVFFIIGVGVQWAGLNRRCPLPE 245
Db      205 RPLRAINRVPMSRLILVLLDTPMLGNVLLLCFFVFFIIGVGVQWAGLNRRCPLDS 264
QY      246 NFSIPLSVD-LERYQTEDESPFICQSPRENGMRSCSRVP---TLRGDGGGPPCGGLD 301
Db      265 AFVRNNNLTLRPPYQTEEGEENPFICSSRRDNGMQKSHIPGRRLR-----MPCTLG 318
QY      302 YEAYN-----SSNNTTCVNNQYNTNCAGHNPKGAINFDNIGYAMIAIFQVITL 354
Db      319 WEAYTQPAEGVGAAARNACINWQYNNVCRSGDSNPHNGAINFDNIGYAMIAIFQVITL 378
QY      355 GWVDIMYFVMDAHSFYNFYIFILLIIIGVSPFMNLCVLIATOFSETKQESQLMREQV 414
Db      379 GWVDIMYFVMDAHSFYNFYIFILLIIIGVSPFMNLCVLIATOFSETKQESQLMREQRA 438
QY      415 RFLSNASTLASPEGSCYBELLYLVILRKAARLAQVSRAGVRVGLSSPAPLGGQ 474
Db      439 RHLNSDSTLASPEGSCYBELLYLVILRKAARLAQVSRAGVRVGLSSPAPLGGQ 498
QY      475 ETQPSSSCSRHRR-LSVHLV-HHHHHHHHVLGNGTLRAPASPEIQDRDANGSRRL 532
Db      499 --GPHRQRAGHTASVHLVHHHHHHHHHHVHSHGSPRPEPGFAGCD-----TRLV 551
QY      533 MLPPPTPALSGAPPGAESVHSFYHADCHLE--PVRCAQPPRSPSEASGR-TVGSGKV 599
Db      552 RAGAPSPSPGPGPDPAESVHSFYHADCHIEGQERARVAHAATAASLRATLGLTM 611
QY      590 -YPTV-----HTSP-----PPTELKEKALVEVAASSGPPTLTSLNIPPGPY 629
Db      612 NYPTILPSGVSGKSTSPGPKWAGGPPGT-----CGHGPLSNS-----PDY 657
QY      630 SSMHKLLETQSTACOS-----SKISPPCLKADSGAGPDSQPCYCARA-GAGEVELA 681
Db      658 EKIPHVVGHEGLGQAPGCHLSGLSPVCPFLPSP--PAGTLTCELKSCPYCTRALEDPEGELS 715

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QY      682 DREMPDSSEAVYETQDAQHSDLRDP-----HRRORSLSGPDABPSV 725
Db      716 GSESGSDSGRGVYETQDVHRGDRWDPTRPRAITDPGPGSGPQRAQAAPGPGWM 775
QY      726 LAFWRLICDTRKIVDSKYFGRGIMIALVNTLSMGIEYHQPELTALISINIVFSL 785
Db      776 GRWTFSGKLRRIVDSKYFSGRGIMIALVNTLSMGVEYHQPELTALISINIVFSL 835
QY      786 FALEMLKLKLVYGGPGYIKPNYIFDGVIVISVMEIVGQGGGSLVTLRFLMRVLKLV 845
Db      836 FALEMLKLKLVYGGPGYIKPNYIFDGVIVISVMEIVGQGGGSLVTLRFLMRVLKLV 895
QY      846 RFLPALQRLVLMKTMNVATFCMLLMFLTFISILGMHLFGCKPASERD-GDTLPDRK 904
Db      896 RFLPALQRLVLMKTMNVATFCMLLMFLTFISILGMHLFGCKPASERD-GDTLPDRK 955
QY      905 NFDLLWAIIVTVFOILLQEDMNKVLVNGMASTSSWAALYFIALMTFCGNVLFNLLVALIV 964
Db      956 NFDLLWAIIVTVFOILLQEDMNKVLVNGMASTSSWAALYFIALMTFCGNVLFNLLVALIV 1015
QY      965 EGFOAEIISKREDASGQLSCILQPLVDSQGGDANKSESEPDFFSPSLDGD-----GD 1015
Db      1016 EGFOAEIISKREDASGQLSCILQPLVDSQGGDANKSESEPDFFSPSLDGD-----GD 1052
QY      1016 RKKCLALVSLGERPELRKSLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRSSGSA 1075
Db      1053 LKMCSTAVTPNGHLEGRGSLSPPLIMCTAATPMPPTKSSPFLDAAPSLPDSRRGSSSGD 1112
QY      1076 EPGAHAEMKPPSPASRSPSPHSPWSAASWTSSRSRNSLGRAPSLKRRSPSGERSLSGE 1135
Db      1113 PP--LGQKQPPASURSPPCAPWPGSGAWSSRSLGRAPSLKRRSQGQERESLSGE 1170
QY      1136 GQESQDEESESSEERASPA--GSDHRRGSLREAKSFDLPDL-----QVPLH--- 1184
Db      1171 KGKSTDE--AEDGRAAPGPRATPLRAESLDPRPLPAALPTKCDRDRGQVVALSDF 1228
QY      1185 --RTASRGSASEHQDCNGKSGASGRALARLPDDPPLDGDGDDADDEGNLSKGERVRAWIRA 1242
Db      1229 FLRIDSHREDAAEIADDSDSCCLRLHKVLEPKP-----QWCRS 1268
QY      1243 RLPACYLERSGAYIFPPQSRRELLCHRIITHKPDHVVVLIIFLNCITIAMERPKIDP 1302
Db      1269 -----RAWALYLFSPQNRFRVSCQKVIITHKPDHVVVLIIFLNCITIALERPDP 1320
QY      1303 HSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSNNVLDGLLVISVIDIL 1362
Db      1321 GSTERVFLSVNYIFTAVFAEMVMKVALGSLGSHAYLQSSNNLDDGLLVLSLVDIV 1380
QY      1363 VSMVSDSGTKILGMLVRLRLRLPLRVLISRAQGLKLVVETLMSSLKPTIGNIVVICAF 1422
Db      1381 VAMASAGGAKILGVRLRLRLRLPLRVLISRAQGLKLVVETLMSSLKPTIGNIVVICAF 1440
QY      1423 FIIFGLIGVQLPKGKFFVCGEDTRNITNKSDCAEASVWRHKNFNDLGOALMSLFLV 1482
Db      1441 FIIFGLIGVQLPKGKFFVCGEDTRNITNKSDCAEASVWRHKNFNDLGOALMSLFLV 1500
QY      1483 ASKQGWIDIMYDGLDVGVDQOPIMHNPMLLIYFISFLIIVAFFVLNMFVGVVWENFHK 1542
Db      1501 SSKDQWNIIMYDGLDVGVDQOPVQNHNPMLLIYFISFLIIVSVFVLNMFVGVVWENFHK 1560
QY      1543 CRHQEEREEARRREERKRLRRERRRSTPPSEARPPYYADYSPTRRSIHSLSCTSHYLD 1596
Db      1561 CRHQEEREEARRREERKRLRRERRRSTPPSEARPPYYADYSPTRRSIHSLSCTSHYLD 1620
QY      1597 LFTITGVIGNVVTMAEHYQQOILDEALKINYIETVIVLESVKLVAFGRRFPQDR 1656
Db      1621 LFTITGVIGNVVTMAEHYQQOILDEALKINYIETVIVLESVKLVAFGRRFPQDR 1680
QY      1657 WNLQDLAIIVLLSIMGITLLEEIEVNASLPINPIIRIMRVLRIRARVLLKMAVGBALLD 1716
Db      1681 WNLQDLAIIVLLSIMGITLLEEIEVNASLPINPIIRIMRVLRIRARVLLKMAVGBALLD 1740
QY      1717 TWNQALPQVGNIGLLIFMLFFIFAALGVLELFGDLECDETHPCPEGLRHATFRFNGAFULT 1776

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QY 499 HHHHHYHLNGTLLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFVH 558
Db 469 -----PEAPA--PAKPGP-----H 480
QY 559 ADCHLEPVRCQAPPPRSPSEASGRTVGSKVYPTVHTSPPTLKEKALVEAASGPPT 618
Db 481 AK--EPRHYQLCPQHSPLDTPHIL-----VQIPATL-----511
QY 619 LITSNIPPGYPSMHKLLTQSTGACOSSCKTSSPCLKADSGACGPDSCPYCAR-----672
Db 512 -----ASDPASCPCQCHEDGRPP 529
QY 673 AGAGEVELADREMPDSDEAVYFTQDAQHSDLRDPHSRRQRSLGDAEPSSVL-----726
Db 530 SGLGSDT-SGQBSGSGSGAGGE--DEADGDSARSEDGASSELGKEEBEEOQAGAVWL 586
QY 727 --AFWELICDTRKIVDSKYFCRGIMAILVNTLSMGIEYHEQPEELTNALISNIVFTS 784
Db 587 CGDWRETRAKLGIIVDSKYFNKGINMALLVNTVSMGIEHHEQPEELTNILEICNVVFTS 646
QY 785 LFALEMLLKLVLVPGFYIKNPVNIPEGVIVISWWEIVGQGGGLSVLRTFRLMRVLKL 844
Db 647 MPFALEMLKLAAPGLFYLRLNPNIEDSIIVISWWEIVGQADGGLSVLRTFRLMRVLKL 706
QY 845 VRFLPALQRLVLMKTMNDVATFOMLLMFIIFISILGMHLFGCKFASERD-GDTLPDR 903
Db 707 VRFPALRQLVLMKTMNDVATFOMLLMFIIFISILGMHLFGCKFASERD-GDTLPDR 766
QY 904 KNFDSLWALIVFQILTOEDMKNVLYNGMASTSSWAALFYIALMTFGNVYVFNLLVAIL 963
Db 767 KNFDSLWALIVFQILTOEDMKNVLYNGMASTSSWAALFYIALMTFGNVYVFNLLVAIL 826
QY 964 VEGFOAEISKREDASQUSCIOLPVDQGDANKSESEDPFSPS-----LDGD 1013
Db 827 VEGFOAE-----GDANRSYSDQSSNIEEFKLEQGLDSS 863
QY 1014 GDRKKLALVSLGHEHPELRKSLPLLIHTAATPMSLPKSTSTGLGALGPASRRT-----1069
Db 864 GDPKLCPIPMTPNGH-----LDP-----SPLGHLGPGAGAAPRLSLQPD 906
QY 1070 -----SSSGSAEPGAHEMKSPSPARSSPHSPMSAASWTSRNRSLGRAPSLK 1120
Db 907 PMLVALGSRKSSVMSLGRMSYDQRLSSRSYVGPWGRSAAWASRRSSWN-----SLK 960
QY 1121 RSPSGERRILLSGE-QESQDDEESSEE--ERASPAGSDH-----RHRG 1162
Db 961 HKPPSAEHSILSAERGCGGARVCEVAADGPPRAAPLHTPHAHHIIHGHPLAHRHRHR 1020
QY 1163 SLEREAKSSFDLPDLOVPGHRTASGR--GSASEHODCNGKASGRALARALRDPDPLD 1220
Db 1021 TSLSDNRSDVDLAEVPAVAGNHPAARAGAPACHEDCNGRMPESIAKOVFTKMGDRGR 1080
QY 1221 GDDADDEGNLSKGRVERAWIRAPLACYLBERDSMSAYIFPQSRFLLCRRIITHKMPDH 1280
Db 1081 GED--EEHIDYTLCFVRKMDIVYKPDNCEVREDWSVYLFSPENRFRVLQCTIIAHLKFDY 1139
QY 1281 VVLVILFNCITIAMERPKIDPHSABRIFLTLNSYITAVFLAEMTVKVALGWCFCGEQA 1340
Db 1140 VVLAFIFNCITIALERPOIBAGSTERIFLTVSNYIETAFIVGEMTLKVSGLGYFGEQA 1199
QY 1341 YLRSSMNVLDGLLVLSVIDILVMSVDSGPKILGMLRVLRLTLRLPLRVISRAQGLKL 1400
Db 1200 YLRSSMNVLDGLLVLSVIDILVMSVDSGPKILGMLRVLRLTLRLPLRVISRAQGLKL 1259
QY 1401 VVETIMSLKPIGNIVVICCAFFIIFGILGVQLFKGPFVCOGEDTRNITKSDCAEASY 1460
Db 1260 VVETIMSLKPIGNIVVICCAFFIIFGILGVQLFKGPFVCOGEDTRNITKSDCAEASY 1319
QY 1461 RWRHRYNFDNLGQALMSLFVLASKGWDIMYDGLDAVQDQOQIPMHNHFWMLLYFTSF 1520
Db 1320 RWRHRYNFDNLGQALMSLFVLASKGWDIMYDGLDAVQDQOQIPMHNHFWMLLYFTSF 1379

QY 1521 LLIVAFVFLNMFVGVVNFHKKROHQBEEBARRREBEXRLRLEKKRKAOCKPYSDYS 1580
Db 1380 LLIVSFFVFLNMFVGVVNFHKKROHQBEEBARRREBEXRLRLEKKRKAORLPYIATYC 1439
QY 1581 RFLIVHLCSTSHYLDLFTITGVIGLVNVTMAHEHYOQOILDEALKICNYITFTVFLVES 1640
Db 1440 HTRLIHSMTCSHYLDLFTITGVIGLVNVTMAHEHYOQOILDEALKICNYITFTVFLVES 1499
QY 1641 VFKLVAFGFRFPQDRMNQOLDLAILVLLSIMGTLEEBIEVNASLPINPTIIRMRVLRIAR 1700
Db 1500 VLKLVAFGLRFRFKDRWNQOLDLAILVLLSIMGTLEEBIEVNASLPINPTIIRMRVLRIAR 1559
QY 1701 VLKLVAFGLRFRFKDRWNQOLDLAILVLLSIMGTLEEBIEVNASLPINPTIIRMRVLRIAR 1760
Db 1560 VLKLVAFGLRFRFKDRWNQOLDLAILVLLSIMGTLEEBIEVNASLPINPTIIRMRVLRIAR 1619
QY 1761 LGRHATERNFGMAELTLFRVSTGDNWNGIMKDTLRDC-DOESTCYNTV--ISPIYFVSFV 1817
Db 1620 MGRHATERNFGMAELTLFRVSTGDNWNGIMKDTLRDC-DOESTCYNTV--ISPIYFVSFV 1679
QY 1818 LTAQFVLNVVAVLVMKHLLEESNKAKEAEAELELEM-KTSLSPQHSPLGSPFLMFG 1876
Db 1680 LTAQFVLNVVAVLVMKHLLEESNKAKEAEAELELEM-KTSLSPQHSPLGSPFLMFG 1738
QY 1877 VEGPDSPD-----SPKFGAL-----HPAAHA-----1897
Db 1739 -RPGGAGGGGTGEGLCRCRCYSPAQDSLEGELTIIDNLSGSIFFHYSPAGCKKCHDK 1797
QY 1898 -----RSAS-----HFSLEHTMQP-----HPTLEFGPDLTLVRKSG--1929
Db 1798 QEVQLAETAFAFSLNDRSSILLGDDLSLEDDTACPPGRKDSKGELDPPEPMRVGDLGEC 1857
QY 1930 --VSRTHSLPN--DSYMCRRHGSTAEQPLGHRGWLKPAQSGSVLSVHSQPADTSYLQLP 1985
Db 1858 FFLSSTAVSPDENELCEMEETPFNPV--RSW--LKHDSSQAPPSPFSPDASSPLPMP 1913
QY 1986 KDAFH-----LLOHSAFTWTPIKLPFG-----RSLAQRLRQAIRTDSDVQ 2034
Db 1914 AEFHPFAVSASQXGPKGTGTGLPKIALQGSWASRSPRVNCTLLRQATGSDTSLD---1970
QY 2035 LGSREDLLAEVSGSPPLARAYFWQSGSTQAQOHSRSHSKI SKHMTTPAPCPGPEPNWG 2094
Db 1971 -----ASFSSAGSLQTLTLEDLSLSDSPRA-----LGFPAPAFGPAGLS 2012
QY 2095 KGPETRSLSLELTELTSWISGDLPLPGQGEPPSPRDLKCYSVFAQSCORRPTSWLDEQ 2154
Db 2013 ---PAARRRLSL-----RGRGLFSLRGLRA-----HQ 2036
QY 2155 RRSIAVSCLDGSGQPHLGTDPN---LGGQPLGGGSRPKKLSPPSIT---IDPPESQ 2208
Db 2037 RSHSSGGS-TSPGCTHDSMDPSDEGRGAGGGAGGAGSEHETLSLSLSLFCFP--2092
QY 2209 GPRTPPSPGHCLRRRAPSDS---KDPASGPPDSMAASPPKCVLSLGLSSDPADL 2264
Db 2093 ---PPAPGLTPARKFSTSTSLAAGPRHAAALHGLARSFMAAD-----RSKDPGR 2143
QY 2265 DP 2266
Db 2144 AP 2145

RESULT 8
US-09-935-541-4
; Sequence 4, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23

QY 1893 --PAA-----HARSAS-----HFSLEHPTMQP-----HPTQLP 1918
 Db 1798 SSPAGCKKHDKQVQAEAFSLNSRSLIILGDDLSLEDPACPPGRKDKSGELD 1857
 QY 1919 GPDLLTVRKSG-----VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWLKPAQSGSVLSVH 1972
 Db 1858 PPEPVRVGLGECFFPLSTAVSPENELCEMEBEPFNPV--RSW--LKHDSSQAPPSP 1913
 QY 1973 SQAFTSYIQLPKDAPH-----LLOPHSAPTWGTIPKLPDPG-----RSLAQRPLRR 2021
 Db 1914 FSPDASSPLLEPAEPFPAVSAOSKQPEKGTGTGLPKIALQGSWASLRSPVNTLLR 1973
 QY 2022 QAARTDSIDVOGLSREDLLAEVSGPSPLARAYFWGSSSTQAQOHSRSHSKSKMT 2081
 Db 1974 QATGSDTSLD-----ASPSSAGSLQTLLEDSLTLSPRRA-----LG 2012
 QY 2082 PPAPCPGPPNMGKPPETRSSLELDTLSWISGDLPLPGQGEPPSPRDLKCYSEVAQ 2141
 Db 2013 PPAPAGPRAGLS--PAARRLSL-----RGRGLFSLRGLRA- 2047
 QY 2142 SCORRETSWLDQRRHSIAVSCLDGSOHLGTDPSN-----LGQPLGGPGSRKKKLSP 2198
 Db 2048 -----HORSHSGGS-TSPGCTHDSMDPSDEGRGAGGAGGAGSEHSETLSL 2095
 QY 2199 SIT--IDPPESQPTPSPGICLRRAPSDS-----KDIASGPPDSMAASPSPKDV 2251
 Db 2096 SUTSLFCPPP-----PPFAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSFNAAD- 2148
 QY 2252 LSLSLGSLSDPADLDP 2266
 Db 2149 -----RSKOPPGRAP 2158

RESULT 9
 US-10-425-800-4
 ; Sequence 4, Application US/10425800
 ; Publication No. US2003018086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dietrich, Paul S.
 ; APPLICANT: McGivern, Joseph G.
 ; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
 ; TITLE OF INVENTION: AND USES
 ; FILE REFERENCE: R0043B-REG sequence listing
 ; CURRENT APPLICATION NUMBER: US/10/425,800
 ; CURRENT FILING DATE: 2003-04-29
 ; PRIOR APPLICATION NUMBER: US/09/404,650
 ; PRIOR FILING DATE: 1999-09-23
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 2188
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-425-800-4

Query Match 46.1%; Score 5484; DB 14; Length 2188;
 Best Local Similarity 51.1%; Pred. No. 0;
 Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;

QY 31 RPPGSAEKDPGSADSEAG---LPYPALAPVVFYLSQDSRPSRSMCLRTVCNPFERI 86
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 Db 85 SMLVILLNCVTLGMYQPCCDDCLSDCKILQVDDFFIFFAWEMVLMVALGFGKCC 144
 QY 147 YLGTWNRDLDFVFIAGLMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSRIILVLLD 206
 Db 145 YLGTWNRDLDFVWAGVMEVSLDLQNLNLSAIRTVRVLRPLKAINRVPSRIILVLLD 204
 QY 207 TPLMLGNVLLLCFFVFFIFGIVGVLWAGLRNRCFLPENFSLPLSVDLERYQTENDE 266

Db 205 TLPMLGNVLLLCFFVFFIFGIVGVLWAGLRNRCFLPENFTIQGDVALPPYQEEDE 264
 QY 267 SPFICSQPRENGMRSCRSVPTLRGGGGPPCGL-----DYEAYNSSNTT--CVNNMQ 318
 Db 265 MPFICSLSGNGIMCHEIPPLKEQ---GRECLSKDDVDFGAGRQDLNASGLCVNNR 321
 QY 319 YITNGSAGEHNPKGAINFDNIGYAWIAIFQVITLEGVVDIMYFMDAHSFNFIYFILL 378
 Db 322 YVNCRTGSANPKGAINFDNIGYAWIVIFQVITLEGVWEIMYVMDAHSFNFIYFILL 381
 QY 379 IIVGFFMINCLVVIATQFSETKQRESOLMEORVRLFSNASTLASPEPCSCYBELK 438
 Db 382 IIVGFFMINCLVVIATQFSETKQREHLMLEQORILYS--SSTVASAEPGDCIEIFQ 440
 QY 439 YIVITLXKAARLAQVSRAGVRVGLLSPAPLGGQETQPSSCSCSRSHRLSVHLLVHH 498
 Db 441 YVCHILKAKR-----RALGIXQALOSRQALG----- 468
 QY 499 HHHHHYHLNGTLRAPRASPEIQDRANGSRRLMLPPSTPALSGAPPGGAESVHSFYH 558
 Db 469 -----PEAPA--PAKEGP-----H 480
 QY 559 ADCHLEPVRQAPPSPSEASCRTVGSKVYVTVHTSPPETLKEKALVEVAASGPPT 618
 Db 481 AK---EPRHYQLCPQSPLDATPHLL-----VQPIPAL----- 511
 QY 619 LTSINIPPGFYSSMHKLLTQSTGACQSSCKISSCLKADSGACGDPSCPYCAR----- 672
 Db 512 -----ASDPACPCQHQHEDGRRP 529
 QY 673 AGAGEVELADREMPDSSEAVVEFTODAOHSDLRDPHSRRQSLGDAEPSSVL----- 726
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 QY 727 --AFWLLICDTFKIVDSKYFEGGIMAILVNTLSMGIEVHEQPEELTNALETSNIVFTS 784
 Db 587 CGDVWRETRAKLRGIVDSKYFNKGIMAILVNTVSMGIEHHEQPEELTNALETSNIVFTS 646
 QY 785 LFALEMLKLLVYGFYIKNPNIFDGVIVVISVMEIVGQGGGLSVLFTFLMRVLKL 844
 Db 647 MFALEMLKLAAGLDYLENPNYIFDSIIVISIMEIVGQADGGLSVLFTFLLRVLKL 706
 QY 845 VRFLPALQOLVVLMTDMNVATFCMLLMFIIFISILGMLFGCKFASERD-GDTLPDR 903
 Db 707 VREMPALRRQLVVLMTDMNVATFCMLLMFIIFISILGMLHIFGCKFSLTDTGDTVPDR 766
 QY 904 KNFDSLILWAIVTVFOILTQEDWNKLVNGMASTSSWAALFYALMTFGNVLFNLVAIL 963
 Db 767 KNFDSLILWAIVTVFOILTQEDWNVVLNGMASTSPWASLYFVALMTFGNVLFNLVAIL 826
 QY 964 VEGFOAEIISKREDASQQLSCIQLPVDOSQGDANKSESEPFPS-----LDGD 1013
 Db 827 VEGFOAE-----GDANRSYDEDEQSSNTEEDFKLEGLDSS 863
 QY 1014 GDRKKCALVSLGHEHPELRKSLPLLIHTAATPMSLPKSTSTGLGALGPASRT----- 1069
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 QY 1070 -----SSGSAEPFAAHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLK 1120
 Db 907 FMLVALGSRKSSVMSLGRMSIDQRLSSSSSSSYGPGWRSNAWASRSSWN-----SLK 960
 QY 1121 RRSPPSGRRRILSGE-QRESQDEESEE--ERASPGASH-----RHRG 1162
 Db 961 HKPSPAHEHSLLSAERGGAARVCEVAADGPPRAAPLHTPHAHIHGHGHLAHRHRR 1020
 QY 1163 SLREAKSSFLPDTLQVPLHRTASGR--GSAHEQDCNGKSGASGLARALRDPDPLD 1220
 Db 1021 TSLSDNDSVDLAEVLVPAVGAHPRAAWRAAGAPCHDCNGRMSIAKVFTKMGDRDR 1080
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Db 505 -----ISAILASD-----PSSCPHQHEA 523
QY 673 -----ACAGEVELADREMPDSDSEAVYEFTODAOHSDLRDPHSRRQSRSLGPDAPSSVLA- 727
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QY 728 -----FWRLICDTRFKIVDSKYFGRGIMIALVNTLSMGIEYHQBPELNTNALBISNIVFT 783
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QY 784 SLFALEMLKLIVYGPFGYIKNPNIPDGVIIVISVWEIVGQGGGLSVLRTFLMRVLK 843
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QY 844 LVRFALQOLQVVLVMTDMNVATFCMLLMFIFISILGMHLFGCKFASERD-GDTLPD 902
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QY 963 LVGEFOAEELSKREDASGQLSCIQLPVDSOGDANKSESEPDFFSPS-----LDG 1012
Db 819 LVGEFOAE-----GDANKSCDESDQSSNLEFFDKLPGLDN 855
QY 1013 DGDRKKCLALVSLGEHPRLKSLPLLIHTAATPMSLPKSTGTGLGEALGPA-SRRTSS 1071
Db 856 SRLKLCPTMTNGH-----LDP-----SLP-----LGAHLGPAGTGTAP 892
QY 1072 SGSAEPG-----AAHEMKSPPSARSSPHSPWSAASSWTSSRRNSL 1113
Db 893 RLSLQDPDVLVALDSRKSVMSLGRMSYDQSLSSRSYYPGWRSSTWASRRSWN-- 950
QY 1114 GRAPSLKRRSPSERRSLSGEQESQDEP-ESSEBE---RASPAGSDH----- 1158
Db 951 -----SLKHKPPSAEHSLLSGEGGSCVRACEGAREEAPTRTAPLHAPHAAHGHPLA 1006
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QY 1213 RPDPPDLGDADDEGNLKGKGERVRAWIRARLPACYLERDSWSAYIFPPQSPRFLLCRI 1272
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QY 1273 ITHKMFHDVVLVIFLNCITIAMERPKIDPHSARIFLTLNSVIFTAVFAEMTVKVVAL 1332
Db 1126 IAHKLFYVVLAFIFLNCITIALERPQIEAGSTERIFLTVNSVIFTAVFVGMTLKVWSL 1185
QY 1333 GWCFGQAYLRSSWNVDGLVLISVIDILVMSVDSGKILGMLRVLRLLRTRPLRVI 1392
Db 1186 GLYFGEQAYLRSSWNVDGLVFSIIDVVSASAGGAKILGLVLRVLRLLRTRPLRVI 1245
QY 1393 SRAQGLKLVVETLMSSLKPIGNITVITCCAPFIIFGILGVQLFKGKFFVCGEDTRNITNK 1452
Db 1246 SRAPGLKLVVETLISLLKPIGNILVICCAPFIIFGILGVQLFKGKFFVCHGLVDTRNITNR 1305
QY 1453 SCACASAYRWRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDVGVDQOQIMHNHP 1512
Db 1306 SDCAANYRWRHKKYNFDNLGQALMSLFVLASKDGWVIMYNGLDVAVDQOQVTHNHP 1365
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QY 1573 KPYYSYRFRLLVHLCTSHYLDLFTITGVIGLNVVTMAHEHYQQOQLDEALKINYIF 1632
Db 1426 LPYATYCPRLLIHSGMCTSHYLDLFTITFICLNVVTMSLEHYNQPTSLTALKYCNMF 1485
QY 1633 TVLIFVLESVPKVAAGFRFRFQRWQOLDLAILLSITMGITLLEEIVNASLPINPITIRI 1692
Db 1486 TTVFVLEAVLKVAFGLRRFRFQRWQOLDLAILLSVMGTLLEEIEINAILNPITIRI 1545

QY 1693 MRVLRIRARVLKLLKMAVGMRALDITVMOALPOVGNLGLLPMLLFFIPAAALGVLEFGDLEC 1752
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QY 1753 DETHPCCEGLRHATFNFPGMAFLTLFRVSTGDNWNGIMKDTLDC-DQBSTCYNTV--IS 1809
Db 1606 NDENPCCEGSRHATFNFPGMAFLTLFOVSTGDNWNGIMKDTLDCDTHDERTCLSSLQFVS 1665
QY 1810 PIYFVSFVLTAQFVLNVVAVLMLKHLERSNKEAKEAELEAELEEM-KTILSPQHSPL 1868
Db 1666 PIYFVSFVLTAQFVLNVVAVLMLKHLDDSNKEAQDAEMDAEIELEMAHGLGPCP---- 1721
QY 1869 GSPFLWPGVEGPDSPKPGALHPAAHARSASHFSLEHPTMQPHTELPDPLLTV--- 1925
Db 1722 -----GPCFG-----PCPCPCPCPCAGPRLPTSSPG 1747
QY 1926 ---RKSGVSRTHSLPNDNSYMRH 1945
Db 1748 APCRSGGAGAGG-DTESHLCRH 1769
RESULT 11
US-10-425-800-5
; Sequence 5, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1835
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-425-800-5
Query Match 45.1%; Score 5366; DB 14; Length 1835;
Best Local Similarity 56.8%; Pred. No. 0;
Matches 1138; Conservative 183; Mismatches 346; Indels 336; Gaps 38;
QY 27 GAGRPGGSAEKDPGSADSEAEAG---LPYPALAPVVPFFYLSQDSRSPSWCLRTVCNWP 82
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QY 83 FERISMLVILLNCVTIGMFRPCEDIACDSQRCILQAFDDFIPAFPAVEMVVMVALGIF 142
Db 79 FECVSMVLILLNCVTIGMYQCDDMECLSDRCKILOVDDDFIFFAMEMVLKMWALGIF 138
QY 143 GKCYLGDTWNRLLDFVIAGLMLEYSLDQNTVSFSAVRTVRLRPLRNRVPSMRLVLT 202
Db 139 GKCYLGDTWNRLLDFVIWAGVVEYSLDQNLNLSAIRVRLRPLKALNRVPSMRLVN 198
QY 203 LLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLPENFSLPSVLDLERYQTE 262
Db 199 LLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLEENFTIQGDVALPPYVQPE 258
QY 263 NEDESFPICQSPRENGMRSCRSPVTLRGDGGGPPCGL-----DYEAYNSSNTT--CV 314
Db 259 EDEMFPICSLTGDNMGIMGCHIEIPPLKEQ---GRECCLSKDDVYDFGAGQDLNAGLCV 315
QY 315 NNNQYVNTCSAGEHNPFKGAINDFNIGYAWIAIFQVITILEGWVDIMFYVMDAHSFYNFYI 374
Db 316 NNNRYNVCTGNANPHKGAINDFNIGYAGIVFQVITILEGWVEIMYVMDAHSFYNFYI 375
QY 375 FILLIIVGFFMNLCLVIAIQFSTKQRESQLMREQRVFLSNASTLASFSEPGSCYE 434

Db 376 FILLIIVGFFMINICLVVIAIOTFSETKQREHRLMLEQRYLS-SSIVASVAREPGDCE 434
Qy 435 ELLKXVLVILKAARILIAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHLL 494
Db 435 EIFQYVCHILKAKRRALGLYALQNR----- 461
Qy 495 VHHHHHHHHVHLNGTLRAPRASPEIODRDANGSRRLMLPPSTPALSGAPPGAESVH 554
Db 462 -----RQMG-----PGTGA-PAKPGP----- 477
Qy 555 SFYHADCHLEPVRCOAPPRSPSEASGRVTSKGVPYPTVHTSPPTTLKELALVEVAASS 614
Db 478 ---HAK---EFSHCKLCPRHPLD-----PTPHLTVQP----- 504
Qy 615 GPPTILTSINIPPGPYSSMHKLLELTQSTGACOSSCKISSPCLKAUSGAGCPDSCPYCAR-- 672
Db 505 -----ISAIIASD-----PSSCPHCQEA 523
Qy 673 ---AGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRRQRSGLPDAEPSSVLA- 727
Db 524 GRRFSGLGST-DQEGSGSGSAREABANGD-----LOSSEDGVSSDLGKEEBEQDGAAR 578
Qy 728 ---FWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFT 783
Db 579 LCGDVWRETRKKLRIGVDSKYFNRGIMAILVNTVSMGIEHEQPEELTNILEICNVVFT 638
Qy 784 SLFALEMLKLLVGPFGYIKNPYNIPGVIVIVISWEIVQGGGLSVLRTFLMRVLK 843
Db 639 SNALEMLKLAALFDFLRNPYNIPDSIIIVISWEIVQADGGLSVLRTFLRLVLK 698
Qy 844 LVRLPALOROLVLMKTMNDVATFCMLLMFIRIFSLTGMHLFCKEASERD-CDTLPD 902
Db 699 LVRFMPALURQVLVLMKTMNDVATFCMLLMFIFIFSLGWHIFGCKESLRTDGTGVFD 758
Qy 903 RKNFDSLWAIWTVFQILTOEDWNKVLNGMASTSSWAALFYFIALMTGNTVLENLVAI 962
Db 759 RKNFDSLWAIWTVFQILTOEDWNVLYNGMASTTPMASLYFVALMTGNTVLENLVAI 818
Qy 963 LVEGQAEIEKREDASQGLSCIQLPVDSDQGDANKSESEDPFSPS-----LDG 1012
Db 819 LVEGQAE-----GDANRSCSDQDQSSNLEEFDKLPEGLDN 855
Qy 1013 DGDRKCLALVSLGHEPELRKSLAPPLIHTAATPMSLPKSTSTGLGEALGPA-SRRSS 1071
Db 856 SRDLKCLPIMPNGH-----LDP-----LGAHLGPAFTMGTP 892
Qy 1072 SGSABPG-----AAHEMKSPPSARSPSPHSPWASASWTSRRSSRNSL 1113
Db 893 RLSLQDPVLVALDSKSSVMSLGRMSYDQSLSSRSYSGYGPWGRSGTWSRRSSWN-- 950
Qy 1114 GRAPSLKRSFGSRRSLLSSEGBQDEB-ESSEEB---RASPAQSDH----- 1158
Db 951 ----SLKHKPSAEHESLLSSEGGSCVRACEGAREEAFTRTAPLHAPHAAHGHPLA 1006
Qy 1159 ---RHRSGLEREAKSFDLPDTLOVPGHLRTAS--GRGSASEHODCNKGSASGLARAL 1212
Db 1007 HRRHRRRLTSLDRDSVDLDELVPVVGAAHRAAWRGAGQAPGHEDCNGRPNIAKVFT 1066
Qy 1213 RPDPPPLDGDADDGNLSKGERVARIARLPACYLBERDSWSAYIFPPQSRFRLLCHRI 1272
Db 1067 KMDRRDRGED-EEBIDYTLCFVRKMDIVYKPCWCEVREDWSVYLFSPENKFRILCQTI 1125
Qy 1273 ITHKMFHDHVLVIFINCITTIAMERPKIDPHSAERIFLTSNIYPTAVFLAEMTVKVVAL 1332
Db 1126 IAHKLFDVVLAFIFLNCITTIALERPOIEAGSTERIFLTVSNYIIFTAIFVGEMLTKVVS 1185
Qy 1333 GWCFCQAYLSSWNVLDGLVLIIVIDILYSVSDSGTKILGMLRVLRLLRTPLRVI 1392
Db 1186 GLYFCQAYLSSWNVLDGFLVFSIIDIVSVASGAKILGVLRVLRLLRTPLRVI 1245
Qy 1393 SRAQGLKLVWETLMSLKPIGNIVVICCAFFIIFGILGVQFGKGFVFCQGEDTNTNKN 1452

Db 1246 SRAPGLKLVWETLSSLPKIGNIVVICCAFFIIFGILGVQFGKGFVHCLGVDTNRITNR 1305
Qy 1453 SDCBAEASVRWRHXYKNEDNLGOALMSLFLVASKDGDWDIMYDGLDAGVQDQPINHNPW 1512
Db 1306 SDCVAANRWYHXYKNEDNLGOALMSLFLVASKDGDWNIMYNGLDAGVQDQPVTHNPW 1365
Qy 1513 MLLYFISFLLIIVAFVFLNMFGVNVFNPKCRQHQEBAEARRRBEKRLRLEKRRKQAC 1572
Db 1366 MLLYFISFLLIIVSFFVFLNMFGVNVFNPKCRQHQEBAEARRRBEKRLRLEKRRKQAC 1425
Qy 1573 KPYSDYSRFRLLVHHLCTSHYLDLFTITGVLNVVNMAMEHYOQPOLDBALKICNVIF 1632
Db 1426 LPYVATYCPTRLIHSMTSHYLDLFTITGVLNVVNMAMEHYOQPOLDBALKICNVIF 1485
Qy 1633 TVIFVLESFVKLVAFGRFRFFODRWNOOLDIAVLLSIMGITLERIEVNASLPINPTIIRI 1692
Db 1486 TTVFVLEAVLKVAFGRFRFFODRWNOOLDIAVLLSIMGITLERIEVNASLPINPTIIRI 1545
Qy 1693 MRVRIARVLLKXAVGMRRALLDTVMQALPQVGNLGLLFMLFFIFAALGVLEFGDLEC 1752
Db 1546 MRVRIARVLLKXAVGMRRALLDTVMQALPQVGNLGLLFMLFFIFAALGVLEFGDLEC 1605
Qy 1753 DETHPCBGLGHATFRNFGMAFLTLFRVSTGDNNNGIMKDTLRDC-DOESTCYNTV--IS 1809
Db 1606 NDENPCGMSRHAUFENFGMAFLTLFQVSTGDNNNGIMKDTLRDCDTHDERTCLSLQFVS 1665
Qy 1810 PIYFVSFVLTAQFVLNVVNVIAVLMKHLSEESKEAEAELEAELEEM-KTILSQPHSPL 1868
Db 1666 PIYFVSFVLTAQFVLNVVNVIAVLMKHLSEESKEAEAELEAELEEM-KTILSQPHSPL 1721
Qy 1869 GSPFLWPGVEGPDSPSPKPGALHPAAHARSASHFSLEHPTMQPHTELPDGLTIV-- 1925
Db 1722 -----GPCPG-----PCPCPCPCAGRLPTSSPG 1747
Qy 1926 ---RKSGVSRTHSLPNDSDSYMCRH 1945
Db 1748 APCRSGGAGAGG-DTESHLGRH 1769

RESULT 12

US-09-030-482B-19
; Sequence 19, Application US/09030482B
; Patent No. US20020009772A1
; GENERAL INFORMATION:
; APPLICANT: Snutch, Terry
; TITLE OF INVENTION: NOVEL HUMAN CALCIUM CHANNELS AND RELATED
; FILE OF INVENTION: PROBES, CELL LINES AND METHODS
; FILE REFERENCE: 38109-20007.00
; CURRENT APPLICATION NUMBER: US/09/030,482B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: US 60/039,204
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1853
; TYPE: PRT
; ORGANISM: Human
US-09-030-482B-19

Query Match 33.3%; Score 3959.5; DB 9; Length 1853;

Best Local Similarity 46.8%; Pred. No. 2.1e-240;

Matches 908; Conservative 158; Mismatches 361; Indels 515; Gaps 42;

Qy 27 GAGCRPG-----PGSAEKDPGSADSEAEGLPYPALAPVVFYLSQDSRSPRSLRTRVC 79

Db 76 GTGMHTGTGFGAEPGSSQHEAQAATYAGCTPAPTGDPTCCFVLD-----LVC 124

Qy 80 NPWERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAEDDFIFAFVMMVMMVAL 139

Db 125 T-WFECVSMVILLNCVTLGMVQPCDDMDCLSDRCKILQVDFDFFIFFAMEMVMMVAL 183

140 GIFGKCYLGDWNRDFFIVIAQMLEYSLDLQNSFSAVRTVRVLRPLRAINRVPMSRI 139
184 GIFGKCYLGDWNRDFFIVIAQMLEYSLDLQNSFSAVRTVRVLRPLRAINRVPMSRI 234
200 LVTLTLLDTLPMGNVLLLCFFVFFIFIGVQVQWAGLRRNRCFLPENFSLPLSDLVRY 259
235 LVNLLDTPMLGNVLLLCFFVFFIFIGVQVQWAGLRRNRCFLPENFSLPLSDLVRY 294
260 OTENEDESPIQCPRENGMRSRCSVPTLRDGGGGPPCGL-----DYEAYNSNNTT- 312
295 QPEEDDEMPICSLSGDNGIMGHEIPPLKEQ---GRECCLSKDDYDFGAGQDLNASG 351
313 -CVNNQOYVNCAGHNPKGAINFDNIGYAMIAIQQVITLGGWVDMVFMVDAHSFYN 371
352 LCNNRYNVNCRGTSANPHKGAINFDNIGYAMIVIFQVITLGGWVEIMVYVMDAHSFYN 411
372 FIYFILLII----- 380
412 FIYFILLIISELHLVMPDCFSFQAQSPKCGDLSLPGVAAESLLLRDSSSVITDEAAM 471
381 ----- 380
472 ENLLAGTSKDESLLRLLAGSQVHSAQOQMLGRGLGPESLETBEEPHSMSPRATRWDPQ 531
381 -----VGSFMINCLVVIATQFSETKQRESQMLRQVRFLSNASTLAS 425
532 COPGQPLPLHFMAQVGSFMINCLVVIATQFSETKQREHRLMLRQRYLS-SSTVAS 590
426 FSPGSCYBELLKYLIVILKKAARRLAQVSRAGVRVGLLSSPAPIGGQETQSSCCSR 485
591 YAFPGCYERIFQVYCHILKAKR-----RALGLYQALQSRQALGPEAPAKP- 640
486 HRRLSVHLLVHHHHHHVHLNGTLRAPRASPEITQDRDANGSRRLMLPPPTPALSGA 545
641 -----GPAKEPRHPPLTWBSILQRABECTLRAA-----AHPSSGAS 679
546 PPG-GAESVHSFYHADCHLEPVRQAPPPRSPSEASGRVTGSGKVYPTVHTSPPTLKE 604
680 HPGVGSSEA-----PELC---PQHSPLDATPHL-----VQIPATL-- 713
605 KALVEAASGPPTLTSLNTPPGYSSMHKLLTQSTGACQSSCKTSSPCLKADSGACGP 664
714 -----ASDP 717
665 DSCPVCAR-----AGAGEVELADREMPDSDSAVVEFTQAOHSDLRDPHRSRQSLGP 718
718 ASCPCQHQEDRRPRLGSTD-SQEGSGSGSAGGE--DEADGDGARSEDGASSELGK 774
719 DAEPSSVL-----AFWRLLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIYHQPE- 769
775 EEEEEQADGAVMLCGDVWRETRAKLGIIVDSKYFNRGIMVAILVNTVSMGIEHHEQASA 834
770 -----ELTNAL------ISNIV----- 781
835 AQPGACRGRQNDPLCMTLAPCLCHNVPSFGQGVLSHPVTPHTAPWRMETGKQHGCE 894
782 -----FTSLFALEMLLKLVYGPFGYKPNYINFDGVIIVISWVEIVGQGGSLVLR 835
895 EGGQSSDFALEMLKLVYGPFGYKPNYINFDGVIIVISWVEIVGQGGSLVLR 954
836 FRMLRVKLVRLPALQRLVLMKMDNVATFCMLLMFIFIFSLGMHFLGCKFASER 895
955 FRLLRVKLVRFMPALRQLVLMKMDNVATFCMLLMFIFIFSLGMHFLGCKFASER 1014
896 D-GDTLPDRKNFSLWVITVQILTOEDWNVKLVNGMASTSSWALYFIALMTGNVY 954
1015 DTGDTVPDRKNFSLWVITVQILTOEDWNVKLVNGMASTSSWALYFIALMTGNVY 1074
955 LFNLLVAILVEGFOAE-EISKREDA-----SGQLSCITQLP 988
1075 LFNLLVAILVEGFOAEVTVVIAEAPPGQRLKTRGREGGLDGGGLQFKLAGNLS-LKEG 1133
989 VDSQGGDANKSESEPDFSPS-----LQDGDGRKKCLALVSLGHEPRLKSLPP 1038

1134 VADEVGDANRSYDESDQSSNIEEPDKLQEGLDSSGDKLCPIMPNGH-----LDP 1186
1039 LIHTAATPMSLPKSTSTGLGEALGPA-----SRRIS----- 1070
1187 -----SLPLGHLGPAAGAPAPRLSLQDPMVALGSRKSGVMSLGRMSYDORS 1236
1071 -----SSGSAEPGAHEMKSP-----PSARSSPHSPWSAASWTSSRS 1109
1237 LVGGLRATAGVQAPGHLVPQPVWCVLWADPNNSFSQSSRSYYPGWSAAWARRSS 1296
1110 RNSLGRAPSKRSPSGERRSLSGE-GOESQDEEESSEE--ERASPAGSDH----- 1158
1297 WN-----SLKHPSPAHEHLSAERGGGARVCEVADEGPPRAAPLPHFAHHVHGP 1350
1159 -----RHGSLERAKSFDLPDLQVPLGHLRTASGR--GSASHQDCNGKASGRILA 1209
1351 HLAHRHRRHRTLSLDRDSDVLAELVPAVGAHPRAAAGAPAGPAGHEDCNGMPAIKD 1410
1210 RALRPDDPPLDGDADD-----EGNLSKGERVRAMIRARLPACYLERSDSWASVIPP 1260
1411 VFTMGDRGDRGBDEEEDIVVSGGGAEGDUTLCFRVRKMDIVYKPDWCEVREDWSYLF 1470
1261 PQSRPR-----LLC-----HRIITHKMFHDHVVVLIIFLNCITAME 1296
1471 PENLRDLGWSLECCQKVGDLVWVYQRRQRQTIIAHKLFYVVLAFIFLNCITALE 1530
1297 RPKIDPHSAERFLTISNYIFTAVFLAEMTVKVALGWCFCGQAYLRSSWNVDGLVLI 1356
1531 RQIEAGSERIFLTVSNYIFTAIFGEMTLKVSGLGYFGQAYLRSSWNVDGLVLFV 1590
1357 SVIDILVMSVDSGKILGMLRVLRLRLRLRPLRVISRAQGLKLVVETLMSLKPICNIV 1416
1591 SIIDIVVSLASAGKILGVLRLRLRLRPLRVISRAQGLKLVVETLMSLKPICNIV 1550
1417 VICCAFFIIFGLVQLFKGFVCOGEDTRNITKSDCAEASRYWRVHRYKPNFNLGOAL 1476
1651 LICCAFFIIFGLVQLFKGFVCHLGVDTNITNRSDCMAANYRWVHRYKPNFNLGOAL 1710
1477 MSFLVLSKDGVDIMYDGLDVGVDQOQPMHNPMLLYFISFLAVFVLMNVGVV 1536
1711 MSFLVLSKDGVMINMYNGLDAVADQOQVNTNPMMLLYFISFLAVFVLMNVGVV 1770
1537 VENFHKROHQBEEARREKRLRLEKRRKAQCKPYYSYRSRFLVHHLCTSHYLD 1596
1771 VENFHKROHQBEEARREKRLRLEKRRKAQRLPYATYCHTLHLSMCTSHYLD 1830
1597 LFTGVIGLVNVTMAMEHYQQP 1618
1831 IFITFIICLVNVTMSLEHYNQ 1852
RESULT 13
US-10-369-493-6836
; Sequence 6836, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6836
; LENGTH: 1657
; TYPE: PR

ORGANISM: Caenorhabditis elegans
US-10-369-493-6836

Query Match 29.9%; Score 3564.5; DB 14; Length 1657;
Best Local Similarity 42.2%; Pred. No. 1.5e-215;
Matches 822; Conservative 231; Mismatches 430; Indels 465; Gaps 50;

QY 15 QPSFMRNLDSGAGRRG-----PSAEKDPG-----SADSEA 48
DB 56 QSQSTRHEDVEALGSTEGSKETQLSEHGHLASSSEASPSRWEGROLEWNEQIEEES 115
QY 49 EGLPYALAPVVPYLSQDSRPSWCLRTVCNPMFERISMLVILLNCVTLQMPKPCED-I 107
DB 116 E-LPYGFAEPALRCFQAPRPRKALQWSPNEDRITMAVINCVTLGNYKPCEDGP 174
QY 108 ACDSQRCLLQAFDDFIPAPFAVEMVVMVAGLFGKCYKLGDTWNRDLDFIVTAGMLEY 167
DB 175 DCDYRCQILDIIDNCIFVYFAFEMVIKIMALGFYGAAYMSDTWNRDLDFIVMAGIAEF 234
QY 168 SLDLQ---NVSFSAVTRVRLPRLPRAINRVPMSRILVTLTLLDTPLMGLNVLLLCFFVFFI 224
DB 235 VLHYLEGGINLTAIRTVRLPRLPRAINRVPMSRILVTLTLLDTPLMGLNVLLLCFFVFFI 294
QY 225 FGIYGVOLWAGLLNRCF--LPENFS-----LPLSVDLERYQTEENDESFFICSQPREN 277
DB 295 FGIYGVOLWAGLLNRCVINLPKTISENQSALEFNNVKLTRFYIPE-DTSLEYICSQPDAN 353
QY 278 GMRSCRVPTRLRGDGGGPPCGLDYEAENSSNTTCVNNVNYNCASG-----326
DB 354 GLHTCSNLPPTVD---GVKCNLTLDYDKVTNDSCINWNIYNECQVNIYPSLMTIAIS 410
QY 327 -----EHNPKGAINEDNIGYAMTAFQVITLGGWDTMYFMDASHFYNFIFILLI 380
DB 411 CFIKWMORNPQGSVDNIGFAWVAFVLSLGGWDTIMYVQDAHSFWMNIYFVLLIV 470
QY 381 VGSFPMNLCLVLTATQFSETKQESQLMRQRVRFISNASTLASFSRPG-----S 431
DB 471 IGAFPMNLCLVLTATQFSETKRTERMLQERKMLNRDSISCTGSEIGGASSKEBGT 530
QY 432 CYEBLLKYLVLKRAARLAQVRAAGVRVGLLSSPAPLGGQETQPSSSCSRHRRLSV 491
DB 531 VYAAFPVRFIGHTFR--TKRAAKKTYAYMEE-----560
QY 492 HHLVHHHHHHHHYHLNGTIRAPASPEIQDRDANGSRRLMLPPSTPALSGAPPGAE 551
DB 561 -----RAERKSSEROOR-----RKSCLDDMAT--LS-----584
QY 552 SVHSFYHADCHLEPVRCPQAPPPSPSEASGRTVSGKVYPTVHTSPPETTLKEKALVEVA 611
DB 585 -----RIEKAEDB--593
QY 612 ASSGPPLTSLNIPPGYSSMHKLETOSTGACOSSCKI--SSPCLKADSGAGDPDPCYC 670
DB 594 --EDETTITREN-----GDDQIEQNGDGVRIKRVKIEEPKIKIGN--GNSNGPHY 640
QY 671 ARAGAGEVELADREMPDSDSEAVYFTQDAHSDLRDPHSRQRSLGPDAPSSVLAFWR 730
DB 641 KHSSSDE-----ESDEGDEQYDGEBAKKKS-----TPSKL--WW-675
QY 731 LICDTFRKIVDSKYFGRGIMIAILVNTLSMGVEHQPEELTNALEISNIVFTSLFALEM 790
DB 676 -FREKIQKFVICHETRGLIVALLVNTLSMGVEHQPEELTNALEISNIVFTSLFALEM 734
QY 791 LKLLVYGFPGYIKNPYNI PDGVIIVISWEIVGQGGGLSVLRTFLMRVLKLVRLPFA 850
DB 735 LKLLVYGFPGYIKNPYNI PDGVIIVISWEIVGQGGGLSVLRTFLMRVLKLVRLPFA 794
QY 851 LQQLVLMKMDNVDATFCMLMLMFIPIFSLGMLHFGCKFASERD---GDTLP--DRKN 905
DB 795 LRYQLVLMKMDNVDATFCMLMLMFIPIFSLGMLHFGCKFASERD---GDTLP--DRKN 854
QY 906 FDSLWLWAVTVFOILTQEDWNNKLVNGMASTSSWAALFYIALMTGNTGVNVLNLAIVLIVE 965

RESULT 14
US-10-627-370-2
; Sequence 2, Application US/10627370
; Publication No. US2004008198A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jason M.

DB 855 FDTLLMALITVQILLTQEDWNNKLVNGMASTSSWAALFYIALMTGNTGVNVLNLAIVLIVE 914
QY 966 GFQABEISKREDAAGQLSCITQLPVDOSGOGDANKSESEPDFFPSLDGDRKCKLALVSL 1025
DB 915 GFQABEISKREDAAGQLSCITQLPVDOSGOGDANKSESEPDFFPSLDGDRKCKLALVSL 949
QY 1026 GEHPELRKSLPLLIHTAATPMSLPKSTGTGLGEALGPASRRSTSSGSAEPGAHMKMS 1085
DB 950 -----IAKTTSPAFNNGVAPA-----ECTQBPSPSPSPSPS 980
QY 1086 PPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSG-----ERRSLLSGEGESQ 1140
DB 981 PRLLSANVH-----PSPERKHSANLDAIDKRLVL-----1010
QY 1141 DEESSSEERASPAAGSHRHGSLERAKSSFDLPDLTQVPLGRLHTASGRSASEHQDCN 1200
DB 1011 --RNSAPFDR--SPY--SEGRDDSRNLNRA--SLVLPVANGVP-----YRRQRVH 1052
QY 1201 GKSASGRALARALRPDDPLDGDADDDEGNLSKGS--RVRAWIRARL--PACYLERDSWSAYI 1258
DB 1053 SWKASQELKQAL-----AEEE--KRNEAKONTFVRKLLKKTCLNRTFESLFL 1098
QY 1259 FPQSRFELLCRRIITHKMFHDVVLVIFLNCITITAMERPKIDPHSAERIFLTISNYIFT 1318
DB 1099 MGPKNPLRIKCLQTTQKKWEDYTVLFFIGINCITLAMERPSPIDPSFERQFLHISGYIFT 1158
QY 1319 AVFLAEMTVKVALGWCFCGEQAYLRSSWNLDDLVLISIDILVSVSDSGTKILGMLR 1378
DB 1159 VIFTGEMMK-----1168
QY 1379 VLRLRLRLPLRVISRAQGLKLVVETLMSLLKPIGNIWICCAFFIIFGILGVOLFPGKF 1438
DB 1169 -----VSHRIPTLKPIGNIWICCAFFIIFGILGVOLFPGKF 1205
QY 1439 FVCGEDTRNITNKSDCAEASR--WVRHKYNFONLQALMSLFLVASKGQVMDIMYDGL 1496
DB 1206 YHCIGPEVGNVTTKADCE--DYRNKNWYHRNFNQLGQALMSLFLVASKGQVMDIMYDGL 1264
QY 1497 DAVGVDQOPINHPNPMWLLYFISFELLIVAFVLMFVGVVVVVENFHKCHQHOEBEARE 1556
DB 1265 DAVGVDQOPINHPNPMWLLYFISFELLIVAFVLMFVGVVVVVENFHKCHQHOEBEARE 1324
QY 1557 EKRLRLLEK-----KRRKQAC-----KPYSDYSRFLLVHHL 1590
DB 1325 EKRLRLLEK-----KRRKQAC-----KPYSDYSRFLLVHHL 1384
QY 1591 TSHYLDLFTTIGVIGLVNVTWAMEHYQOILDEALKICNYIFTVIFVLESFVKLVAFGR 1650
DB 1385 TSKYFDLAIARVIGINVISMAEFYMMPMGLKYVLKALNYFTAVFTLEAAMKLIAGFK 1444
QY 1651 RFFQDRWNLDAVLVLSIMGITLEEBEVNASLDPINTIIRMRVLRARVLRKLVKMAVG 1710
DB 1445 RFFQDRWNLDAVLVLSIMGITLEEBEVNASLDPINTIIRMRVLRARVLRKLVKMAVG 1503
QY 1711 MRALLDTVMQALPOVGNLGLLPMLLFFIFALGVLFGLDECDETHPCGELGRTATPNF 1770
DB 1504 IRSLLDTVGEALPOVGNLGLLPMLLFFIFALGVLFGLDECDETHPCGELGRTATPNF 1563
QY 1771 GMAFLTFRSTGDNWNGIMKDTLR--DCD-----QESTCVNTVISPFIYFVSVLTAQFVL 1824
DB 1564 GMAFLTFRSTGDNWNGIMKDTLR--DCD-----QESTCVNTVISPFIYFVSVLTAQFVL 1623
QY 1825 VNVVAVLMKHLSEENKEAEAELEAE 1852
DB 1624 VNVVAVLMKHLSEENKEAEAELEAE 1648

Db 812 HLDRLVLVGLRGDARGVGGKARPEAAEAPGVDPDRRHRHRDKDKTPAAGDQDRAEA 871
Qy 1074 ----SABPGA-----AHMKGPPSARS-----SPWSAASSW 1103
Db 872 PKAESGPGAREPRHRSHKAEAGPPARERGRGPGEGRRHRHRSFEEAARE 931
Qy 1104 TSR-RSRNSLGRAPS LKRRSPGERSLLSGEQESQDEESSEE-----ERASP- 1153
Db 932 PRHRAHRH--QDPSEKACAGKERRARHGGPRAGPREAESGEEFARRHRAHKAQPA 988
Qy 1154 ----AGSDHRHRSGLEREAKSSFDLPDTLOVGLHRTASGRG 1191
Db 989 HEAVEKETTEKEAEIADKEKELRNHQREPHCDLETSGITVGMPTLPTCL 1048
Qy 1192 SASEHODCNKSGASRLARLRDPD-----PLDGDADDEGNL-----SKGE 1234
Db 1049 QKVEEQPEDADNORNVTRMCSQPDENTIVHPMLTGPGLGEATVPSGNDVLESQAEGK 1108
Qy 1235 R-----VRAMTRARLPACYLERSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVIIF 1287
Db 1109 KEVEADDMRSGRPIVPYS-----SMFCLSPNLLRRFCHVITMRVFEVILVIA 1161
Qy 1288 LNCITITAMEPKIDPHSAERIFLTLNYSIETAVFLAEMTKVVALGWCFCGEQAYLRSSWN 1347
Db 1162 LSSIALAARDP-VRTDSPRNALKYLDYIFTFVTFPEWIKMIDLGLLHPGAYFRDLWN 1220
Qy 1348 VLDGLLVLISVIDI-LVSMVSDSGTKILGMLRLRLRPLRVISRAOGLKLAVETLM 1406
Db 1221 ILDFIVVSGALVAFSSFFVGGSGKDINTIKSLRVLRVLRLPLKTELKPLKAVFCVV 1280
Qy 1407 SSKLPTGNIVICAPFIIPGILGVQLFKGKFFVCGE-----DTRN--ITNKSDCAEA 1458
Db 1281 NSLKNVLNILLVWLMFIFPAVIAVQLFKGKFFVCTDESELERDCRGQYLDVEKEVEA 1340
Qy 1459 SYR-WVRHKYNFNLCQALMSLVLASKDGMVIMYDGLDAVGVDQOPIMNHPWMLLYF 1517
Db 1341 QPQWKXYDHYDNVILWALLTLFTVSTGEGWVLVSKHSDVATYEEQGPSGYRMELSFY 1400
Qy 1518 ISPELLIAVFFVLMVGVVNFHKKRQHOOEEEAAREERKRLRLEKRRKA-----QC 1572
Db 1401 VVYFVVFPPFFVNI FVALIIITF-----QEOGDKWSE-----CSLEKNERACIDFAISA 1450
Qy 1573 KPY--YSDYSR--FRLLVHLCTSHYLDLFTIGVGLNVVTVMAVHYQQOQIILDEALKIC 1628
Db 1451 KPLTRYMPONRQSFQYKWTFTVVSPPPEYFIMAMIALNTVLMKMFYDAPYEVELMKCL 1510
Qy 1629 NYLFTVLEVSFKLVAFGRFRFQDRNQDLAIVLSIMGITLEEI-EVNASLPINP 1687
Db 1511 NYFTSMFSMECVKIIIAFGVLNFRDAMNVDFVTVLGSIITDILVTEIAETN-----NF 1565
Qy 1688 TIIRIMRVLRIARVLLKLMAGVMRALLDTVMQALPOVGNLGLLFFLFFIFAALGVLELF 1747
Db 1566 INLSFLRLPEARLILKLRQGYTIRILLWTFFVQSEKALPVVCLLIAMLFYIYALIGMQVF 1625
Qy 1748 GLECEBETHCEGLGHAFRNGMAPLTLFRVSTGDNWNGIMKDTLRD--CDOE--STC 1803
Db 1626 GNIALDDD--TSINRHNFRTEFLQALMLLFRSATGEAWHEIMLSCLSNQACDOANATE 1682
Qy 1804 YNTVIGPIYFVSFVLTAQFVLNVNVIATVLM-----KHLEE----- 1838
Db 1683 CGSDFAFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDEFIRVWAEYDP 1742
Qy 1839 ----- 1838
Db 1743 AACGRISYNDMEBMLKXMSPPGLGKKCPARVAVKRLVRNMNMPISNEDMTVHFTSTLMAL 1802
Qy 1839 -----SNKEAKEAELEAELEBMTLSLSPHSPGLSPFLWPCVEGDPSPD 1886
Db 1803 IRTALEIKLAPAGTKQOCDAELRKETSIVVWNL-FQKTLDDLVP-----PHKPEDEM 1853
Qy 1887 KPGALHPA-----AHARSASHFSLEHTM-----QPHPTLPD 1921
Db 1854 TVGKVYAALMIFDYFKONKTTROMQOAPGGLSQMGFVSLFHLKATLEQTQAVLRGAR 1913

Qy 1922 LLTVRKSGVSRTHSLPNDNSYCRHSGTAEGPLGHRGMLPKAQSGSVLSVHSOPADTSYI 1981
Db 1914 VFLRQKSTSLN-----GGAIQNESGIKESV-----SWG 1944
Qy 1982 LQLPKQAPHLLOP-----HSAPTWTGTPKLPPPGRSPLAQRLRRQAIR-----TDS 2029
Db 1945 TQRTQDAPHEARPLERGHSTEI-----PVGSRGALAVDVQMOSITRRGPDGEPQG 1996
Qy 2030 LDVOGLGSRREDLLAEVSGP---SPPLARAYSFWGQSQSTQAOQHRSRSHSKISKHMTTPAPC 2086
Db 1997 LESQGRAASMPRLAAETQPVTDASPMKRST-----STLAQRPRGTHLCST---TPDRPP 2047
Qy 2087 PG-----PEPNWKGPPETRRSGSLELDTLSWITSGDILLPPGGOEPPSP 2129
Db 2048 PSQASSHHHHRRCHRRDRKQRSLEKP---SLSADMDGAPSSAVNGPLPG--EGTGC 2102
Qy 2130 RDLKICYVEAQSCORR-PTSWLDEORRHIAVCLDSG-----SOPHLG 2173
Db 2103 RRRERRQERGRQERRQPSSSSEKQRF---YSCDRFGGRPPKPKPSLSHPTSPTAG 2159
Qy 2174 TDP-----SNLGGOPL-----CGPSRPPKKLSP-PSITI-----DPPESQ 2209
Db 2160 QEPGPHPGSGSVNGSPLLSTSGASTFGRGRRLQFQTPLTTPRPSITYKTANSPIHFAG 2219
Qy 2210 PRT--PP-SPG-----ICLRRRAPSDSKDPLASGPPDSMAASPSPKDVLISLGL 2257
Db 2220 AQTSLPAFSPGRSLRGLSEHNALLQRDPLS---QPLAPG-----SRI 2258
Qy 2258 SSDP 2261
Db 2259 GSDP 2262

Search completed: November 18, 2004, 13:59:31
Job time : 210.672 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:21 ; Search time 50.2671 Seconds
(without alignments)
4337.375 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEDGAGAEESGQPRSF.....PKKDVLSLGSLSDPADLDP 2266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10945	91.9	2254	2 T09053	low voltage-activa
2	3564.5	29.9	1657	2 T15838	hypothetical prote
3	1746.5	14.7	2339	2 A42566	omega-conotoxin-se
4	1741	14.6	2237	2 T45115	N-type calcium cha
5	1711	14.4	2336	2 A45386	omega-conotoxin-se
6	1706	14.3	2288	2 S41080	calcium channel al
7	1697	14.3	2259	2 S29236	calcium channel pr
8	1689	14.2	1810	2 T31092	probable voltage-g
9	1681	14.1	2178	2 S29237	calcium channel pr
10	1681	14.1	2272	2 C54972	voltage-dependent
11	1665	14.0	2270	2 A54972	voltage-dependent
12	1664.5	14.0	1891	2 T43262	calcium channel al
13	1663.5	14.0	2251	2 B54972	voltage-dependent
14	1658	13.9	2223	2 A47447	calcium channel pr
15	1651.5	13.9	2222	2 A37490	voltage-dependent
16	1633	13.7	1911	2 T43048	calcium channel al
17	1632	13.7	1873	2 A30063	dihydropyridine re
18	1626	13.7	1993	2 T30902	sodium channel sca
19	1625.5	13.7	1852	2 A37860	calcium channel pr
20	1612	13.5	2143	2 JH0427	voltage-dependent
21	1602.5	13.5	2139	2 A44467	voltage-dependent
22	1597.5	13.4	1559	2 T30535	calcium channel al
23	1596.5	13.4	2166	2 S11336	calcium channel pr
24	1591	13.4	2019	2 A33996	sodium channel pro
25	1590	13.4	1783	2 T37258	probable voltage-d
26	1586	13.3	2016	2 A38195	sodium channel pro
27	1583.5	13.3	1873	2 A55645	calcium channel, v
28	1583	13.3	1977	2 S54771	sodium channel alp
29	1581.5	13.3	2171	2 S05054	calcium channel al

30	1578	13.3	1917	2	C88728	protein C48A7.1 [i
31	1573.5	13.2	1983	2	A60054	sodium channel pro
32	1572.5	13.2	2212	2	A41098	calcium channel pr
33	1568.5	13.2	1687	2	S41742	calcium channel al
34	1566.5	13.2	2203	2	T42742	voltage-dependent
35	1565.5	13.2	1951	2	S00320	sodium channel pro
36	1564.5	13.1	2181	2	A38198	calcium channel al
37	1561	13.1	2326	2	B47447	calcium channel pr
38	1560.5	13.1	1610	2	A46227	voltage-dependent
39	1557.5	13.1	2161	2	JH0564	calcium channel al
40	1555	13.1	2220	2	A45290	calcium channel pr
41	1554	13.1	2262	2	T30890	calcium channel al
42	1553.5	13.1	2005	2	A46269	sodium channel alp
43	1550	13.0	1957	2	S68453	sodium channel pro
44	1549.5	13.0	2009	2	A25019	sodium channel pro
45	1549	13.0	1646	2	JH0422	voltage-dependent

ALIGNMENTS

RESULT 1
T09053
low voltage-activated, T-type calcium channel alpha chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09053
R:Peres-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox
Nature 391, 896, 1998
A:Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium
A:Reference number: Z16538; MUID:98154730; PMID:9495342
A:Accession: T09053
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2254 <P>
A:Cross-references: UNIPROT:O54898; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g3
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Map position: 17
A:Note: CACNA1G
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C:Keywords: calcium channel; voltage-gated ion channel

Query Match 91.9%; Score 10945; DB 2; Length 2254;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2107; Conservative 34; Mismatches 101; Indels 36; Gaps 6;

Qy	1	MDEEDGAGAEESGQPRSF	FMRLNDLSGAGRGPGPSAEKDPGSADSEAGLPYPALAPVV	60
Db	1	MDEEDGAGAEESGQPRSF	FMRLNDLSGAGRGPGSTKDPGSADSEAGLPYPALAPVV	60
Qy	61	FFYLSQSRPSRSC	LRVTCNPWFERRISMLVILLNCVTLGMFRPCDIACDSQRRILOAF	120
Db	61	FFYLSQSRPSRSC	LRVTCNPWFERRISMLVILLNCVTLGMFRPCDIACDSQRRILOAF	120
Qy	121	DDRTFAEFVEMVVMV	ALGIFGKKCYLGTWRLDFFIVLAGMLYSLLDQNVSFSAVR	180
Db	121	DDRTFAEFVEMVVMV	ALGIFGKKCYLGTWRLDFFIVLAGMLYSLLDQNVSFSAVR	180
Qy	181	TVRVLRPLRAINR	VPMSRIILVTLTLLDPLMGLNVLLICFFVFFIFGVGVQLWAGLNR	240
Db	181	TVRVLRPLRAINR	VPMSRIILVTLTLLDPLMGLNVLLICFFVFFIFGVGVQLWAGLNR	240
Qy	241	CFLPENFSLPLSV	LDLERYQYOTENEDSPFICSPRENGMRSRCSVPTLRGGGGGPGCGL	300
Db	241	CFLPENFSLPLSV	LDLERYQYOTENEDSPFICSPRENGMRSRCSVPTLRGGGGGPGCGL	300
Qy	301	DYAYSSSTNTCV	NNQYVYVTCNSAGEHNPFGKAINFDNIGYAWIAIPQVITLEGWDIM	360
Db	301	DYAYSSSTNTCV	NNQYVYVTCNSAGEHNPFGKAINFDNIGYAWIAIPQVITLEGWDIM	360
Qy	361	YFVMDAHSFYNF	YFILLITVGSFFFMINLCVVIATQFSETKQRESOLMEQVRFLSNA	420

Db 361 YFVMDAHSYNFYFIYFILLIIVGSFFMINILCLVVIATQFSETKQRBSQLMRQVRFLSNA 420
QY 421 STLASFBPGSCYEBELLKYLVVILKAAARLQAQRAAGVRVGLLSSAPLGGQETQPS 480
Db 421 STLASFBPGSCYEBELLKYLVVILKAAARLQAQRAAGVRVGLLSSAPLGGQETQPS 480
QY 481 SCRSRHRLLSVHLLVHHHHHHHHHVLGNGTILRAPRASPEIORDANGSRRLMLPPSP 540
Db 481 SCTRHRRLSVHLLVHHHHHHHHHVLGNGTILRAPRASPEIORDANGSRRLMLPPSP 540
QY 541 ALSGAPPGGAESVHSHADCHLEPVRCQAPPPRSPSEASGRVTGSGKYPTVHTSPPE 600
Db 541 TFGGPPRGAESVHSHADCHLEPVRCQAPPPRSPSEASGRVTGSGKYPTVHTSPPE 600
QY 601 TLKEALVEAASSGPPLTSLNIPPGPYSSMHKLELTOSTGACOSSCKISPPCLKADSG 660
Db 601 ILKDALVEAPSPGPPLTSLNIPPGPYSSMHKLELTOSTGACOSSCKISPPCLKADSG 660
QY 661 ACPGDCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQSDLRDPHS - RRQSLGPD 719
Db 661 ACPGDCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQSDLRDPHS - RRQSLGPD 720
QY 720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIALVNTLSMGIEYHQPEELTNALEISN 779
Db 721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIALVNTLSMGIEYHQPEELTNALEISN 780
QY 780 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIIPGVIVVISVWBIVGQGGGLSVLRTFRML 839
Db 781 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIIPGVIVVISVWBIVGQGGGLSVLRTFRML 840
QY 840 RVKLVRFLPALQROLVLMKTMNDVATECMLLMFLFIFISILGMHLFCKEASERDGT 899
Db 841 RVKLVRFLPALQROLVLMKTMNDVATECMLLMFLFIFISILGMHLFCKEASERDGT 900
QY 900 LPDRNFDLSLWAIIVTFQILLTOEDWNKVLVNGMASTSSWAALYFIALMTFGNYVFNLL 959
Db 901 LPDRNFDLSLWAIIVTFQILLTOEDWNKVLVNGMASTSSWAALYFIALMTFGNYVFNLL 960
QY 960 VAILVEGQAEIISKREASGQISCIQLPVDQGGDANKSESEPPFFSLDGDGRKCC 1019
Db 961 VAILVEGQAEIISKREASGQISCIQLPVDQGGDANKSESEPPFFSLDGDGRKCC 997
QY 1020 LALVSLGHPRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRSTSSGSAEPGA 1079
Db 998 LALVALGHAELKSLPLLIHTAATPMSHPKSSSTGVGEALGSGSRSTSSGSAEPGA 1057
QY 1080 A - HEMKSPSARSPHSPWSAASSWTSRRSSNSLGRAPSLKRRSPGSRRLLSGEGQE 1138
Db 1058 AHHEMKCPPSARSPHSPWSAASSWTSRRSSNSLGRAPSLKRRSPGSRRLLSGEGQE 1117
QY 1139 SODESESEERASPAQSDHRRGSLEREAKSSFDLPDTLQVPGHRTASGRGSAEHQD 1198
Db 1118 SODESESEERASPAQSDHRRGSLEREAKSSFDLPDTLQVPGHRTASGRGSAEHQD 1177
QY 1199 CMGKSASGRLARALRPDPPDLGGDDADDEGNLSKGERVRAWIRARLPACYLBERDSWSAYI 1258
Db 1178 CMGKSASGRLARALRPDPPDLGGDDADDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI 1237
QY 1259 FPQQRFLLCRIITHKQFDHVLVIFPLNCITIAMERPKIDPHSAERIFLTLGNLYIPT 1318
Db 1238 FPQQRFLLCRIITHKQFDHVLVIFPLNCITIAMERPKIDPHSAERIFLTLGNLYIPT 1297
QY 1319 AVFLAEMTVKVALGWCFOEQAYLRSSWNVLGDLVLISVIDILVSWSDSGTKILGMLR 1378
Db 1298 AVFLAEMTVKVALGWCFOEQAYLRSSWNVLGDLVLISVIDILVSWSDSGTKILGMLR 1357
QY 1379 VLRLTLRLPLRVISRAQGLKLVWETLMSLKPIGNIVVICCAFFIIFGILGVLQFKGF 1438
Db 1358 VLRLTLRLPLRVISRAQGLKLVWETLMSLKPIGNIVVICCAFFIIFGILGVLQFKGF 1417
QY 1439 FVCOGEDTNIITNKSDCAEASVRRVHRKYNFNLGOALMSLFLVLSKQGWDMIMVDGLDA 1498
Db 1418 FVCOGEDTNIITNKSDCAEASVRRVHRKYNFNLGOALMSLFLVLSKQGWDMIMVDGLDA 1477

QY 1499 VGVDOOPIMNHNPNMMLLYFISLLIIVAFVLMFVGVVVENPHKCRQHQEERREARK 1558
Db 1478 VGVDOOPIMNHNPNMMLLYFISLLIIVAFVLMFVGVVVENPHKCRQHQEERREARK 1537
QY 1559 RLRREKERR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTTGVIGLVNVTMA 1611
Db 1538 RLRREKERRSKQMAEAAQCKPYSDYSRFRLLVHHLCTSHYLDLFTTGVIGLVNVTMA 1597
QY 1612 MEHYQOQLDALKICNYIFTVIIVLESVFKLVAFGFRFRFPQDRWNQDLDAIVLLSIMG 1671
Db 1598 MEHYQOQLDALKICNYIFTVIIVLESVFKLVAFGFRFRFPQDRWNQDLDAIVLLSIMG 1657
QY 1672 ITLEIEVNASLIPNPTIIRIMRVLIARVLKLLKXVGMRAALLTVMQALPQVGNLGL 1731
Db 1658 ITLEIEVNLSPNPTIIRIMRVLIARVLKLLKXVGMRAALLTVMQALPQVGNLGL 1717
QY 1732 FMLFFIFAALGVELFGDLECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1791
Db 1718 FMLFFIFAALGVELFGDLECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1777
QY 1792 DTLRCDQESTCYNTVISPITYFVSFVLTAQFVLVNVVIAVLMKHLBEESKEAKEAELEA 1851
Db 1778 DTLRCDQESTCYNTVISPITYFVSFVLTAQFVLVNVVIAVLMKHLBEESKEAKEAELEA 1837
QY 1852 ELELEMKTLSPHPSPLGSPPLWPGVEGPDSPSPKPGALHPAAHARSASHESLRHPTWO 1911
Db 1838 ELELEMKTLSPHPSPLGSPPLWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMV 1897
QY 1912 PHFTBLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTARGPLGHRGWGLPKAQSGSV 1968
Db 1898 PHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAESLSLGRGWGLPKAQSGSI 1957
QY 1969 LSVHSQADTSTVILQIPKDAAPHLLOPHSAPTWTGTPKLPPLPPGSRPLAQRPIRQAIRTD 2028
Db 1958 LSVHSQADTSTVILQIPKDAAPHLLOPHSAPTWTGTPKLPPLPPGSRPLAQRPIRQAIRTD 2017
QY 2029 SLDVQGLSREDLLAEVSGSPPLARAYSFWQSGSTOAOHRSRSHSKSHMTTPPAPCPG 2088
Db 2018 SLDVQGLSREDLLAEVSGSPPLARAYSFWQSGSTOAOHRSRSHSKSHMTTPPAPCPG 2077
QY 2089 PEPNWKGPPTETRSLELDTLSTWISGDLPLPGGQEEPPSPRDLKKCYSAEQSCORRT 2148
Db 2078 LEPNWKGPPTETRSLELDTLSTWISGDLPLPGGQEEPPSPRDLKKCYSAEQSCORRT 2136
QY 2149 SWLDQRHRSIAVSCLDGSGQPHLGTDFSNLGGQPLGGPGSRPKKLAPPSTIIDPPESQ 2208
Db 2137 FWLDQRHRSIAVSCLDGSGQPHLGTDFSNLGGQPLGGPGSRPKKLAPPSTIIDPPESQ 2196
QY 2209 GPRTPPSGICLRRRAPSSDKPLASGPPDPSMAASPSPKDVLISLGLSSDPADLDP 2266
Db 2197 GSRPPCSGVCLRRRAPASDKDPSVSSFLDSTAASFPKDTLSLGLSSDPTDMDP 2254

RESULT 2

T15838

hypothetical protein C54D2.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text_change 17-Mar-2000

C:Accession: T15838

R:Minx, P.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid C54D2.

A:Reference number: Z18415

A:Accession: T15838

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1657 <MIN>

A:Cross-references: EMBL:U37548; NID:g1017804; PID:g1017809; PIDN:AAA79201.1; CESP:C54D2.5

C:Genetics:

A:Gene: CESP-C54D2.5

A:Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; 334/2; 370/2; 439/3; 470/3; 51/3

C:Superfamily: sodium channel protein

Query Match	29.9%;	Score 3564.5;	DB 2;	Length 1657;
Best Local Similarity	42.2%;	Pred. No. 6.5e-210;		
Matches	822;	Conservative 231;	Mismatches 430;	Indels 465; Gaps 50;
QY	15	QPSRPMRLNDLSGAGRG-	-----PGSAEKDPG-----	SADSEA 48
Db	56	QSQSTRRHEDVEALGSI	EGSKETQLQSHGLASSSEASPRWEGRQI	EWGNEEQIBES 115
QY	49	EGLPYPALAPVFFVYLS	QDSRPSRCLRTVCNPFERISMLVILLNCV	TGLGMPRCPD-I 107
Db	116	E-LPYGPAEALRCFYQ	ARPRKVALQVMSPDFRITMAVINNCV	TGLGMPRCPDGP 174
QY	108	ACDSQRCRILQAFDDF	IPAFFAVEMVVMKVALGIFGKKCYLGD	TWNRLLDFFIAGMLEY 167
Db	175	DCDTRCQILDIIDNCI	FVYFAFEMVIKIMALGFYGPAAVMSD	TWNRLLDFFIWAGIARF 234
QY	168	SLDLQ---NVSFSAVR	TVRLRPLRAINRVPDSMRILLVTL	LLDTTIPMLGNVLLCFFVFFI 224
Db	235	VLHEYLGNNILTAIR	TVRLRPLRAVNRIPSMRILVNL	LLDTTIPMLGNVLLCFFVFFI 294
QY	225	FGIVGVQLWAGLLNR	CF---LPENFS-----LPLSVDLERY	QYQENEDSPFICSQPREN 277
Db	295	FGIVGVQLWAGLLNR	CVINLPKTIENQSALEFNNVKLTR	YIPE-DTSLEYICSQPDAN 353
QY	278	GMRSRCSVPTLRG	GGGGPPCGGLDYEAYNSSNTTCVN	WQYYTNCAG-----326
Db	354	GLHTCSNLPPTVD---	GVKCNLTLDYDKVTNDCINWNI	YNECQVNIYPSLMTAIS 410
QY	327	-----EHNPFK	GAINDFNIGYAWIAFQVITILEGW	TDIMYFVMDAHSFNFYFILLII 380
Db	411	CFIKVMQRNPFQGS	VDNIGFAWIAFLVISLEGWTDIM	YVYQDAHSFNNWYFVILLIV 470
QY	381	VGSPFMNLCLV	VIATQFSEKTESQLMREORVRLFS	NASTLASRSEPG-----S 431
Db	471	IGAFFMNLCLV	VIATQFAETKRETERMIQERKML	NRDSISCTGSEIGASKEGDT 530
QY	432	CYEBLLKYLVI	ILKKAARRIAQVSRAGVRGLLS	PAPLGGQETQSSCSRSRRLSV 491
Db	531	YVAAFVRFIGHTPR-	TKRAAKKYTAYMBE-----	560
QY	492	HHLVHHHHHHYH	LGNGTILRAPASPETQDRDANGSR	RLMLPPPTPALSGAPPGA 551
Db	561	-----RAERKSS	RQOR-----RKSLDDMAT--	LS-----584
QY	552	SVHSFVHADCHLE	PRVRCQAPPRSPSEASGRTVGSG	KVYPTVHTSPPTLKEKALVEVA 611
Db	585	-----RIBES	ABDE-----593	
QY	612	ASSGPPTLSL	NIPPGPYSSMHKLETQSTGACQSS	CKI--SSPCLKADSGACPDSPYC 670
Db	594	--BDETITREN---	GDQIEQNGDGVIRKVKIEEPK	IKIGN---GNSNGPHY 640
QY	671	ARAGAGEVELADRE	MPDSDSEAVYFTQDAQHSDRLD	PHSRRRORSIGPDAPSPSVIAFWR 730
Db	641	KHSSDSDE-----	ESDEDEEDQVYDGEBAKKS----	TPSKL--WW-675
QY	731	LICDTRFKIVDS	KYFGKGIMAILVNTLSMGIEV	HEQPEELTNALATISNIVTSLFALEM 790
Db	676	-PREKTQKFI	CHDFTRGILUVALVNTLSMGV	BYHQOPEILTVILEYSLNFFTFALFALEM 734
QY	791	LLKLLVYGP	FGYIKNPYNIPDGVIWISVMEI	VGQQGGLSVLTRFRLMRVLKLVFLDA 850
Db	735	LLKIIASGLFGY	LADGFNLFDGGIVALSVLEL	FQEGKGGLSVLTRFRLRILKLVFMFA 794
QY	851	LQROLVLMK	TMDNVATFCMLMLFTIFPSIL	GMHLFGCKFASERD---GDTLP--DRKN 905
Db	795	LRYLQVLM	LRTMDNVTFVFFGLLVLFIFPS	ILGMNLFQCKFCKVEEFLGGLAKKERKN 854
QY	906	FDLSLLWAI	VTVFQILLTOEDWKNVLYNG	MASTSSWAALYFIALMTFGNYVFNLLVAIIVE 965
Db	855	FDTLLWALI	TVFQLTQEDWNWVLFNGMA	TNPAAALYFVALMTFGNYVFNLLVAIIVE 914

RESULT 3

A42566

omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively spliced)
C/Species: Homo sapiens (man)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
C/Accession: A42566
R/Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; MCCI Science 257, 389-395, 1992

A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type
A;Reference number: A42566; MUID:92335886; PMID:1321501
A;Accession: A42566
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2339 <MUI>
A;Experimental source: IWR32, hippocampus (NCBIP:109168)
A;Note: sequence extracted from NCBI backbone
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.7%; Score 1746.5; DB 2; Length 2339;
Best Local Similarity 24.2%; Pred. No. 2.2e-98;
Matches 641; Conservative 361; Mismatches 823; Indels 819; Gaps 86;

QY	27	GAGRGPGSGAEKPGSADSEAEGLPYEPALAPVVF-----FYLSQDSRP 70
DB	25	GAGGAGGPGGLQGQGVLYKQSIQAQARTMALYNPIVKQNCFTVNRSLFVSEDNV 84
QY	71	RSWCLRTVCNPFERISMVILLNCVTLMGFPCEDIACDSQRCILQAFD---FIFAF 127
DB	85	KYAKRITETWPPFYMILATIANCIVLAL-----EQLPDGDKTMSERLDDTEYFIGI 140
QY	128	FAVEMVVKVALG-IFGKKCYLGDWNRDLDFIVLAGMLEYS---LDLQNVSFSAVTRV 183
DB	141	PCFEGAGIKIILGTFVHGKSYLRNGWVDFVVLITGILATAGTDFDLR-----TLRAVR 195
QY	184	VLRPLRAINRVPSMRILVTLTLLDPLMLGNVLLCFFVFFIPGIVGVQVWAGLLNRCP 243
DB	196	VLRPLKLVSGIPSLQVWLKSIKMAVPLLIQILLFFAILMFAIIGLEPYMGKFKACG- 254
QY	244	PENFSLPSVLDLERYQTEDEDESPICQSPRENGKRSRCSVPTLRGDCGGGPPCGLDYE 303
DB	255	-----PNSDAB-----PV-----GDFPCQKEAP 273
QY	304	AYNSSNTTCVMNOYNTMCSAGEHNPFGKAINFGNIYAMTIAFQVITLEGWDMIVFV 363
DB	274	ARLCGDTFC-----REYWP-----GPNFGITNFNILLFALTIVQCITMEGWTILYNT 323
QY	364	MD-AHSFYNFIYFIILLIIVGSPFMNLCIVTATOFSETKORES-----QLMRQVRVF 416
DB	324	NDAAGTNWNLVFIPLIIIGSFPMNLVLGSLGFEKAKERVENRRAFLKLRQOOQIB- 382
QY	417	LSNASTLASFPSPGCBELLYVILRKARRLAQVSRAGVRVGLLSAPLGGQGT 476
DB	383	-----RELNGYLEWIFKAEVUMLAEEDRNA-----EEK 410
QY	477	QPSSSCSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPP 536
DB	411	SLDLVKRAATKKSNDLIH-----AEEGEDRFAD----- 440
QY	537	PSTPALSGAPPGGAESVHSFYHADCHLEPVRQAPPSPRSEASGRTVSGKYPTVHTS 596
DB	441	----- 440
QY	597	PPPETLKALVEVAASSGPPTLTSLNIPPGPYSSMKLELTQSTGACQSSCKIISPCCLK 656
DB	441	-----LAVGSPFAR 450
QY	657	ADSGAGCPDSCPCYCARAGAVEVELADREMPDSDSEAVYBFTQDAQSHDLRDPHSRQRL 716
DB	451	ASLKGKTESSSYFR-----KERWFRF----- 473
QY	717	GPDAEPSSVLAFWRLICDTRKLVDSKYGRGMIAILLNTLSMGLEYHQEELTNALE 776
DB	474	-----FIRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTLTY 515
QY	777	ISNIVTSLFALEMLKLLVYGPFGIKNPYNIFDGVIVVISVWEIVG---QOQG--GLS 831
DB	516	FAEFVFLGLFTLSLWYGLGRSFRSFCNCFDGVIVGVSFVFWAAIKGSGSGFIS 575
QY	832	VLRTFLMRVLKLVRLPALQRLQVLMKTMNDVATFCMLMLFIPTFISILGMHLGCKF 891
DB	576	VIRALRLLRIFKTYKWSLRLNVLWSLNSMKSIIISLLFLLFIVVFAALLGMQLFGGQF 635

QY	892	ASREDGTLPRKNFDSLLWALIVTVFOILLTOEDWNKVLNCGM-----ASTSSWAAIFYA 946
DB	636	NFODETPT-----TNFTDTPAAILTVFOILLTGEDNWNVWYHGIESQGGVSKMGFSFFIV 691
QY	947	LMTEGNYVLFNLVAILVEGF-QAEISK-----REDASGQ-----LSCIQ 986
DB	692	LTLTEGNYVLLNVLVIAVDNLANAQELTKDBEEMEAANQKLQKAKEVAEVSFMSAAN 751
QY	987	LPVDSQGDANKSESEDPFSPSLDGDGRKCKIALVSLGE-----HPELRK 1033
DB	752	ISIAARQONSAKARSVMEOQRASQLRQLNRASCALYSEMDPEERLRFATTHRLRPMK 811
QY	1034	SLLPPLIHTAATPMSLP-----KSTSTGLCEALGPASR-----RTSSSG----- 1073
DB	812	HLDRPLVVELORDGARGPVGKARPEAAEAGEVDPRRHHRRDKDKTTPAAGQDRAEA 871
QY	1074	-----SAEFGA-----AHEMKSPSPARS-----SPH-----SPWSAASSW 1103
DB	872	PKAESGEPGAREERPRPHRSKSEAAGPPEARSEGRGPGEGGRHRRHRSPEEAERE 931
QY	1104	TSR-RSSNSLGRAPSLKRRSPSGERRSLLSSEGESODEBESSE-----ERASP- 1153
DB	932	PRRRAHRH-----QDPSKECAGKERRARHRRGGPRAGPREASGEEPPARRHARKAQPA 988
QY	1154	-----AGSDHRRHRSLEAREAKSSFDLPDTLOVPGHLRTASGRG 1191
DB	989	HEAVEKETTEKATEKEAEIVAEKELRNHQPREPHCDLETSGTVVGPMTLPSTCL 1048
QY	1192	SASEHQDCKGSASGRALARLPDDP-----PLGDDDDADDGNL---SKGER- 1235
DB	1049	QKVEQPEDADNQRNVTRMGSPDPDNTIVHPVMTGLTGLGEATVPSGNDLESQAEQK 1108
QY	1236	-----VRWIRARLPACVLRDSWSAYIFPQOSRELLCHRIITHKMPDHVVLIIF 1287
DB	1109	KEVEADDMRSGPRDIVPYS-----SMFCLSPNLLRRPCHYIVTWRYFEVLIIVIA 1161
QY	1288	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSGW 1347
DB	1162	LSSIALAEADP-VRTDSPPNNALKYLDYIFTGVFTFEMVIMDLGLLLHPCAYFRDLWN 1220
QY	1348	VLDGSLVLIISVIDILVSV-SDSGTKILGMRLVRLRLTLRLPLVIRSAQGLKLVETILM 1406
DB	1221	ILD-----FTWSGALVAFAFSGSGKDINTIKSLRVLRLVRLPKTIKSLPKLKAIVDCV 1276
QY	1407	SLKPIGNIWVICCAFFIIFGLVQLPKGKFEVCGE-----DTRN--ITNKSQDABA 1458
DB	1277	NSLKNVNLILVYMLFMFIFAVIAVOLFKGKFFCYCTDESKELERDCRGGLDYEEKVEEA 1336
QY	1459	SVR-WVRHKYNFDNLGQALMSLFLVASKDGWVDIMYDGLDVGVDQOQIMNHNPMMLLYF 1517
DB	1337	QPRQWKYDFHYDNLVWALLTLFTVSTGEGWPMVLKHSVDATYEEQGPSGPGYRMELSIY 1396
QY	1518	ISFLILIVAFVLMVGVVVVENFHKCRQHOBEERARRREKRLRLEKERRKA-----QC 1572
DB	1397	VVVFVVFPPFFVNFVALLIITF-----QEQDKVMSB-----CSLEKNERACIDFAISA 1446
QY	1573	KEY--YSDYSR--FRLLVHLLCTSHVLDLFTIGVLGNVTVWVMAHEHYQOQILDEAKIC 1628
DB	1447	KPLTRVMPQNRQSFOYKWTFTVVSPPFFIWMALNTVLMKMEYDAPYEVELMKCL 1506
QY	1629	NVIFTVIFVLESVKLIVAFGRFRFQDRWNQOLDLAIVLLSIMGITLERI-EVNASUPINP 1687
DB	1507	NIVFTSMFMECVCKLIAAGVLNYPFDMANVDFVTVLGSITDILVTEAETN-----NF 1561
QY	1688	TIIRNVRIRARVLKLLKNAVGMRLTLTVQALPQVGNLGLFLMLFFIAPALGVELF 1747
DB	1562	INLSFLRIFRAARLIKLRQGYTRILLWTVQSFKALPYVCLLIAMLFIIAILIQWVF 1621
QY	1748	GDLECDTEPCGELGHATFRNFGMAFLTLFRVSTGDNWNGIMKOTLRD--CDQE--STC 1803
DB	1622	GNIALDDD---TSINRHNFRFLQALMLLFRSATGEAHEIMLSCLSNQACDQANATE 1678

Qy	1034	SLLPPLIIHTAATPMSLP-----KSTSTGLGEALGPASR-----RTSSSG-----	1073
Db	812	HLDRPLVVELRGDARGCPVGKARPAAEAPEVDPPRRHHRDXDKTTPAAGDQDRAEA	871
Qy	1074	-----SAPPGA-----AHEMKSPSPARS-----SPH-----SPWSAASWS	1103
Db	872	PKAESGPGAREERPRHRSHKEAAGPPPEARSGKPGCGEGRHRHRRGSPPEEAARE	931
Qy	1104	TSR-RSRNSLGRAPSLKRSPSGERSLLSGGQSQDBEESSE-----ERASR-	1153
Db	932	PRRERARRH--QDPSEKACAGERRARRHGGFRAGPRAESGEGEPARRHRAHKAQPA	988
Qy	1154	-----AGSDHRHRGSLEREAKSFDLPDTLQVPLGHLRTASGRG	1191
Db	989	HEAVEKETTEKEATEKEAEIVADKEKELHNQPRPHCDLETSGVTVGPMTLSTCL	1048
Qy	1192	SASHQDNCNGKSASGLARLARDPP-----PLDGDADDEGNL-----SKGE	1234
Db	1049	QKVEEQPEDADNORNVTWMSQPPDPNTIIVHIFVMLTGPLGEATVVPNGVDLSEQAEG	1108
Qy	1235	R-----VRAMIRARLAPACVLERDSVAIFPPQSRFLLRHRIITHKDFHVLVITF	1287
Db	1109	KEVEADVMRSGPRPIVPS-----SMFLSGTNLRRFCHYIVTMRYFVVLIVVIA	1161
Qy	1288	LNCTIIAMERPKIDPHSAERIFLTLSNYIIFTAFLAEMTVKVALGWCGEQAYLSSWN	1347
Db	1162	LSSIALAAEDP-VRTDSPRNNAKYLDYITFGVTFEMVKIMIDGLLHPGAYFRDLWN	1220
Qy	1348	VLDGLLVLISVIDILVMV-SDSGTKILGMLRVLLRLTLPRLVRSRAQGLKLVVETLM	1406
Db	1221	ILD----FIVVSGALVAFASGSGKQDINTIKSLRVLRVLRLPKTKRGLPKLKAVDCCV	1276
Qy	1407	SSLKPIGNIVVICCAFFIIFGILGVQLFGKGFVQCGE-----DTRN-----ITNKSDCAEA	1458
Db	1277	NSLKNVNLILVYMLFMEIFAVIAVQLFKGFFCTDSEKELRDCRGQYLDYEKEVEHA	1336
Qy	1459	SYR-WVRHKYNFDLGOALMSLFLVLSKGDGVNDIMYDGLDAGVDQOPIMHNPWMLLYF	1517
Db	1337	QPRQWKKYDHYDYNVWALLTFTVSTGEGWPMVLKHSVDATYEBEQSPSPGYRMEISIFY	1396
Qy	1518	ISFLLIIVAFVILNMFVGVVFNPHKQHQCEEBEAREEKLRLRLEKKRKA-----QC	1572
Db	1397	VYVFWFVFFVFNIFVALIITF-----QBQDKVMSE-----CSLEKNERACIDFAISA	1446
Qy	1573	KPY--YSDYSR--FRLAVHHLCTSHYDLFTIGVILNVVTMAHEHYQQQPIIDLEALKIC	1628
Db	1447	KPLTRYMPQNPQSQYKWTWTFVSPPEYFIMAMALNTVVMKMFYDAFVEVELMKCL	1506
Qy	1629	NYITFTVFLVESVKLVAFGPRRRFPQRWNOLDIAIVLLSIMGITLBEI-EVNASLPINP	1687
Db	1507	NIVFTSMFSMECVLKIIAFGVLNFRDANWNFDFTVLGSIITDLVTEIAETN-----NF	1561
Qy	1688	TIIRIMRVLRARVILKILKMAVGRAILDTVMQALPOVGNLILLEMLLFTIFALGVLEF	1747
Db	1562	INLSFLRFRARLRLKLURQGYTRILLTWFVQSFKALPYVCLLIAMLFIFYALIGNQVF	1621
Qy	1748	GDLECDETHPCPEGLRHATFRNFGMAFUTLFRVSTGDNWNGIMKDTLIRD--CQOE--STC	1803
Db	1622	GNIALDDD--TSINRHNNTFLQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE	1678
Qy	1804	YNTVISPIYFVSFULTAQFVLNVNVIAM-----KHLEE-----	1838
Db	1679	CGSDFAFYFYVSFIFLCSFLMLNFVAVIMDNFYLTRDSSILGPHLHDEFIRWAEYDP	1738
Qy	1839	-----	1838
Db	1739	AACGRISYNDMEELKHMSPPLGLGKCKPARVAYKRLVRMNPISNEDMTVHTSTLMAL	1798
Qy	1839	-----SNKEAKEAEARLEAELEBKMTLSFQPHSPDGSEFFLWPGEVGDSPDSP	1886
Db	1799	IRTALEIKIAPAGTKHQCDALRKEISVWVANL-PORTDLDP-----PHKDEM	1849

Qy	1887	KPGALHPA-----AHARSASHFSLEHPTM-----QPHTEPLPGPD	1922
Db	1850	TVGKVAAALMIFDYKONKTTEDMOQAQGLSQMGVSLFHLPKATLEQTQPAVLRGAR	1909
Qy	1922	LLTVRKSGVGRTHSLPNDSTYMCRHGSTAEGPLGHRGWGLPKAOSGVSLSVHQSOPADTSYI	1981
Db	1910	VFLRQKSTSLSN-----GGAIQNESGIKESV-----SMG	1940
Qy	1982	LQLPKDAPHLLQP-----HSAPTWTGTPKLPPLPGRSPLAQRPLRROAIR-----TDS	2029
Db	1941	TQTQDAPHEARPELGRGHSTEI-----PVGRSGALAVDVQMOISITRERPDGEPQPG	1992
Qy	2030	LDVQGLSGREDLLAIFYSGP---SPPLARAYSFWGQSGTQAQHSRSHSKISKHMTDPAPC	2086
Db	1993	LESGRAASMPRLAAETQPTVDASPMKRSI-----STLAQRFGTHLCST---TPDRPP	2043
Qy	2087	PG-----PEPNWKGKPPETRSRSLDELTSLSIGSDLLPPGQOEPPSP	2129
Db	2044	PSQAASSHHHRRCHRRDRKQRSLEKGP---SLSDMDGAPSSAVGGLPPG---EGPTGC	2098
Qy	2130	RLDKKYSVFAQSCORR-PTSWLDQRRHSIAVSCLDGSG-----QPHLGTDPNS--LG	2180
Db	2099	RRERERQGRGSRQERRQPSSEKQRF---YSCDRFGGRPPKPKPSLUSHTSPSTAG	2155
Qy	2181	GOPLGGPGSRPKKLSPPSITIDPESQGRPTPPSP-----GIC	2219
Db	2156	QEP--GHPQAGSANGVFNTT--PCCRETSAAPWLALELALTLTWGSVMTVRPLSTPC	2211
Qy	2220	LRRRAPSDSKDPLASGPPDSMAASP	2245
Db	2212	LRTRSLSRLLWPPTRAAPPGGLTCTPP	2237
RESULT 5			
A45386			
omega-conotoxin-sensitive calcium channel alpha-1 subunit r1b-I - rat			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004			
C:Accession: A45386			
R:Dubel, S.J.; Starr, T.V.; Hell, J.; Ahljianian, M.K.; Enyeart, J.J.; Catterall			
Proc. Natl. Acad. Sci. U.S.A. 89, 5058-5062, 1992			
A>Title: Molecular cloning of the alpha-1 subunit of an omega-conotoxin-sensiti			
A:Reference number: A45386; MUID:92279265; PMID:1317580			
A:Accession: A45386			
A>Status: preliminary; not compared with conceptual translation			
A:Molecule type: nucleic acid			
A:Residues: 1-2336 <DUB>			
A:Cross-references: UNIPROT:O89089			
A:Experimental source: brain			
A>Note: sequence extracted from NCBI backbone (NCBIP:104355)			
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain			
Query Match			
Best Local Similarity 14.4%; Score 1711; DB 2; Length 2336;			
Matches 644; Conservative 365; Mismatches 810; Indels 860; Gaps 93;			
Qy	27	GAGGRPGGSAEKDPGSADSEAGELPYALAPVVF-----FYLQSQRSP	70
Db	25	GAGGAGGPGQGLPGQGRVLYKQSIQARFARTMALYNIPVKNQCFVTNRSLSLFVSEDNVV	84
Qy	71	RSWCLRTVCNPFERRISMLVILLNCVTLTGMFPCEDIACDSQRCKILLQAFDD---FIFAF	127
Db	85	RYAKRITETWEPFEMILLATIANCIUAL-----EQHLPGDKTFPMSERLDDTFYFIGI	140
Qy	128	FAVENVVRVVALG-IFGKKCYLGTNRRLDFFVIAGMLEYS---LDLQNVSFSAVTRVR	183
Db	141	FCFEAGIKIIALGFVFKHKS YLRGNWNVDFVWLTEILATAGTDFDLR-----TLRAVR	195
Qy	184	VLRLPRAINRVPSMEILLTLLDTPMLGNVLLLCFFVFETFGVGVQLWAGLLNRNCFLL	243
Db	196	VLRLPUKVSIFPSIQGVLUKSIWKAWVPLQLGLLFFAILMFAIIGLEFYMKFKHACF-	254
Qy	244	PENFLSPLSVLDERYQVTEDESPFICSPQRENGMRSRCSVPILRGDGGGPGCLGDYE	303

2110 LSWISGDLPPGQBEPPSPRDLKKCYSEVAQSCORRPTSMWDEQRHSHIAVSCLDGSG- 2168
2080 PSTAAGSGLPHG--EGSTGCRERKQGRSQE--RRPSSSSSEKQRF--YSCDRFGSR 2133
2169 -----QPHLGTP-----SNLGGQPL-----GGPGSRPKKLS 2196
2134 EPPQKPSLSHPSPTAALRPGHPQSGVNGSFLMSTGASTPGRRQLPQTPLT 2193
2197 P-PSITIDPPRS-----QGRTPP--SPG-----ICLRRAPSDSKDPASGPP 2238
2194 PRPSITYTANSSPVHRAEQGGLFAFSPGRSLRGLSEHNALLQKEPLS--QPLASGRS 2250
2239 -----DSMAASRSPKDVLSL-----SGLS 2259
2251 IGSDFYLGRLDSEASAHNLPEDTLTFBEAVATNSGRSS 2289

RESULT 6
S41080
calcium channel alpha-1 chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S41080
R:Coppola, T.; Waldmann, R.; Borsotto, M.; Heurteaux, C.; Romey, G.; Mattei, M.G.; Lazdu
REES Lett. 338, 1-5, 1994
A:Title: Molecular cloning of a murine N-type calcium channel alpha-1 subunit. Evidence
A:Reference number: S41080; PMID:94139884; PMID:8307146
A:Accession: S41080
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2288 <COP>
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.3%; Score 1706; DB 2; Length 2288;
Best Local Similarity 24.5%; Pred. No. 6.6e-96;
Matches 646; Conservative 363; Mismatches 802; Indels 828; Gaps 98;
27 GAGRPGGSAKDGSDSEAGLPYPALAPVVF-----FVLSQDSRP 70
25 GAGGAGGPGGGLPGQGVLYKQSIQAARTWALYNPIPVKQNCFTVNSLFFVESDNVV 84
71 RSWCLRTVCNPFERISMLVILLVTLGWFRPCEDIAQDSORCRILQAFDD---PIFAP 127
85 RYAKRITWPFEPFYMILATIANGVLAL---EQHLDGDKTTPMSERLDDTEPYFIGI 140
128 FAVEMVVMKVALG-IFGKCYLGDWNRLLDFFIVTAGMLEYS---LDLQNVSESAVRTVR 183
141 FCFEAGIKIILGFPVFKGSLRNGWVMDVFWVLGTILATAGTDFDLR-----TLRAVR 195
184 VLRLPAINRVPSMRILVILLDTLPMIGNVLLICFVFFIFGIVGVQWAGLLNRCEL 243
196 VLRLPLKLVSGIPLSVLKSIMKAMVPLQIGLLFFAILMFGIIGLEFYMGFHKACF- 254
244 PENFSLPLSVDLERYQYOTENEDBSPICSPRENGMRSCRVPTRLRGDGGGPPCGLDYE 303
255 -----PNSDTIE-----PV-----GDFPCGKDP 273
304 AYNSSENTTCVNNQVYTCSGAHEHNPFGKAINPDNIGYAWIAI FQVITLEGWVDIMYFV 363
274 ARQCDGTEC---REYWP-----GPNFGITNFDNILFAILTVPFQCITMEGWTDILYNT 323
364 MD-AHSFYNTFYIILAIIVGSEFMNLCVNIATOPSETKQES-----QLMREORVRF 416
324 NDAAGNTWNLWYFIPLIIIGSFPMNLVLJVLGSEFAKERVENRRAFLKLRQQOIE- 382
417 LSNASTLASFERGSCVEEILKYLIVTLRKAARLAQVSRAAGVRVGLLSPAPLGGQET 476
383 -----RELNGYLEWTFKAEVWMAEEDKNA-----EEK 410
477 QPSSCSRSRRRLSVHLLVHHHHHHHHHLLNGTLLAPRASPEIQDRDANGSRRLMLPP 536
411 SPLDVLKRAATKKSRNDLIH-----

537 PSTALSGAPPGCAESVHSFYHADCHLEPVRQAPPPRSPSEASGRTVGSKVPTVHTS 596
431 ----- 430
597 PPEPTLKEKALIVFAAAGSPPTLSLNTIPPGYPYSMHKLLETQSTGACQSSCKISSPCIK 656
431 -----AEEGEDRFVDL-----CAVGSPPAR 450
657 ADSGACGPDSPCYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRQSL 716
451 ASLXSGKTESYFR-----KEKMPF----- 473
717 GPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHHEPEELTNALE 776
474 -----FIRMVKAQSFYVVLVCVALNTLCVAMVHYNQFORLTTALY 515
777 ISNIVFTSLFALEMLLKLLVGPFGYIKNPYIPGVIVIVSVVMEIVGQ-----QGGGLS 831
516 FAEFVFLGLFLEMSLKNYGLPRSYFRSSFCDFGVIVGSIFEFVWAAIKPGTSFGIS 575
832 VLRTFLMRVLKVRFLPALORQLVLMKTMNDVNATFCMLLMFLFIIFSILGMHLFGCKF 891
576 VLRLRLRIKFIKVIYNSLRNLVSLNSMKSIISLFLFLFVIVFALLQWQLFGQGF 635
892 ASERDGDLPDRKPNFDSLLWAIIVTFQILTOEDMNKVLNGM-----ASTSSWAALYFTA 946
636 NFQDETPT---TIFDTPAALLTVFQILTGDMNAVVMYHGIESQGVSKGMFSFYFIV 691
947 LMTFQNYVFLNLLVAILVEGF-QAEISK---REDASQ-----LSCIQ 986
692 LTLFNGYTLNVLNLAIVDNLANAQELTKDEEMEEAANQKALOKAKEVAEVSMPMAAN 751
987 LPVDSQGGDANKSESEPPDFSPSLDGDGRKCLALVSLGE-----HPELRK 1033
752 ISIAAQNSA-KARSWEQRASQLNLNLRASCEALYSEMDPEERLYASTHRVREDMKT 810
1034 SLLPPLIIT-----TAATPMS-LPK-----STSTGLGEALGPASR 1067
811 HMDRLVIVPEGRDGLRGPVGSKPEGTEATESADLPRRHRHRDRDKTSATAPAGEQD 870
1068 RTSSSGS-----APGAAHENKSPS-----ARSSHPSPSAASSWTSR-----RSSR 1110
871 RTESTETGPREERAPRKRSHKETPGADQVRCESRRHRRGSPREATERPRCHRAHR 930
1111 NSL-----GRAPSLKERSPSGRRSLLSGE---GQESQDEESSESEERASPAGSDHRHG 1162
931 HAQDSKGETVPVL---VPKERRARHGRPTGPREAENNEBPTRRHRA-----RHK- 979
1163 SLEREAKSSFDLPDTLQVFLHRTASGRGSAHQDCNGKASGRILARALRDPDDPLD-- 1220
980 -----VPPTLQPP--ERAAEKESNPFVEGD-----KETRNHQPKPEHCDLE 1018
1221 -----GDDADDEGNLSK-----GE 1234
1019 AIAVTDVGPLHMLPSTCLOKVEQEDADNRQVNTVMGSPQSDPSTTVHVVTLTGPPGE 1078
1235 R-----VRWIRARLPACYLERDSWSAYIFPPQSRFRLLC 1269
1079 TPVVPNGNMLEQAGKKEAEADDVLRGPRFIVPYS-----SMFCLSPTNLPRRFC 1131
1270 HRIITHKMFHVVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNVIYFATVLAEMTVKV 1329
1132 HYIVIMRYLXEMVLVIVIALSSIALAAEDP--VRTDSPNNALETMDYIFTGVFCFVWIRM 1190
1330 VALGWCFCGEOAYLRSSWNVLGDLVLSVIDILVSMV-SDSGTKILGLMLRVLRLTLRP 1388
1191 IDLGLLHPGAYFRDLWNILD-----FIVSGALVAFAGSKGKDINTIKSLVLRVLRP 1246
1389 LRVISRAQGLKLVVETIMSLKPEIGNIVVICCAFFIIFGILVOLPKGKPFVCOQE----- 1444
1247 LKTIKRLPKLKPVFDVSNLSKNVLNIIIVMLFMFIFAVIAVLQFKGKFFYCTDESKE 1306

Qy	826	QCGGLSVLRTFLRMVLKLVRFELPALORQOLVLMKTMNVATFCMLMLFIPIFSLGMH	885
Db	564	TSFGISVLRALRLIRFKIKYKWSLRNIVVLSLMSSKGISULLFLLFVIFVFPALLGMO	623
Qy	886	LFGCKPASERDGTLPDRKNFDLGLLWAIIVTFQILTEQDWNKVLNGM-----ASTSSWA	940
Db	624	LFGGRF-NFNDG---TPSANFDIFPAIMIVFOILTGEDWNEMWYNGIRSQGVSSGMS	679
Qy	941	ALYFIALMTFGNYVLFNLLVAIVLEGF-QABEITSK-----REDASGQLSCIQLPVDISOGD	995
Db	680	AVYFIVLTLFGNTVLLNFVIAVDLNLANAQEITKDEQEEEAFFKHALQAKEV----	735
Qy	996	ANKSESPDPFSPSLDGDGRKKCLAL-----VSL	1025
Db	736	--SPMSAPNV--PSIEDRRRRHHMSWEPFSSHLRERRRRHHMSVWEQRTSQLRHHQM	791
Qy	1026	GEHPELAKSLLPPIIHTAATPM-----LPKSTGTGEGALGPASRTSS	1072
Db	792	SSQBALNKEEAPMNPPLNPLSPALNPLNAHPSLYRRPRPMB--GLALGLEKCEEBHVR	850
Qy	1073	GSAPFGAAHEMKSPPS-ARSSPHSPNSA-----ASSMT-----SRSS	1108
Db	851	GGSLKGLALDCQRSPLSLGRREP--PWLARPCGNCEPALOETAGETVTFEDRARHROS	908
Qy	1109	SRNSLGRAPSLKRSPSGERRSLLSGBQBSQDEEESSEERASPAGSDHRHGS-----	1163
Db	909	QRRSRHVRTEAKESSASRS-RSVQBSRLDEGASTEGER-----DHEARGSHGKE	961
Qy	1164	--LERAKSSFDPLDTLOVP-----GLHRTAS-----GRGSASEHODCNCKS	1203
Db	962	PTIHEERAAQRLRRTDSIMVPKSGSLAGGLDEAGTPLVLSPEBGVGEAKAAPTQEHADGSG	1021
Qy	1204	ASGRLL-----ARALR-----PDDPPL-----	1219
Db	1022	BPALLGHVQLDVGRAISOSEPLDSCTVATTDKVTTESTDVTVAIPDAEPLVDSTVVHGN	1081
Qy	1220	--DGD-----DADDEGNLSKGERVRAWIRARLPACYLERSDSWSAIFFPQSRFRL	1267
Db	1082	KTDGEASPFOBAEMKEABOETEKKKXERPASGKAMVPHS-----SMFIFSTSPIRR	1134
Qy	1268	LCHRIITHKMDHVVLVILFNCITIAMERKPIDPHSAERIFLTLNVIETAYFLAEMTV	1327
Db	1135	ACHYVNVNRYEMCILLVIAASSIALAAEDPLVLTNSERNRV-LRYFDYFVTGTFTEMVI	1193
Qy	1328	KVVALGWCFGQAYLRSWNVDLGLLILISVIDI-LVSMVSDSGTKILGMLRVLRLTL	1386
Db	1194	KXIDOGILIQDSYFRDLWNILDFVVVVGALVAFALANALGTNKGRIKTIKSLRVLRL	1253
Qy	1387	RPLRVISRAQGLKLVETLMSLKPIGNIVVICAPFIILGILQVLPKGFPPVC--QGE	1444
Db	1254	RPLKTIKRLPKLVAFDCVWTSLSKNVFNILIVYLFMFIFAVIAVQVLPKGFPPCYCTDSSK	1313
Qy	1445	DTNN-----ITNKSDCAEASVR-WVRHKYFNDLGQALMSLFLVASKGOWIMDIMGDL	1497
Db	1314	DTEKSCIGNYVDHEKXNKEVKGREKREFFHYDNIWALLTLFVSTGEGMPQVLOHSVD	1373
Qy	1498	AVGVDQQPTMHNHPMLLYFISFLLIIVAFFVLNPFVGVVVENFHKKRQHOEBEERREE	1557
Db	1374	VTEEDRGFSRNRMEMSIFVYVYVFPFPFVNFVFIALLIITF-----QEQDKXMEE	1426
Qy	1558	XELRLEKKRKA-----QCKPY--YSDYSR--FRLVHLHCLTSHYLDLFTGTGVLNVV	1608
Db	1427	---CSLEKNNERACIDFATSAKPLTYMPCNRHTQYRVVHVFPVSPSEYIIMAMALNTV	1483
Qy	1609	TMAMEHYQOQLDALKTCINYIFTVIFLBSVFKLVAFGRFRFQDQRNOLDIAIYLLS	1668
Db	1484	VLMKYSPACTYELALKVLYNTAFTWVFSLECVLKVIAFGFVNYFRDWNIFDFTIVGS	1543
Qy	1669	IMGITLEETEVNASLPINTIIRMRVLRIARVLKLVKQAVGMALLDTVMQALPQVGNL	1728
Db	1544	ITFIVLTDLSKLVNTTGFNMSFLKLFRA---ARLIKLRQGYTIRILLMTQSPKALPYV	1600

QY	1729	GLIFMLFFIFAALGVVLFGLDLECD--ETHPCGELGRHATPRNFGMAFLTLFRVSTGDMWN	1787
Db	1601	CLLIAMLFFIYALIGMVFGNIRLDRESH-----INRHNNFRSFFGSLMLLSRSATGEAWQ	1656
QY	1788	GIMKDTL--RDCLD-----QESTCYNTVISPIYFVSFVLTAQFVLNVNVIAMVKHL	1836
Db	1657	EIMLSCLGKGCBCBDTTAPGQQQBSERCGTDLAYIVFVSFFFCFSLMLNLFFVAVIMDNF	1716
QY	1837	EESNKEAK-----EEAELEAELE-----LEMKTLSPQPHSPGLSGPFLWPQ	1876
Db	1717	EYLTRDSSILGPHLHDFVRVWAEYDRAACGRHIVTEWYEMLTLM-----SPPLGLG	1768
QY	1877	VEGDPSPDSKPGALHAAHARSASHSLSLEHTPQPHTELPDGDLLTVKRSVGRTHSL	1936
Db	1769	KRCPSKVAYKRLVILNMNFEVADMTVHT--STLMALINTALD-----IKIAGGADROOL-	1821
QY	1937	PNSYMCRHGSTABEPLGHRGWGL-----PKAOSGVLVSHSQPADTSYI-----	1981
Db	1822	--DSELQKETIATWPHLSQKMLDLLVMPMKASDLTVGKIYAAMIMDYKQSKVKKQRRQ	1879
QY	1982	LQLPKADAP--HLLOPHSAP-----TWGTIPKLPP-----PGRSPLAQPLRRQ	2022
Db	1880	LEEQKNAPFMFORMEPSSLPOEIIANAKALPCLPQGPAGLGRSGCCPAMSPSLQIFQIT	1939
QY	2023	AAIRTD-----SLDVQGLGRESDDLAEVSGPSPPLARAYSPW-----QOSSTQ	2065
Db	1940	CMDPADDDGQEQORSRLVTTDPGMRRSFSTIRD-----KSSSSWLEEFSEWERSDNTY	1994
QY	2066	AQOHSRHS--KISKHMTTPAPCPGPEPNWKGPPETPRSSLELDTLSWISGDLPLPPGQ	2123
Db	1995	KSRRSYHSSLRLSAHL-----NSDSGHKSDTHRS-----GGR	2028
QY	2124	EEPPSPR-----DLKKCYVEA-----OSQRRPTSWLDEQRHRSIAVSLDGSQP	2170
Db	2029	ERGRSKEREHLSDADVRCSSSEERGAQADWDSPEHPSPSPSEGRSQS-----	2076
QY	2171	HLGTDPSNLGGQLPGGSRPKKLSPSIITDPES--QGPRTPSPGICLRRRAPSSD	2228
Db	2077	-----PSR-----QGTGSLSESIPIVSDTSTPHSRRLQPLPPVPPKRPLL--SYSSL	2122
QY	2229	SKDPLASGPP-----DSMAASPPSKDVLISGLSSDP	2261
Db	2123	KQPSNFPFPADGSGQGLLASPALESQVGLPSSSDSP	2161
RESULT 8			
T31092			
probable voltage-gated sodium channel - Aiptasia pallida			
C:Species: Aiptasia pallida			
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004			
C:Accession: T31092			
R:White, G.B.; Pfahnl, A.; Haddock, S.; Lamers, S.; Greenberg, R.M.; Anderson, P.A.V.			
Submitted to the EMBL Data Library, January 1998			
A:Description: Structure of a putative sodium channel from the sea anemone Aiptasia			
A:Reference number: Z20975			
A:Accession: T31092			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-1810 <WHI>			
A:Cross-references: UNIPROT:044930; EMBL:AF041851; NID:92791840; PID:92791841; PIDN:AAH			
C:Genetics:			
A:Gene: Nal			
C:Superfamily: sodium channel protein			
Query Match 14.2%; Score 1689; DB 2; Length 1810;			
Best Local Similarity 25.8%; Pred. No. 5.3e-95;			
Matches 520; Conservative 343; Mismatches 721; Indels 428; Gaps 65;			
QY	78	VGNPWERISMVILINCVTLMGFRPCEDIACDSQRCILQAFDDFI-F-AFFAEVWVVKM	136
Db	110	ITNQFEFFILLTIIVNCIFAL-----RDAPEQPEYVFAAIYTFEMLLKI	155

A;Cross-references: UNIPROT-Q02343; EMBL-X67856; NID:gl474; PIDN:CAA48041.1; PID:gl475
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein

Query Match 14.1%; Score 1681; DB 2; Length 2178;
Best Local Similarity 23.9%; Pred. No. 2.1e-94;
Matches 605; Conservative 366; Mismatches 811; Indels 752; Gaps 83;

Qy	28	AGGRPGSGSAKDPGSADEAEGLPYPALA-----PV-----	59
Db	8	AAGRPGSGSDGQ---RNLPGTPVPASGSAAYKQSAQARTMALYNIPYRQNCFT	64
Qy	60	---VFFYLSQDSRSPRSLRVCMFWPERISMVILLNCVTLGWR--PCEDIAQDSORC	114
Db	65	VNRSLETFGEDIYKVKAKLIDPPPPFYMLATLIANCIVLALEQHLPEDDKTPMSRR-	123
Qy	115	RILQAFDDIFAFFAVENVMVMVAIG-IFGKKCYLGDVTWNLDFEVIAGMLEXSLDQN	173
Db	124	--LEKTEFYFIFCFEAGIKIVALGFIFHGSLYLRNGMVMDFIVLWSGILATAGTFN	181
Qy	174	--VFSAVRTVRVRLPRAINRVSMRILVTLILLDTLPMLGNVLLLCFFVFFICIVGVQ	231
Db	182	THVDLRTLRAVRVRLPLVSGIPSLQIVLKSIMKAMVPLLQIGLLFFAILMFAIGLE	241
Qy	232	LWAGLLRNCFLPENFSLPLSVDLERYQYQTEDESPFICQPRENGMRSCRSVPTLRGD	291
Db	242	FYSGKLHRCACFVNNSGVL-----EGFDP-----PHPCGVQC-----	273
Qy	292	GGGGPCGLDYEAVNSSNTTCVNNQYVYTNCSAGEHPFKGAINFDNIGYAMIAIFOVI	351
Db	274	-----PAG--YE-----CKDW-----IGPDNGITQFDNILFAVLTVFCOI	306
Qy	352	TLEGWVDIMYFMDA-HSFYNYFIPIILLIIVSGFPMINCLIVIAIQSETQKRSQMLR	410
Db	307	TMEGVTTLVNTNDALGATMNLWYFIPIIIIGSFVFLNLVLGSLGEFAKERERV----	361
Qy	411	FORVFLNASFLASFSPGSCYEELLYVILKAARLLAQVRAAGVRVGLLSPPAP	470
Db	362	ENRRAPMK-----LRQOOI-----	376
Qy	471	LGQGETQPSSCSRSHRLSVHLLVHHHHHHHHLGNGTLRAPRASPEIQDRDANGER	530
Db	377	-----ERELNGYR	384
Qy	531	RLMLPPPTPALSGAPPGGAESVHSFYHADCHLEPVRQCAPPRSPSEASGRTVSGKYI	590
Db	385	AMI-----	387
Qy	591	PTVHTSPPTLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKILETOSTGACQSSCKI	650
Db	388	-----DKAEVMAEENKNSGTSALVLRRAIKRSRTTEAMTRDSDHCVDISSV	438
Qy	651	SSPCLKADSGAGDPSCPYCARAGAGEVBLADREMPDSDSEAYVEFTQAOHSDLRDPS	710
Db	439	GIPLARASIKSAKVDGASY-----FRHKE-----	462
Qy	711	RQRSIGPDAPSSVLAFWELICDTPRKIVDSKYFGRGIMIALIVNLSMGLIEHYRQPEE	770
Db	463	-----RLRISVRHAKVSQFYVWILSVLNTACVAIVHHNQPOW	503
Qy	771	LTNALBSINFTSLFALEMLKLLVYGPFGYIKNPYNIPDGVIVIVISVMEIVGQ-----	825
Db	504	LTHLLYAEFLFGLFLEMSLKMVGMPRLYFHSFNCDFDGVTVGSIFEVWVAIFRPG	563
Qy	826	QGGLSLVRLTRMLRVKLVRFLPALQROLVLMKTMNDVATPCMLLMFLIFPISILGMH	885
Db	564	TSFGISVLRALRLRIFKITYKVASLENVLSMSSMKSIISLLFLFLFVIVFALLGMQ	623
Qy	886	IFGCKFASERDGTLPDRKNFDSILWALIVTFOILLQEDMKNKYLNMG-----ASTSSWA	940
Db	624	LFGGRF--NFNDG---TFSANFDTPPAIMTVFQILTGEDNNEVWYNGIRSQGVSSGMWS	679
Qy	941	ALYPIALMTFGNYVFLNLLVAILVEGF-QAEELISK-----REDASGQLSC:QLPVD	995

Db	680	AVTIFVLTLCGNYTLLVFLAIAVDNLNAQELTKDEEEAPNOKHALQKAKEV-----	735
Qy	996	ANKSESEPDFSPSLDGDGDRKKCLAL-----VSL	1025
Db	736	--SPMSAPNV--PSIEDRRRRHHHSMWEPSSHLRERRRRHHHSMVWEQRTSQLRRHQM	791
Qy	1026	GEHPDLKSLPLPLIIHTAATPMS-----LPKSTGGLGALGPASRRRTSS	1072
Db	792	SSQALNKEEAPPNPLNPLNPLNPLNAHPSLYRRPRME--GLALGLEKCEEEHVSR	850
Qy	1073	GSAPGGAHEHMSPPS-ARSSPHSPWSA-----ASSWT-----SRSS	1108
Db	851	GGSLKGLADCCORSPLSLGRREP--PWLAPCHGNCPEALQTAGETVVTEDRARHQS	908
Qy	1109	SRNSIGRAPSLKRSPSGERSLLSGEQSDSEESSEERASPAAGSDHHRGS-----	1163
Db	909	QRRRHRRVTEAKESSASRS-RSVQERSLDEGASTEGER-----DHEARGSHGKE	961
Qy	1164	---LEREAKSSFDLPDLQVP-----GLHRTAS-----GRGSAHEQDCNGKS	1203
Db	962	PTIHEERAQDLRTDSLMVPKSGLAGLDEAGTPLVLSPEGVGKEAAPTQHADGSG	1021
Qy	1204	ASGRLL-----ARALR-----PDDPL-----	1219
Db	1022	EPALLGHVQLDVGRAISQSEPDLSCTATTDKVTTESTDVTVAIPDASPLVNDSTVVHGN	1081
Qy	1220	--DGD-----DADDEGNLSKGERVRAWRARLPACYLERSWSAYIPPPQSRPL	1267
Db	1082	KTDGEASFQBAEMKEAEQETEKQKKERPASGKAMVPHS-----SMFESTSNPIRR	1134
Qy	1268	LCHRIITHKMFHDVVVLIIFLNCITIAMERPKIDPHSAERIFLTISNIFTAVFLAEMTV	1327
Db	1135	ACHYVVNLRYPFEMCILLVIAASSIALAAEDPVLNTSERNRV-LRYEDYVFTGVTFEMVI	1193
Qy	1328	KVVALGWCFGEQAYLRSSNVLDGLLVLSVIDI-LVSMVSDSGTKILGMLRVLLRLT	1386
Db	1194	KMIDQGLIJDGYSYFRDLWNILDFFVVVGALVAFALANALGNTKGRDITKSLRVRL	1253
Qy	1387	RPLRVISAQGLKVVTETLMSLKPIGNIVTICCAFFIIFGILGVQLFKGFVC--QGE	1444
Db	1254	RLPKTIKRLPKLKAVIDCVVTSLKVNFLIIVYKLFMFIAVIAVQLFKGFYCTDSK	1313
Qy	1445	DTRN-----ITNSDCAEASYSR-WVRHKYNFDNIGQALMSLFVLASGKGDWIDMDGLD	1497
Db	1314	DTEKECIGNYVDHEKNMEVKREWKREHYDNIWALLTLFTVSTGSGWQVLQHSYD	1373
Qy	1498	AVGVDOQPMNHNPMMLLYFISFLIIVAFVLMVGVVVENFHKCRQHQEERARRRE	1557
Db	1374	VTEEDGRPSRNRMEMSIFYVYVVFVFFVFNIFVALIITF-----QSQGKMMEE	1426
Qy	1558	KRLRLKRRKA-----QCKEY--YSYSR--FRLLVHHLCTSHYLDLFTITVIGLVNV	1608
Db	1427	---CSLEKNERACIDFAISAKPLTRYMPQNRHTFQYRVWHFVVSFVETIMAMIALNTV	1483
Qy	1609	TMAMHYOQOILDEALKICNVIFTVIVLESVKLVAEPRFRFPQDRWNQDLALVILS	1668
Db	1484	VLMMKYSPACTVELALKYLNIAFTMVFSLECVLKVIAFGVNYFRDTWNIEDFITVIGS	1543
Qy	1669	INGITLEEVNASLPINFTIIRVLAIRVLAIRVLAIRVLAIRVLAIRVLAIRVLAIRVLA	1728
Db	1544	ITEIVLTDKLVNTTGFNMSFLKLFRA---ARLIKLRQGYTIRILLTFTVQSFKALPYV	1600
Qy	1729	GLILFMLLFFITFAALGVLEFGLDECD--ETHPECEGLGRHATFRNFGMAFLTLFRVSTGNNN	1787
Db	1601	CLLIAMLFYIALLIGVQVGNIRLDESH---INRHNFRSFFGSLMLLFRSATGEAWQ	1656
Qy	1788	GIMKOTL--RDCD-----QESTCYNTVTSPIYFVSFVLTAQVIAVNVVIAVLMKHL	1836
Db	1657	EIMLSCLGKGBCEPDTTAPSGQOQESERCCTDLAIVYFVSFIFPCSFMLNLFVAVINDNF	1716
Qy	1837	EESNKEAK-----EEAELEAELE-----LEMKTLSQPQHSPLGSPFIWPG	1876

Db 1717 EYLTRDSSILGPHLHDEFVRVWAEYDRAACGRHXYTEMVMTLM-----SPPLGLG 1768
QY 1877 VEGPDSPPSKPCALHPAAHARSASHESLHPTMQPHPTLPGLLTVRKSGVSRTHSL 1936
Db 1769 KRCPSKVAYKVLVMMMPVAEDMTVHFT--STLMALIRIALD-----IKIAGGADRQQL- 1821
QY 1937 PNDYVCMRHGSAEGLHGRMGL-----PKAQSGLSVLSVHSPADTSYI----- 1981
Db 1822 --DSELQKETTALWPHLQKQKLDLAVPMFKASDLTVGKIYAAMMIMDYKSKVKQKRRQ 1879
QY 1982 LQLPKDAP--HLQPHSAP-----TWGTHPKLP--PPGRSPLAQRLRRQAAIRTDSDLV 2032
Db 1880 LEEQKNAPWFORMPSSLPQBIANAKALPCLPQGPFA----- 1917
QY 2033 QGLASREDLLAEVSGPSPPLARAYFWGQSSTQAQCHSRSHSKHMTTPAP-----C 2086
Db 1918 -GLGRSGCPA-----MSPLSPQIFQUTC 1940
QY 2087 PGPEPNWKGPPETRSSLELDELTELISWISGDLPLPGQBEPPSPRDLKKCYVEAQSCORR 2146
Db 1941 MDPADDDQGF-QEQRSLVVD-----PGSMRFSFTIRD--KRS 1976
QY 2147 PTSMLDE-----QRHSIAVSC-----LDGSGPHLGTDPNGLGQPLGG 2186
Db 1977 SSSWLEEFMERSDNTYKSRSSYHSSRLSAHRLNDSGHK-----SDTHRSGRERG- 2031
QY 2187 PGSRPXKKLSPSITIDPESQG-----PRTPSPGICLRRAPSSDSKDPPLAS 2235
Db 2032 -RSKERHLLSADVSRCSERGAQWDSERHPSRSPSEG-----RSQSFSRQGTGLSE 2087
QY 2236 GPPDSMAASPPKK 2249
Db 2088 SSIPSVSDTSPRQ 2101

RESULT 10
C54972
voltage-dependent calcium channel alpha 1E - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Accession: C54972
R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil
J. Biol. Chem. 269, 22347-22357, 1994
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A;Reference number: A54972; MUID:94350992; PMID:8071363
A;Accession: C54972
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-2272 <MIL>
A;Cross-references: UNIPROT:Q61290; GB:L29346; NID:G522330; PIDN:AAA59206.1; PID:G522331
A;Note: authors translated the codon AGG for residue 788 as Lys, and CCT for residue 886
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.1%; Score 1681; DB 2; Length 2272;
Best Local Similarity 23.7%; Pred. No. 2,2e-94;
Matches 607; Conservative 375; Mismatches 844; Indels 740; Gaps 82;

QY 30 GRPGSGAEKDPGASDSEAEGLPYALAPVV----- 60
Db 11 GRPGSGDGSDD---QSRNQGTVPVSGPAAAYKQKAQARTMALYNPIPVQNCFVTN 67
QY 61 --FFYLSQDSRRPSWCLRTVCNPFWRISMLVILLNCVTIGMPF--PCEDIACDSORCI 116
Db 68 RSLDFIGEDNVRKYAKKLDWPPFYMILATIANCIVLAEQHLPEDDKTPMSRR--- 124
QY 117 LQAFDDFIFAFAVEMVVMWALG-IFGKKCYLGDTWNRLDFFVIAGLMEXSLDLQN-- 173
Db 125 LKTEPYFIGIFCFEAGIKIVALGFIHFHKGYSYLRNWNWMDFTVLSGLATAGTHFNTH 184
QY 174 VGSFAVRTVRLPLRAINRVSMRLTVLLDITLPMGLNVLLCFFVFFIFGIVGVQLW 233
Db 185 VDLRALRAVRVRLPLKIVSGIPSLQIVLKSIMKAMPVLLQIGLLLPFAIMFAIIGLEFY 244

QY 234 AGLLRNCFLPENFSLPLSVLRLRYQTENEDESPFIQSPRENGMRSCRSVPTLRGDGG 293
Db 245 SGKLHRCFMNMSGIL-----EGFDP-----PbPCGVQGC----- 274
QY 294 GPPCGGLDYEAYNSSNTTCVNNQYITNCAGEHNPFGKAINFDNIYAMTAITQVITL 353
Db 275 ---PAG--YE-----CKDW-----IGPNDGITQFDNILLFAVLTVFQCITM 309
QY 354 EGWVDIMYFVMDA-HSFYNFIYFILLITVGSFFMINLCLVVIATQFSTKQRESQLMREQ 412
Db 310 EGWTVLNTNDALGATWMLYFPLIIIGSFFVLNLVGLVSGEFKERV-----EN 364
QY 413 RVRLSNASTLASPEGSCYBELLYLILKAARLAQVSRAGRVVGLLSPAPLG 472
Db 365 RRAFMK-----LRRQQOI----- 377
QY 473 QGETQPSSSCSHRRLSVHHLVHHHHHHHHLNGTLPRAPRASPEIQDRDANGSRRL 532
Db 378 -----BRELVGYRAW 387
QY 533 MLPPPTPALSGAPPGAESVHSFYHADCHLEPVRQAPPSPSPSEASGRVTGSGKVYPT 592
Db 388 I----- 388
QY 593 VHTSPPETLKEKALVEVAASSGPPPTLTSNIPPGYSSMHKLETOSTGACQSSCKISS 652
Db 389 -----DKAEVMLAENKNSGTSALEVLRRATIKRSRTEAMTRDSDHCHVDISSVGT 441
QY 653 PCLKADSGACGPPSCPYCARAGAGEVELADREMPDSEAVYEFTQAOHQSHLDLRHRR 712
Db 442 PLARASTKSTKVDGASY-----FRHKE----- 463
QY 713 QRSIGPDABPSSVLAFWRLICDTRFKIVDSKYFGRGIMIAIIVNTLSMGLEYHQBELT 772
Db 464 -----RLLRISIRHMVKSOVFWIVLSVVALNTACVAIVHNNQPOWLT 506
QY 773 NALISNIVFTSLFALBMLKLIVYGPFGYIKNPYNIFOGVIVVISWEIVGQ-----QG 827
Db 507 HLLYYAEFLFLGLLEMSLMYMGPRLYFHSSFCNCFDGVTVGSIFVFWAIFRPGTS 566
QY 828 GGLSVLRTPRLMLVLRPLPALQOLVLMKTMNDVATFCLMLLFIIFISILGHMFL 887
Db 567 FGISVLRALRLKLFKITKWSLRNLVLSMSKMSIISLLFLFLFIYVFFALLGOLF 626
QY 888 GCKFASERDGTLPDRKNFDSLWAIIVTFQIITQEDWNKVLNGM-----ASTSSWAAL 942
Db 627 GGRF-NFNDG---TPSANFDTFPAIIMTVFQIITGEDWNEVMYNGIRSQGVSSGWSAI 682
QY 943 YFTALMTFGNYVLFNLLVAILVEGF-QAEISK-----REDASQLSCIQLPVDSQGGDAN 997
Db 683 YFIVLTIFGNITLLNVLAVDNLANAQELTKDEQEEBAFNQKHALQAKEV----- 736
QY 998 KSESEPDFFSPSLDGDGRKKCLAL-----VSLGE 1027
Db 737 SPMSAENM--PSIERDRRRHHMSWMEPRSSHLRERRRRHHMSVWEQRTSQRLEHHQMS 794
QY 1028 HPELRKSLPPIIHTAATPMS--LPKSTSTGL-----GEALGPA-----SRTSSS 1072
Db 795 QEALNKEEAPPNPLNPLNPLNAHPSLYRRPRPIEGLAGLGLGLEKCEEEERISRG 854
QY 1073 GSAAE-----PQAAHEMKSPPS-ARSSPHSPMSAASWTS----- 1105
Db 855 GSLKGDIGLTSALDNQSRSLSLGKREP--PMLPRSCHGNCDPDIOQAGGGETVTVFEDR 912
QY 1106 ---RBSRNSLGRAPSLKERSPSGERRSLLSGEGQESODEEESSEERASPDGHRHG 1162
Db 913 AHRQSQRARRHRRVRTEGOSASASRS-RSASQERSLDEGVSGVEKEHEPHSHRSKE 971
QY 1163 SLEREAKSFDL--PDTLQVP---GL-----HRTASGRGSAHEHQDCNGK 1202
Db 972 PTIHEERTQDLRRNTSLMVPRGSLGVGALDEATPLVQPOPELEVGVKDALTEGAEGS 1031
QY 1203 SAS-----GRLARALRPD-----DPPLD----- 1220

A;Cross-references: UNIPROT:O97017; EMBL:U64465; NID:g4204978; PID:g4204978; PIDN:AAD114
 C;Genetics:
 A;Gene: CACHL
 C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.0%; Score 1664.5; DB 2; Length 1891;
 Best Local Similarity 25.2%; Pred. No. 1.8e-93;
 Matches 486; Conservative 316; Mismatches 510; Indels 617; Gaps 55;

QY 11 EESQPSRSMRLND-----LSGAGRGPGSAEKDPSADSEAEGLPYP 54
 DB 2 EONGYPRANFTQSGSKIWPNGTDLMOFTEARLNGHGKVAKSAAKRQKKSGNTVR--PKR 59
 QY 55 ALAPVVFYLLSQDPRSRWCLRTVCNPW--FERISMLVILLNCVTLGMRFCEDIACDSQ 112
 DB 60 AL-----LCLSLGNPIRSAANLV--EMKPTDVMILITIFANCAALAAFEELPE--KDS 110
 QY 113 RCRILQAPDDFIF-AFFAEMVVMKVALG-IFGKKCYLGDTWNRDLDFIYIAG---MLE 166
 DB 111 BINONLEVAEYVFLAVFTNEAVLKIAYGFLEHPCAYLRNGWNILDFVIVVGLATILVK 170
 QY 167 YSLDLQNVFSFSAVTRVLRPLRAINRVPSMRILVTLTLLDPLMGNVILLCFVFFPIFG 226
 DB 171 ATLSSGSFDVKALRAFRVLRPLRLVSGVPSLQVWLSIKALIPLFHIALLVFVVIYA 230
 QY 227 IVGVOLWAGLLRNRCFLPENFSLPLVDLERYQYQTEDESPFICSQPRENGMRSCRVP 286
 DB 231 IIGVELFMGLHKTGY--DNVT-----GAESF-----EHPHCS----- 262
 QY 287 TLRGGGGGPGCLDYEAYNSSNTTCVNNQYTYNCAGENHPFKGAINFDNIYAMIA 346
 DB 263 -----SGSGGFQC-----DKAAGQV-----CEGWKGNPHGINTFNIGLACWT 301
 QY 347 IPQVITLEGVDMYFVMDA-HSFYNFIYFIILLIIVGSPFMNLCLVVIATOFSETKOR- 404
 DB 302 VFQCTILEGTVLVWINDAVGNSWPVYFVTLIIWGSFVLNLVLGSLGSFEFAKEKARR 361
 QY 405 -----ESQLMREGR-----VRFLSNASTLASSEPCSCYBEELLKYLIVILRKAAREL 451
 DB 362 QKSGBFQKREKQVEDAYNGYLDITQAEDELEGSESESGDES-----KASKKT 411
 QY 452 AQVSRAGVRVGLLSPAPLGGQETQPSSSCSRSHRLSVHHLVHHHHHHHHYHLGNCT 511
 DB 412 S--SRQS-----RTEDIEMDRNEHQDSI-----SQDTHY----- 441
 QY 512 LRAPRASPEIQDRDANGSRRLMPPSTPALSGAPPGAESVHSFYHADCHLEPVRCQAP 571
 DB 442 ----- 441
 QY 572 PPRSPSEASGRITVSGKVYPTVHTSPPTLKEKALVEVAASSGPPTLTSLNIPPGYSS 631
 DB 442 ----- 441
 QY 632 MHKLELTQSTGACQSSCKISSPCLKADSGACGDCPCYCARAGAGEVELADREMPDSE 691
 DB 442 -----GWCHNEKV----- 450
 QY 692 AVYEFTQDQSHDLRPHSRQRSLGPDAPSSVLAFWRLLICDTFRKIVDSKYFGRGIMI 751
 DB 451 -----LKKWHRRQTEL-----RAVKTQAFYWIVIV 477
 QY 752 AILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKPNYNI 811
 DB 478 VVFNLSLTALEHYDQDWLTUKFLDKLANKFLGFIETIEMVVMYCLGFGHYFASLNRFD 537
 QY 812 GVTVW-----ISVMEIVGQGGGLSVLRTFLMRVLKLVRLPALQQLVVLAKMTDNVA 866
 DB 538 CIVVISLLELAITEALKQPIGIVLCIRILLRIFKVTYWSGLNSLNASLLNSMERIA 597
 QY 867 TFCMLMLFIIFISILGMHIFGCKFASERGDITLPDRKNFDSLLMAITVTFQILTOEDWN 926
 DB 598 GLLLLSLFLMLICLLGQVFGGKF--NTDDEIP-RSNFDSFWRALITVFQILUTGEDWN 654

QY 927 KVLNGMAS-----TSSWAALYFIATMTFGNVVLNLLVAILVEGF-----QAE 971
 DB 655 AVMYDGIWAGGIGEGGSAIALLYFIFLVVGNYILLNVLAVDAENLTEMEE 714
 QY 972 ISKREDASQSLSCIQL--PYDSQGDANKSESEPDPSLDGDRKKCLALVSLGHP 1029
 DB 715 KKKKEKAREKALKMGKSDSQ-----RIDQG----- 744
 QY 1030 ELRSLPLPLIITAA--TPMSLPKSTSTGLGEALGPASRRTSSSGSABGAHEMKSPP 1087
 DB 745 ----AIVPN--HSSASRSNVLDKST-----QELHSTGT----- 772
 QY 1088 SARSPSPHSAASWTSSRSRNLGRAPSLKRRSPSGRRSLISGEG--QESQDEEE 1144
 DB 773 -----LNGNGVARTASHDDVE 788
 QY 1145 SSEERASPAGSDHHRGSLEREAKSFDPLDTLQVPLGHRHTASGRGSAHQDCNGKSA 1204
 DB 789 AQSTDISEIVGS-----KSAVSNNESASASS 815
 QY 1205 SGRLARLRPDPPPLDGGDDADDEGNLSKGERVRAMIRARLPACYLERDSWAGYIPPOSR 1264
 DB 816 SDDIDRAPMPESAL-----FIPSPNTI 838
 QY 1265 FRLLCHRIITHKMFHDHVVLIIFLNCIITIAMERPKIDPHSAERIEFLTILSNYIFTAVELAE 1324
 DB 839 FRVVCYKIATNTYFVNFILICLIIVSSILLAAEDP--LNASAKRNQVNLVDFYFTSVFTPE 897
 QY 1325 MTVKVVALGWCFGEQAYLRSSNVLGGLLVISVIDILVSMVSDSGTKILGMLRVLRLR 1384
 DB 898 ILVKFISYGLILHKGSCFRSAFNLLDLVSVSVISLSR-----TSQFSVVRILVLR 951
 QY 1385 TLRLPLRVISRAQGLKLVVETILMSLKIPIGNIVVICCAFFIIFGILGVQLFKGKFFVQGE 1444
 DB 952 VLRLPLRAINRAKGLKHVVQSVFVAVKTIQNIKLVMTLQFLPAVIGVOLFKGTFSCNDE 1011
 QY 1445 DFRNITNKSDCABASY-----RWVRKYNFNPLCGALMSLVLASKQGM 1488
 DB 1012 ---KILTABEC--QGNVYIDFKGFLSNPVVYKEREWRHDFNFONVGNAMJTLFTVMFEGW 1067
 QY 1489 VDIMYDGDVAGVDOQPTMNNHPMLLYFISPLLIIVAFVLMFVGVVVVVENFHKCRHOE 1548
 DB 1068 PGLIENSIDSTBVDKGPONNRPWAIYIYIIIIIAFPMVNI FGVFVIVT----- 1119
 QY 1549 EBEARRREERLRLEKKERKA-----QCKPY--YSDYSRFRLLVHLCTSHYDLFLNG 1601
 DB 1120 --QSEGREBFKCELDKNORQCTEFALKAKPLKRYIPENRLOFHWPVVTSSQAFYLIFA 1177
 QY 1602 VIGLVVTVAMEHYQCPQLIDALKICNVIFTVFLSVFKIVAFGFRFFFDORWNQD 1661
 DB 1178 FIVCVTVLMQYQEPKLYTRVLDGFGNIGFTAVFILLICILKLIKAFKPNYFTDRNLF 1237
 QY 1662 LAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKILKMAVGMRLALDTVM-- 1719
 DB 1238 FIIVGSIIDITWNEVSSQMFAG-----FFRLFEALRVLLKLNQSGSIGKTLTWTFIKS 1292
 QY 1720 -QALPQVGNLGLLMLLFFIIFALGVVELFGDLECDETHCEGLGRHATFRNFGMAETLF 1778
 DB 1293 FQALPV--ALLIVMFFIYAVIGMQEGRIAINSD--TAINRNNNTQTFFQSLMVLV 1346
 QY 1779 RVSTGNWNGIM-KDILRD---CDQE-----STCVNTVISPITYFVSFVLTAQFVLNVV 1828
 DB 1347 RSATGNGWQIIMLACTHRDDVKDONADPQPSGLCGSDFAFYFVSFVSCISFLINLF 1406
 QY 1829 IAVLMKHLE 1837
 DB 1407 VAVIMDNFD 1415

RESULT 13
 B54972
 voltage-dependent calcium channel alpha 1E-1 - human
 C;Species: Homo sapiens (man)

C>Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
C/Accession: B54972
R/Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil
J. Biol. Chem. 269, 22347-22357, 1994
A/Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A/Reference number: A54972; MUID:94350992; PMID:8071363
A/Accession: B54972
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-2251 <WTL>
A/Cross-references: GB:L29384; NID:g495867; PIDN:AAA59204.1; PID:g495868
C/Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.0%; Score 1663.5; DB 2; Length 2251;
Best Local Similarity 24.2%; Pred. No. 2.6e-93;
Matches 617; Conservative 383; Mismatches 815; Indels 735; Gaps 89;

QY 31 RPPGSAKDPGSADSEAEGLPYPALA-----PV----- 59
DB 11 RPSGGDGDSD---QSRNRQGFVFPASGQAAYKQTKAQRATMALYNPIVRQNCFTVNR 67
QY 60 VFFYLSQDSRPSCLRTVCNMPERISMLVILLNCVTLGMFR--PCEDIACDQRCKIL 117
DB 68 SLFIFGEDNIVRKAKLIDWPPPEYMLATIIANCIVLALEQHLPEDDKTPMSRR--L 124
QY 118 QAFDDFIPAFPAFVEMVVMVALG-IFGKKCYLGDITWNRDLDFIAGMLEYSLDQN--V 174
DB 125 EKTEPYFIFGFCPEAGIKIVALGFIFHKGSLRNGVMVDIVLGSILATAGTHFNTHV 184
QY 175 SPSAVRVRVLRPLRAINRPSMRILVLLDTPMLGNVLLCFFVFFIGVIGVQLWA 234
DB 185 DLRTLRVLRVLRPLKVGSPISQIVLKSIMKAMVPLLIQILLLFFAILMFAIIGLEFYS 244
QY 235 GLLRNRCFLPENFSLPLSVLDLERYIYOTENEDESFFICSPRENGWRSCRSVPTLRGGG 294
DB 245 GKLHRACFMNSGIL-----EGFDP-----PHPGCVQGC----- 273
QY 295 GPFCGLDYENYSSNTTCVNMNQYTNCSAGEHNPKGAINFDNIGYAMIAIIFOVITL 354
DB 274 --PAG--YE-----CKDW-----IGPNDGITQFDNIIIFAVLTVFQCITME 309
QY 355 GWWDIMYFVMDA-HSFVNFYIFILLIIVGFFMINCLVIAVIAQFSKTORES-----Q 407
DB 310 GWTTVYNTNDALGATWNWLYFIPIIIGSFVNLVGLVSGEFAKERERVENRRAFMK 369
QY 408 LMREQRVRLSNASTLASPEPCGYEELLYVILKARLQAQVSRAGVRLGSS 467
DB 370 LRQQQIE-----RELNGYRAWIDKAEVMLAENKNAG----- 403
QY 468 PAPLGGQETQPSSCSRSHRRLSVHHLVHHHHHHHHLGNGTLRAPASPIQORDAN 527
DB 404 -----TSALEVLRRATI-----KSRTEAMTRDS- 427
QY 528 GSRRLMLPPSPITPALSAPPGGAESVHSFHADCHLEPVRCAQPPRSPSEASGRVTGSG 587
DB 428 -----SDEH----- 431
QY 588 KVPYVHTSPPTLKEKALVEAASSGPPTLTLNLIPCPYSSMHKLJSTQSTGACQSS 647
DB 432 -----CVDI 435
QY 648 CKISSPLKADGACGPDSPCYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRD 707
DB 436 SSVGTPLARASIKSAKVDGVS-----FRHKE----- 462
QY 708 PHSRQRSLGPDAPSPSVLAFRLICDTPRKIVDSKYFGRGIMAILVNTLSMGIEYHQ 767
DB 463 -----RLLRISIRHMVKSQVFWIWLVALNTACVAIVHNNQ 500
QY 768 PBEELNALSINIVFTSLFALEMLLKLIVYGPYIKNPYINFDGVIIVISWEIVGQ-- 825
DB 501 PQWLTHLLYABFLGLFLEMLSLKQVGMGRPLVPHSSFNCFDFGVTVGSIPEVWMAIF 560

QY 826 ---QGGGIVLRTFLMRVLKLVRLPALQROLVVMKTMQNVATFCMLLMFIPIFSTL 882
DB 561 RPTGTSVLRALRLRIFIKITKWSLRNLVSLMSSMKSIISLLFLFLFVIFVALL 620
QY 883 GMHLFGCKFASERGCDTLPDRKNPDSLWAVTVFQIILTQDWNKVLNMG-----ASTS 937
DB 621 GMQLFGGRF-NFNDG---TPSANFDTPAALIMTVQIILTGEDWNEVMYNGRSQGVSG 676
QY 938 SWAALYFIALMTFGNYLVFLNLLVAILVEGF-QAEISK---REDASQLSCIQLPVDSQ 992
DB 677 MWSAIYFIVTLFGNYTLNVLFAIVDNLANAQELTKDEQEEAEAFNQKALQXAEV- 735
QY 993 GGDANKSESEPDFFSPSLDGDGRKKCLAL-----VSLGEHPERLK----- 1033
DB 736 -----SPMSAPNM--PSIERERRRHMSVWEQRTSQLRKHQMWSQSQALNREAPTWP 788
QY 1034 -----SLPLLIHTAATPMSLPKSTSTGLGALGPA-----SRTSSSGS-----AE 1076
DB 789 LNPLNPLSSLNPLNAHP-----SLYRPRRAIEGLALGIALEKFEERISRGSLKGDGD 843
QY 1077 PGAAHEMKSPSARSSPHSPMSA-----ASSWTSRASSR 1110
DB 844 RSSALDQRTPLSLGQREPPWLARPCHGNCDPDQOEAGGCEAVVTFEDRARHRSQRRS 903
QY 1111 NSLGR-----APSLKRRSPSGERRSL--LSGQEBSQD-----BEESSEERASPA 1155
DB 904 HRRVTEKSSASRSASQERSLDEAMPTEGKDHELGRGNHGAKEPTIOEERA--- 959
QY 1156 SDHRHRSGLEREAKSSF-----DLPTLTQVCLHETASGRGSASHODCNKXAS- 1205
DB 960 QDLRTNLSLMVSRGSLAGLDDEADTPLVPHPELE---VGKHVVLTEQEPGSSQOALL 1016
QY 1206 -----GRLARALRPD-----DPLLDG----- 1221
DB 1017 GNVQDMGRVISQSEPDLSCTITANTDKATTESTSVTVVAIPDVPLVDSTVHISNKTG 1076
QY 1222 -----DDADDEGNLSKGERVRAWIRARLPACYLBERDSWSAVIFPQSRFLLCH 1270
DB 1077 ASPLKRAETREDEEVEKKQKKEK-RETGKANVPHS-----SMFIFSTNPIRRACH 1128
QY 1271 RIITHRMFDHVIIVIFLNCITIAMERPDKIDPHSAERIFLTLSNYLFTAVFLAEMTVKV 1330
DB 1129 YIVNLYFENCILLIVIAASIALAADPVLNTERNKV-LRYDYVFTGVTFTFEMVKMI 1187
QY 1331 ALGWCFEQAYLRSSNNVLDGLLVLSVIDI-LVSMVSDSGTKILGMLRLRLTLRPL 1389
DB 1188 DQGLIILQDGSYFRDLWNILDFVVGALVAFALANALGINKGRDIKTIKSLRVLRLRPL 1247
QY 1390 RVISRAQGLKLVVETLMSLSKPIGNIVITCCAFFIIFGILGVQLFKGKFFVC--QGEDTR 1447
DB 1248 KTIKRLPKLKAQVPCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFFYCTDSSK 1307
QY 1448 N-----ITNKSDCAEASVR-WVRHKYNFDNLGOALMSLFLVASKDGVMDIMVDGLD 1500
DB 1308 KECIGNYVDHEKNKMEVKGREWKREHFYDNIILWALLTLFTVSTGEGWFPQVILQHSVD 1367
QY 1501 VQOQPMNHNPMWLYFISFLILVAFVLMFVGVVNFHRCRQHQEHEEARRREKRL 1560
DB 1368 EDGFSRSNRMEMSIFVYVYVFFVFVFFVFIIVALLIITF-----QEQDKMEE- 1417
QY 1561 RLEKKRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYDLFITGVIGLNVVTWA 1611
DB 1418 CSEKNERACIDFAISAKPLTRYMPQNRHTFYRVYVHVFVVSFEYTIMATIALNTVLM 1477
QY 1612 MEHYQOQILDEALKICNYIFTVIFVLSVFLKVAQFRRPFQDRNQDLDAIVLLSIMG 1671
DB 1478 MKYISAPCTYELALKYLNIAFTMVFSLCEVLVIAPGFLNYPFRDTWNIFDFITVIGS 1537
QY 1672 ITLEIEVNASLPIINPTIIRIMRVLRIARVLKLLKMAVGMALDITVMQALPQVGNLGL 1731
DB 1538 IILTDSKLVNTSGFNMSFLKLFRA---ARLLKLFQGYTIRILLWTFVQSFKALPYVCL 1594
QY 1732 PMLFFPIAALGVLELFGDLECD-ETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIM 1790

Db 1595 IAMLFYAIAGVQFNKIDBESH-----INRNNERSFFGSLMLFRGATGAWOEIM 1650
Qy 1791 KDTL--RDCQESTC-----YNTVISPIYFVSFLTAQFVLVNVVIAVIMKHLBES 1839
Db 1651 LSCGEGCEPDTTAPSQONENECGTDLAVYVIFVSIFFCFLMLNLFAVIMDNFEYL 1710
Qy 1840 NKEAK-----EEAELEABLE-----LEMKTLSPQPHSLGSPFLWPGVEG 1879
Db 1711 TRDSSLILGPHLDEFVRVWAEYDRAACGRIHYTEMYEMITLM-----SPPLGLGKRC 1762
Qy 1880 PDSFDSKPGALHAAHARSASHPSLEHTWQPHTELPAGPDLLTVRKSGVSRTHSLPND 1939
Db 1763 PSKVAIKELVLMNMFVADMTVHTF--STLMALIRTALD-----IKIAGGADRQOL---D 1813
Qy 1940 SYMCRHGSTARGLCHRGWGL-----PKAQSGSVLSVHSQPADTSYI-----LQL 1984
Db 1814 SELQKETILAIWPHLSQKMLDLLVPMFKASDLTVGKIYAAMIMDYKQSKVKKQOQLEE 1873
Qy 1985 PKDAP--HLLOPHSAP-----TWGTIPKLP-----PCRSPLAQRPPLRQAAI 2025
Db 1874 QKNAPMFQRMPEPSSLQPIIANKALPYLQDPVSLGSRGYPGMSPLSPQDIPQLACM 1933
Qy 2026 RTDSLIVQGLSREDLLAEVSGSPPLARAYS-----FWQGSSTOQAQHSR 2071
Db 1934 --DPADGQFOFQKSLV--VTDPS--SMRSGFTIRDKSNSWLEEFMSRSENTRYKSR 1988
Qy 2072 SHSKISKHMTPPAPCPGPEPNWKGPPETRSLELDT--ELSWISG---DLIPPGQREPP 2127
Db 1989 RRS-----YHSSLRLSAHRLNDSGHKSDTHPSGGRRERR 2023
Qy 2128 SP-----DLKKCVSAQCORRPTSWLDEQRHSTAVSLDSSGSPHGLTDPNSLG 2180
Db 2024 SKERKHLSPDVSRCNSEB-----RGTOADWESPERRQSRSPS--SGRSQ-----TPNR-- 2070
Qy 2181 GQPLGSGSRPKKLSPPSITIDPPES--QGRTTSPGICLR-----RRAPS----- 2226
Db 2071 ----QGTGSLSSSPSVSDTSTPRSRRLQEPVPPKRPILLSLIRHAGSISPPADG 2126
Qy 2227 SDSKDPPLASCPDMSAA-----SPSPKK 2249
Db 2127 SEEGSPLTQALSNNAWLTSSNSPHQ 2156

RESULT 14
A47447
calcium channel protein alpha-1 chain (variant doe-1) - electric ray (Discopyge ommata)
C:Species: Discopyge ommata
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47447
R:Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; T sien, R.W.; Schwarz, T.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993
A:Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray Discopyge
A:Reference number: A47447; PMID:93248175; PMID:7683405
A:Accession: A47447
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2223 <HOR>
A:Cross-references: UNIPROT:P56699
A>Note: sequence extracted from NCBI backbone (NCBI:P130671)
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.98; Score 1656; DB 2; Length 2223;
Best local similarity 24.28; Pred. No. 7.3e-93;
Matches 595; Conservative 385; Mismatches 811; Indels 668; Gaps 89;
Qy 35 GSAEKDPSGADSAEGLPYDAL---APV-----VFFYLSQDSRPSRWCLRTVCNPW 82
Db 44 GAQAGSGFGKQTAQARTWALYNPIPVHNCITANRSLFLGEDNIVKRSARVIEWPP 103
Qy 83 FERISMLVILNCVTLMGFR--PCEDIACDSQRCLIQARDFDFAFAFVAVMVMVALG 140
Db 104 FEYMILATITANCVLALQHLNGD---KTPAKSLQETPYPIGIFCFEAGIKIVALG 160

Qy 141 -IFGKKCYLGDWTNRLLDFFIVIAAGMLEYSLDLQNVFSASVTRVVRVLRPLAIRNRPVPMRI 199
Db 161 FVHKSGYSLNGWNVDMDFIVLSGLL--ATAATHENLRTLRVAVLRPLKIVSGIPSLQI 218
Qy 200 LVTLLLTPLMGLNVLCCFFVFPFIVGVQLWAGLLRNRCFLPENFSLPLSDVLEERY 259
Db 219 VLKSIKAMVPLQIGLLFFAILMFAIIGLEFYTGKLRHTCYTDDAAAEELDIQF----- 274
Qy 260 QTENEDESPFCSPRENGMESCVRFLTRGDGGGPPCGLDYEAYNSSNTTTCVNNQY 319
Db 275 -----PCGTQETRLCPNGTVCYSW--- 294
Qy 320 YTNCSAGEHNPFGKAINFDNIGYAMIAIFQVITLLEGWVDIMYFVMDA--HSYFNFIYFILL 378
Db 295 -----IGNDGIGTQDNILFALLITVFOCITMEGWTTILYNTDDALGAMWNMLYFIPL 346
Qy 379 IIVGSPMINICLVVIATQFSETQORBS-----OLMREORVRLSNASTLASFEPCGC 432
Db 347 IIGSFFVLNLVGLSGEFAKERERVENRRSFJKLRKQOQIE----- 389
Qy 433 YEEILKYLVLTRKAARLAQVRAAGVRVGLLSAPLGGQETQPSSSCSRSHRRLSVH 492
Db 390 -RELNGYRAMIDKAEVWMLLEENKNAEKSAI----- 420
Qy 493 HLVHHHHHHHHHHLNGTTLRAPRASPEIODRDANGSRRLMLPPSTPALSGAPPGAES 552
Db 421 -----HVLRRATIKKGR----- 432
Qy 553 VHSFYHADCHLEPVRCQAPPRSPSEASGRIVGSKVYTVHTSPPTLKEKALVEVAA 612
Db 433 -----MEMIQTES----- 450
Qy 613 SSGPPTLSLNIPTPGYPMHKLLETQSTGACQSSCKISSPCLKADGACGDCPDPCYCAR 672
Db 451 VGSPLARASI-----KSTYKLEGS----- 470
Qy 673 AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRPHRRRQSLGDBAPSSVLAFWRLI 732
Db 471 -----YFRKKE-----RML 479
Qy 733 CDTFRKIYVDSYFGRGIMAILVNTLSMGIEYHEOPELTNALEISNIVFTSLFALEMLL 792
Db 480 RISIRHWKSHAFYIVLGLVALNVCVAVHVALQPLMLSNFLYFAETFFLGLFSEMEFL 539
Qy 793 KLLVYGPFGYIKNPYNIEDGVIVLSVMEIV-----GQGGGLSVLRTFRLMRVLRVLP 847
Db 540 KMYGCGPRLYFHSSFNCFDCGVIGSIPDVVWTLIRPETSFGISVLRLRLRIFKITKY 599
Qy 848 LPALQRLVYLMKTMNVATPCMLMLFTIFISILGMHLFGCKFASERDGLTLPDRKND 907
Db 600 WASLRNLVSVLSSMKSIISLLFLFLFVIFVALLGMQLFGGQNFEE--GTTP--TNFD 655
Qy 908 SLLWALIVTVFOILTQEDWKNVLYNGAS-----TSSWAALYFIALMTFGNYVFLNLLVAI 962
Db 656 TFPAAIITVFOILTGEDWNEVMYNGIKSGGVNSGMWSSVYFVILFLFGNYTLLNVLAI 715
Qy 963 LVEGF-QABEISK-----REDASQLSCIQ-----LPVDSQGGDANKSE----- 1000
Db 716 AVUNLANAQELTKEEQQEEBENQHALQKAEVSPMSAPGPPSTREFFRRHKHMSIWEA 775
Qy 1001 -----SEDPFFPSLDG-DGDRKK-----CLALVSLGEHPELRKSLPL 1039
Db 776 RTSQLRRRMQSSREALFTDALQLEGSRYYRHRIRFEABSURRLAEQQAESHQJGEV 835
Qy 1040 IITHAATPMSLPKSTGTGLGEALGPASRRTS-----SSGSAEPGAAHMKPSPA 1089
Db 836 GRREAFKSRLENS-----WQAPGPKRSSSIKVNQEGQFALGRSVEAGASPRMABPIRA 890
Qy 1090 RSSPHSPFW-----SAASWTSSRRSSNLSGR-APSLKRRSPSG---ERRSLLSGEQ 1137
Db 891 RRRYSLSYKEAKGLEESAEISLRRPGKNKEGRLQLQCESESQOLTQTPFVMDAQGG 950

QY	1138	ES-----QDEESESBERASPAGSDHRHRSLERE-----AKSSFDLPD-----	1178
Db	951	MKAFSWQGEPHSSMTRTPDVTD-PSGCLNEKESGRTPENGKEESANTSEQVNEQSNWL	1009
QY	1177	TLQV-----PGLHRTASGGSASEHQ-----DCNGKSASGRLARALURDPDDPLD--	1220
Db	1010	NLOLQOQATPGDRELTGTTRDTKQDKOQTEQTEIDVDCEN-----TETPMDSL	1056
QY	1221	---GDDADDEGLSKGERVRAWIRARLPACYLERDSWASYIFPPQSRFRLLCHRIITHKM	1277
Db	1057	VTPGNAYSSSSVKEDEKKS---XALIPYT-----SMFLRKTNPIRVCHFIWNLRY	1106
QY	1278	FHVVLVLIIFNCITIAMERPKIDPHSAERIFLTLSNYIETAFVLAEMTVKVVALGWCFG	1337
Db	1107	FMCIILLVIAASSVALAAEDP-IHKDSARNQVRYFDYVFTGVFTPEWVKMIDIGLVFH	1165
QY	1338	EQAYLRSSNNVLDGLLVLSVIDI-LYSWSDSGTKILGMLRVLLRLLTURLTURPURVSRQA	1396
Db	1166	EGSYFEDVNNILDFIVVSGALVAFAPNLIGSSGKDINTIKSLRVLRVLRPLKTKRLP	1225
QY	1397	GLKLVETLMSLKPIGNIVVICCAFFIIFGILGVOLFKGKFFVCGEDTRNTKSDCA	1456
Db	1226	KLKAVEDCVTSLKNVENILIVYKLFMFIFAVIAVQLFKGKFFYC--TSSKMT-KQDC-	1281
QY	1457	EASYRWVRHK-----YNFNLGOALMSLFVLASKDGWMDIMYDGLDAGVDQO	1504
Db	1282	RQGFVLYRQRTKLSIENGNTVTFHYDNVNWALLTLFTVSTGEGWPQVLQHSVDVTEADQ	1341
QY	1505	PIMHNHPMLLYFETSELLIAFFVLNVFVGVVENFHKCRHOEBEABRRREKRLRLE	1564
Db	1342	PIPGNRMEGSFYIVFVFPFFPNVIFALIIITF-----QEOGDWLEES---SLE	1391
QY	1565	KRRRKA-----QCKPY--YSDYSR--PRLLVHLCTSHVLDLFTICVIGLVNVVTWMBHY	1615
Db	1392	KNERACIDFAISAKPLRYMPQNRQTPQYVWQFVPSFSEFYITLTMIALNTVVLMMKH	1451
QY	1616	QOQOILDEALKNYITFVIVFVLESVKLVAFGRFPQDRNQDLDAIVLLSIMGITLE	1675
Db	1452	SPPPGFASVLKMLNIAFTITFTLECIKIIAFGLNVFRDSMNWDFVTVVGSISEIIVT	1511
QY	1676	EIE---VNASIPINPTIIRTMVLRITARVLRKLKMAVGMRALDVTMQALPOVGNLGLLF	1732
Db	1512	ECNLKFNLIS-----FLKLFRAIRLIKLRQGITIRILLWTFFVQSFKALPYVCLLI	1562
QY	1733	MLJFFIFAAJGVELFGDCEDETHPCBGLGRHATFRNFCMAFLTIFRVTSGDNNGIMKD	1792
Db	1563	AMLFFIIVAILGMQFGNIGLDDHTP---INRHNHHTFFNALMLFRATGESWQEIMLA	1619
QY	1793	TL--RDCD--QESTCYNTVISPTYFVSFVLTAQVLVNVVIAVLMKHLSEENKEAK----	1844
Db	1620	CLSGKECEGTREPC-GTDVAYFYFVSFIFLCSFIMLNLFAVIMDNFEYLTROSSILGP	1678
QY	1845	---EBAELEABLE-----LEMKTL-SQPHSLGSPFLWFG-----VE	1878
Db	1679	HHLDEFVRVWAEYDRAACRIHYTDMYQMLTMSPP-----PUGLKKCKPSKVAYKRLVLMN	1734
QY	1879	GPDSPD-----SPKPGALJHPAAHARSA-----SHFSLEHPTMQPHTELPGPDL	1922
Db	1735	MPVTEDKTVHFTSTLMGLRTALQIKLARGGADKQDLAEURKEIMTIWPHLSQ-KTIDL	1793
QY	1923	L-----TVRSGVSRTHSL-----PNSYMCRHGSTAEGPLGHR-----	1956
Db	1794	LVPMHVTSDLTVKGIYAAWMMIDYKQSNKKYQKLQEEQSRTPMFQRMSEASSLPQIIS	1853
QY	1957	-GWGLPKAOGSVLSVHSGPADTSYIQLPKDAPHLLQPHASPTWGTIPKLPPPGRSPL	2014
Db	1854	STKGLPYLQGTGPDVDSR-SEFTFLVPLP---PVMFOQGRSTSSQGEIHKQRPKELKI	1909
QY	2015	AQR-----PIRRQA-AIRTDSDLVOGLGSRDILLAEVSGPPPLIARVSPWGSSSTQ	2065
Db	1910	KLEYPHYGVLPIENGRAVSPRLEIE---SAED-----TSPLKRSU-----STF	1952
QY	2066	AQOHSRSHSKIKHMTTPPACPGPE-----PNMGKGP--PETRSSLELTELISWISGDLPP	2120

Db 1953 AANHNSG-TWLNEYSLERA---GPEDLKYRWSRRPLRPPSRSS-----N 1992

QY 2121 GGQEEPPSPDLKKCYVEAQSCQRRPTSWLDQRRHSIAVCLDSGSPHLGTDPSNLG 2180

Db 1993 AGSRGRGRSRERKHLLSPERSVCS-----TGQCAH-----PSQHRGLD-QLRS 2034

QY 2181 GQPLGGGSPKKKLSPPSITIDPPESQGRPTTSPGICLRRRAPSSDSKD-PLASGPP 2238

Db 2035 RSPSPGYSHRPREQVN--SSVSESPVPSSSGTSPPKQG---QRLPQTSPKRPPLVSYSP 2089

RESULT 15

A37490

voltage-dependent calcium channel alpha 1E - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A37490

R:Soong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P. Science 260, 1133-1136, 1993

A:Title: Structure and functional expression of a member of the low voltage-activated calcium channel family

A:Reference number: A37490; MUID:93262464; PMID:8388125

A:Accession: A37490

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-2222 <SO>

A:Cross-references: UNIPROT:Q07652; GB:L15453; NID:g310082; PIDN:AAA40855.1; PID:g310083

A:Experimental source: brain

A:Note: sequence extracted from NCBI backbone (NCBIP:132101)

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.9%; Score 1651.5; DB 2; Length 2222;
Best Local Similarity 23.6%; Pred. No. 1.4e-92;
Matches 591; Conservative 374; Mismatches 831; Indels 707; Gaps 77;

QY 62 FYLSQDSRPSRCLRTVCNPFERISMLVILLNCVLGMFR--PCDIACDSQRILQOA 119

Db 21 FIFGDNIVRYAKKLIDWPPPEYMTLATIANCIIVALEQHLPEDDKTPMSRR---LEK 77

QY 120 FDDFIFAFFAVEMVVMKVALG-IFGKKCYLGDTWNRLDFFVIAGMLEYSLDLQ--VSF 176

Db 78 TEPVFIGIFCFEAGIKIVALGFIFHKGYLRNGWNWDFIVLSGILATAGTHNTHVDL 137

QY 177 SAVRTVRVRLPRLNRNVPSPMILVTLDTPLMLGNVLCCFFVFFIFGIVGVQLWAGL 236

Db 138 RTLRAVRVRLPLKLVSGIPSLQIVLKSIMKAMVPLLIQILGLLFFAILMFAIIGLEFYSGK 197

QY 237 LRNCFPLNFSLPLSVDLERYQYOTENEDESPFICSPQENGMRSCSVPTLRDGGGGP 296

Db 198 LHRACFMNNSGIL-----EGFDP-----PHPCGVQGC----- 224

QY 297 PCGLDYEAYNSSNTTCVNNQYTNCSAGEHNPFKGAINFDNIGVAMIAIFOVITILEGW 356

Db 225 PAG--YE-----CKDW-----IGPNDGITQFDNILFAVLTVFCQITMEGW 262

QY 357 VDIMEYFVMDA-HSFYNFIYFILLIIVGFFMNLCLWIATQFSETKQESQLMREQVR 415

Db 263 TTVLNTNDALGATNWMFLYFIPLIIGSFVFLNLVLGVLGSGEFAKERERV-----ENRRA 317

QY 416 FLSNASTLASPSFGSCVEELKVLVYLIRKAARLAQVSRAGVRVGLLSSPAPLGQGE 475

Db 318 FMK-----LRQQQI----- 327

QY 476 TQPSSCSRGHRRLSVHHLVHHHHHHHHHHLNGTLAPRASPEIQDRDANGSRRLMLP 535

Db 328 -----ERELNGYRAWI-- 338

QY 536 PPSTPALSGAPPGAESVHSFYHADCHLEPVRCAQAPPPRSPSEASGRTVSGKVYPTVHT 595

Db 339 ----- 338

QY 596 SPPPETIKKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCL 655

339 -----DKAEVMAEENKNGSALSLEVLVRATIKRSRTEAMTRUSSDHCVDISSVGTFLA 394
656 KADSGACGPDSCPCYCARAGAGEVELADREMPDSDSEAYEFTQDAQSHDLDRPHSRQRS 715
395 RASIKSTKVDCASY-----FRHKE-----413
716 LGPDAEPSSVLAFWRLICDTERKIVSKYGRGIMIAILLVNTLSMGLYEHOPEELTNAL 775
414 -----RLLRISIRHMVKSQVFYIIVLSVALNTACVAIHHNQOMLTHLL 459
776 EISNIVETSLEALEMLKLLVYGPYKIPNYNFDGVIVVISWEIVGO-----QGGGL 830
460 YYAEFLGLGFLLEMSLUKMGMPRLPHSHSFCNCFDGVTVGSIFEVVWALFRPGTSFGI 519
831 SVLRTFLMRVLKVLRLPALQORQLVLMKTMNDVATFCMLMLFIIFISILGHLGCK 890
520 SVLRALRLRIFKITYKASLRNLVSLMSSMKIISLLEFLFLFVIVFALLGNQLFGR 579
891 PASERDGTLLPDRKNFDSLLWAIIVTVFOILTQEDWNVKLVNKM-----ASTSSWAALFYI 945
580 F-NENDG---TPSANFDTFPAIIMTVFQILTGEDWNEVYNGIRSQGGVSSGMSAIYFI 635
946 ALMTFGNVLPNLVAIIVVEGF-QAEEETSK-----REDASGQLSCTQLPVDVSDGGDANKSE 1000
636 VLTUFGNTLLNVFLAIADVNLANAQELTKOEDEEAFNOKHALQKAEV-----SPM 689
1001 SEPDIFFSPSLDGDGRKCLAL-----VSLGEHPE 1030
690 SAPNM--PSIERDRRRHMSWEPSSHLRERRRRHMSVMEQRTSQLRRHMQSSQEA 747
1031 LRKSLPLLIITHAATMS-----LPKS-TSTGGEALGPASRRTSSGSAE 1076
748 LMKEEAPMNPPLNPLNPLNPLNAHPSLVRRPRPIEGLAUGLGLKECEBERIRGGSL 807
1077 PGAAHEMKSPPSARSPPHS-----PW-----SAASWT 1104
808 KGDICGLTSLVDNQSPSLGKREPPWLPSCRCHGNCDPQQTGGGTVTVPEDRARHQ 867
1105 SRRSRNSLGRAPSLKRSPSGERRSLLSGEGESQDEBESSEERERASPAGSDHHRGSL 1164
868 SQRRSRHRRVRTEGESASASR-----SASQERSLDEGVSDGEKEHPEQSHRSKEPT 923
1165 EREAKSSFDL--PDILQV--GL-----HRTASGRGSASEHDCDNGKSA 1204
924 IHEBERTQDLRTNSLMVPRGSLVGLVALDEATPLVQPOPELEVGDAAALTEQAEAGSSE 983
1205 SGRLA-----RALRPDDPPL-----1219
984 QALLADVLDVGRGISQSEPDLSCTMTNMDKATTESTSVTVAIPDVPDPLVDSTVVMISNK 1043
1220 -DGDDA-----DDEGNLSKGER---VRAMIRAPKLPCYLERSDSWASAYIPPPQSRFL 1267
1044 TDGEASPLKEAETKEEBEVEKKQKRETKAMVPHS-----SMFIFSTTPIRK 1096
1268 LCHRIITHKMFHDVHLVIIFLNCITITAMERPKIDPHSAERIPLTLNRYIFTAVFLAEMTV 1327
1097 ACHYIVNLRYFEMCILLVTAASIALAEDPVTNSERNKV-LRYDYVFTGVFTFEMVI 1155
1328 KVALGWCFOEQAYLRSSWNVDGLIIVLISVIDI-LVSMYSDSGTKILGLMLRLVRLRTL 1386
1156 KMIDQGLILLQDGSYFRDLWNILDFVVVGVALVAPALANALGTNKGDRDIKISLRVLRVL 1215
1387 RPLRVTSRAQGLKLVVETLMSLKPIGNIVVICAPFIIFGILGVOLFCKGFFVC--QGE 1444
1216 RPLKTIKRLPKLKAVIDCVVTSLSKNVFNILIVKLFMFIFAVIAVQLFKGFFVCTDSSK 1275
1445 DTRN-----ITNKSDCABASYR-VYRHKYFNFNLGALMSLFVLASKDGMVDIMYDGLD 1497
1276 DTEKECTGNVVDHEKNKQKVKGEWKKEHFEHYDNI I WALLITLFTVSTGEGWPQVLQHSVD 1335
1498 AVGVDOQOPIMMHNPMWLLYFISFLIIVAFVFLNMVGVVFNPHKCHQOHEEERREE 1557
1336 VTEEDRGPSRNRMEMSIFVYVYVFPFVFVFNIFVALLIITF-----QEQGDKNMEE 1368

1558 KRLRLLEKERRKA-----QCKPY--YSDYSR--FRLLVHLCTSHYLDLBITGIVGLNVV 1608
1389 ---CSLEKNERACIDPAISAKPLTRYMPQNRHTFOYRVWHFVSPSEYTIMAMIAINTV 1445
1609 TMAMEHYQOQIILDEALKICNYIFTVIFVLESVKLVAFGFRFFODRWQOLDLAIVLLS 1668
1446 VLMMKYASPTVELALKYLNIAFTWVFSLECVLKVIAFGLNRYFROTWNIFDITVIGS 1505
1669 IMGITLLEEIEVNASLPINPTIIRIMRVLRARVLKLVKVAVMGFMALDITVQALPOVGNL 1728
1506 ITEILITDSKLVTSGENMSFLKLFRA---ARLIKLRQGYTHILLWTFVQSFKALPYV 1562
1729 GILFMLFFFAALGVLEFGDLECD-ETHPCEGEGRHATFRNFMALFELTFRVSTGNWN 1787
1563 CLLIAMLFFIIVAIIGMQVFGNIKLEDSH---INRHNFRSFFGLMLLFRSATGSAWQ 1618
1788 GIMKDTL--RDCQESTC-----YNTVISPIYFVSFVLTAQFVLNVVIAVLMKHL 1836
1619 EIMLSCLGKGECEPDTTAPSGQNESERCGTDLAYVYFVSFFFCFLMLNLFAVIMDNF 1678
1837 EESNKEAK-----EEAELEAELE-----LEMKTLSPQSPHSPGLSGFFLWPG 1876
1679 BYLTRDSILGPHLDEFVRVWAEYDRAACGRIHVTEMYEMLTLM-----SPPLGLG 1730
1877 VEGPDSPDSPKPGALHPAAHARSASHPSLEHPTWQHPTELPGLDILLTVRKSGVSRTHSL 1936
1731 KRCFSKVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD---IXIARGGADROQL- 1783
1937 PNDSYMCHRGSTAEGPLCHRGWGL-----PKAOSGSLSVHSQPADTSVI-----1981
1784 --DSLOKETLAIWPHLSQKMLDLVPMKPSADLTGVGKIYAAMTMDYKQSKVKKQKQ 1841
1982 LOLPKDAP--HLLOPHSAP---TWGTIPKLP-----PGRSPLAQRPL---2019
1842 LEEQKNAPMFORMEBSLPOEIIISNAKALPYLQQDPVSLSGRSGYPSMSPSLPQEIFOL 1901
2020 -----RROQAIRTDSDVOGLGSR-----EOLLAESVSGSPPLARAY 2056
1902 ACMDFADDGQFQEQQLVVTDPSSMRRSFSTIRKRSNSWLFEFSMERSSENTYKSRRR 1961
2057 SFWGSOSTQAQOH-----SRSHKISKHMTTP-----AP 2085
1962 SY--HSSLRLSAHLNSDSGHKSDTHRSGRGRGRSKERKHLSDVSKCNSEERGTQAD 2019
2086 CFGPBNWKGPPETRS-----SLE-----LDTELSWISGDLPLPPGQBEPPSP 2129
2020 WESPERRQSRSPSEGRSQTNPQGTCSLSESIPISTSTTPRRSRRLPP---VPPKP 2075
2130 RDLKCKYSVEAOSCORRPTSWLDEORRHSAIVSCLDGSOPLHGTDPNLGGQPLGGPGS 2189
2076 RPLLSYSSL-----MRHTGGISPPDPGSE-----GSGPLASQAL 2109
2190 RPKKK-LSPSITIDPPESQGRTP---PSPGICLRRRAPSSD 2228
2110 ESNACLTESSNSLHPQOQGHSPQYIIEPYIALHEDSHASD 2152

Search completed: November 18, 2004, 13:35:23
Job time : 97.2671 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:06:30 ; Search time 251.833 Seconds
(without alignments)
5177.235 Million cell updates/sec

Title: US-09-611-257A-37

Perfect score: 11904

Sequence: 1 MDEEDGAGAEESGQPRFSM.....PKDVLISLGLSDPADLDP 2266

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	11815.5	99.3	2377	1	CCAG_HUMAN	O43497 homo sapien
2	11133.5	93.5	2295	2	Q9WUT2	Q9wtu2 mus musculus
3	11111	93.3	2288	2	Q9WUB8	Q9wub8 rattus norv
4	10945	91.9	2254	1	CCAG_RAT	O54898 rattus norv
5	10945	91.9	2254	2	AAG35186	Aag35186 rattus norv
6	10913	91.7	2248	2	Q6P8V8	Q6pfv8 mus musculus
7	10913	91.7	2248	2	AAH57399	Aah57399 mus muscu
8	6573	55.2	1389	2	O62PX4	O62px4 mus musculus
9	6573	55.2	1389	2	BAC98104	Bac98104 mus muscu
10	6217.5	52.2	2359	1	CCAH_RAT	Q9eq60 rattus norv
11	6210	52.2	2353	1	CCAH_HUMAN	O95180 homo sapien
12	6176.5	51.9	2365	1	CCAH_MOUSE	O88427 mus musculus
13	5496.5	46.2	2223	1	CCAI_HUMAN	Q9p0x4 homo sapien
14	5383	45.2	1835	1	CCAI_RAT	Q9z0y8 rattus norv
15	4836	40.6	1994	2	Q7PQV4	Q7p6s8 homo sapien
16	4200.5	35.3	1762	2	Q7Z6S8	Q7pqv4 anopheles 9
17	4180	35.1	2893	2	Q9M433	Q9w433 drosophila
18	3855	32.4	1837	2	Q967R4	Q967r4 caenorhabdi
19	3845.5	32.3	1852	2	Q7Z002	Q7z002 caenorhabdi
20	3845.5	32.3	1852	2	AAR25651	Aar25651 caenorhab
21	3828.5	32.2	1844	2	Q7YZR6	Q7y2r6 caenorhabdi
22	3828.5	32.2	1844	2	AAR25653	Aar25653 caenorhab
23	3823	32.1	1885	2	Q7Z003	Q7z003 caenorhabdi
24	3823	32.1	1885	2	AAR25652	Aar25652 caenorhab
25	3683.5	30.9	1460	2	Q80TJ2	Q80tj2 mus musculus
26	2925.5	24.6	1418	2	Q7JPB4	Q7jpb4 caenorhabdi
27	2925.5	24.6	1418	2	AAR30210	Aar30210 caenorhab
28	2866	24.1	1942	2	O869H0	O869h0 lymnaea sta
29	2089	17.5	1211	2	Q8MQ95	Q8mq95 caenorhabdi
30	1746.5	14.7	2339	1	CCAB_HUMAN	O00975 homo sapien
31	1740.5	14.6	2333	2	O89089	O89089 rattus norv

RESULT 1

CCAG_HUMAN

ID CCAG_HUMAN STANDARD; PRT; 2377 AA.
AC O43497; O43498; O94770; Q9NYU4; Q9NYU5; Q9NYU6; Q9NYU7; Q9NYU8;
AC Q9NYU9; Q9NYV0; Q9NYV1; Q9UHN9; Q9UHP0; Q9ULU6; Q9UNG7; Q9Y5T2;
AC Q9Y5T3;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-gated calcium channel alpha subunit Cav3.1) (Cav3.1c) (NER13).
DE gated calcium channel alpha subunit Cav3.1 (Cav3.1c) (NER13).
GN Name=CACNA1G; Synonyms=KIAA1123;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 4 AND 5).
RC TISSUE=Brain;
RX MEDLINE=20014446; PubMed=10548410;
RA Mittman S., Guo J., Agnew W.S.;
RT "Structure and alternative splicing of the gene encoding alpha1G, a human brain T calcium channel alpha subunit.";
RL Neurosci. Lett. 274:143-146(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=20115462; PubMed=10648811;
RA Cribbs L.L., Gomora J.C., Daud A.N., Lee J.-H., Perez-Reyes E.;
RT "Molecular cloning and functional expression of ca(v)3.1c, a T-type calcium channel from human brain.";
RL FEBS Lett. 466:54-58(2000).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 1-2 AND 6-13).
RC TISSUE=Brain;
RX MEDLINE=20158909; PubMed=10692398;
RA Montell A., Chemin J., Bourinot E., Mennessier G., Lory P., Nargeot J.;
RT "Molecular and functional properties of the human alpha1G subunit that forms T-type calcium channels.";
RL J. Biol. Chem. 275:6090-6100(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 14).
RC TISSUE=Brain;
RX MEDLINE=22158633; PubMed=12168954;
RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
RT "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones.";
RL DNA Res. 9:99-106(2002).
RN [6]

ALIGNMENTS

32	1732.5	14.6	2327	1	CCAB_MOUSE	O55017 mus musculus
33	1729.5	14.5	2331	2	Q9TTH4	Q9tta4 bos taurus
34	1722	14.5	2336	1	CCAB_RAT	Q02294 rattus norv
35	1712.5	14.4	541	2	Q6PE92	Q6pe92 mus musculus
36	1712.5	14.4	541	2	AAH58206	Aah58206 mus muscu
37	1710	14.4	2339	1	CCAB_RABIT	Q05152 oryctolagus
38	1697.5	14.3	2357	2	Q9PUM6	Q9pum6 gallus gall
39	1697	14.3	2259	1	CCAE_RABIT	Q02343 oryctolagus
40	1689	14.2	1810	2	O44930	O44930 aiptasia pa
41	1688.5	14.2	2295	2	Q923K6	Q923k6 rattus norv
42	1685	14.2	2346	2	Q9PW47	Q9pw47 gallus gall
43	1683	14.1	2332	2	Q9PW45	Q9pw45 gallus gall
44	1681	14.1	2272	1	CCAE_MOUSE	Q61290 mus musculus
45	1666.5	14.0	2312	1	CCAE_HUMAN	Q15878 homo sapien

Qy	1990	HLLQPHSAPTWTIPKLPDPSRPLAQPLRQAAIRTDSDVOGLSGREDLLAEVSGPS	2049
Db	2101	HLLQPHSAPTWTIPKLPDPSRPLAQPLRQAAIRTDSDVOGLSGREDLLAEVSGPS	2160
Qy	2050	PPLARAYFWQSGSTQAOQHRSRSHKSKHMTTPAPCPGPEPNWKGPPETRSSLELDT	2109
Db	2161	PPLARAYFWQSGSTQAOQHRSRSHKSKHMTTPAPCPGPEPNWKGPPETRSSLELDT	2220
Qy	2110	LSWISGDLPLPGQOEPPSPDLKKCYSEVAQSCORRPTSWLDEQRRHSIAVCLDSGSQ	2169
Db	2221	LSWISGDLPLPGQOEPPSPDLKKCYSEVAQSCORRPTSWLDEQRRHSIAVCLDSGSQ	2280
Qy	2170	PHLGTDPNGLGQPLGGPSRPKKLSPPSTIIDPPESQGRTPPSPGICLRRRAPSSDS	2229
Db	2281	PHLGTDPNGLGQPLGGPSRPKKLSPPSTIIDPPESQGRTPPSPGICLRRRAPSSDS	2340
Qy	2230	KDPLASGPPDMAASPSPKKDVLSSLGLSSDPADLDP	2266
Db	2341	KDPLASGPPDMAASPSPKKDVLSSLGLSSDPADLDP	2377
RESULT 2			
Q9WUT2			
AC	Q9WUT2	PRELIMINARY; PRT: 2295 AA.	
ID	Q9WUT2		
DT	01-NOV-1999	(TREMELrel. 12, Created)	
DT	01-NOV-1999	(TREMELrel. 12, Last sequence update)	
DT	01-OCT-2003	(TREMELrel. 25, Last annotation update)	
DE	Voltage-gated calcium channel, alpha-1-G subunit.		
GN	Name=Cacna1g;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RC	MEDLINE=99189326; PubMed=10087148;		
RA	Klugbauer N., Marais E., Lacinova L., Hofmann F.;		
RT	"A T-type calcium channel from mouse brain.";		
RL	Pflugers Arch. 437:710-715 (1999).		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).		
CC	-!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.		
DR	EMBL; AJ012569; CAB40793.1; -.		
DR	MGD; MGI:1201678; Cnca1g.		
DR	GO; GO:0005886; C:plasma membrane; IDA.		
DR	GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.		
DR	InterPro; IPR001682; Ca/Na_pore.		
DR	InterPro; IPR002111; Cat_channel_TrpL.		
DR	InterPro; IPR002077; Ca_channel_alpha.		
DR	InterPro; IPR005821; Ion_trans.		
DR	InterPro; IPR005820; M+channel_nlg.		
DR	InterPro; IPR005445; TVDCCAlphal.		
DR	Pfam; PF00520; Ion_trans_4.		
DR	PRINTS; PR00167; CACHANNEL.		
DR	PRINTS; PR01629; TVDCCALPHA1.		
KW	Calcium channel; Calcium-binding; Ion transport; Ionic channel;		
KW	Transmembrane; Transport; Voltage-gated channel.		
SQ	SEQUENCE 2295 AA; 253957 MW; FE817D054ED26984 CRC64;		
Query Match 93.5%; Score 11133.5; DB 2; Length 2295;			
Best Local Similarity 93.3%; Pred. No. 0;			
Matches 2142; Conservative 32; Mismatches 91; Indels 31; Gaps 5			
Qy	1	MDEEDGAGAEESGQPSRFMLNDLSGAGRGPGSGAEKDPGSADSEAGLPPALAPVV	60
Db	1	MDEEDGAGAEESGQPSRFMLNDLSGAGRGPGSGAEKDPGSADSEAGLPPALAPVV	60
Qy	61	FFYLSQDSRRPSWCLRTVCNPFWRISMLVILLNCVILGFRPCEDIACDSQRCRILQAF	120
Db	61	FFYLSQDSRRPSWCLRTVCNPFWRISMLVILLNCVILGFRPCEDIACDSQRCRILQAF	120

Qy	121	DDTFAFAFVAVMVKVALGIFGKKCYLGDWTNRDLDFVIAGMLEYSLDIQNVSFSAVR	180
Db	121	DDTFAFAFVAVMVKVALGIFGKKCYLGDWTNRDLDFVIAGMLEYSLDIQNVSFSAVR	180
Qy	181	TVRVLRPLRANRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVOLWAGLLNR	240
Db	181	TVRVLRPLRANRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVOLWAGLLNR	240
Qy	241	CFLPENSLPLSVLERYOTENEDESPFICQPRENMRSCRSVPTLRGDDGGGPPCGL	300
Db	241	CFLPENSLPLSVLERYOTENEDESPFICQPRENMRSCRSVPTLRGDDGGGPPCGL	300
Qy	301	DYEAYNSSNTTCVNNQYITNCAGAHNPFKGAINFQNIYAWIAIFQVITLEGWVIM	360
Db	301	DYEAYNSSNTTCVNNQYITNCAGAHNPFKGAINFQNIYAWIAIFQVITLEGWVIM	360
Qy	361	YFVMDAHSFYNFIFILLIIVGSPFMINI.CLVATATOFSETKQESQMRQVRFLNA	420
Db	361	YFVMDAHSFYNFIFILLIIVGSPFMINI.CLVATATOFSETKQESQMRQVRFLNA	420
Qy	421	STLASFSPPGSCYEELLYVILKKAARLAQVSRAGVRVGLLSSPAPLGQGTQPS	480
Db	421	STLASFSPPGSCYEELLYVILKKAARLAQVSRAGVRVGLLSSPAPLGQGTQPS	480
Qy	481	SCSRSHRSLSVHHLVHHHHHHHHYHLGNGTLRAPASPEIQDRDANGSRRLMLPPSTP	540
Db	481	SCSRSHRSLSVHHLVHHHHHHHHYHLGNGTLRAPASPEIQDRDANGSRRLMLPPSTP	540
Qy	541	ALSGAPPGAESVHSFYHADCHLEPVRCQAPPSRSEASGRTVSGKVPVHTSPPE	600
Db	541	TPSGGPPRGAEVHSFYHADCHLEPVRCQAPPSRSEASGRTVSGKVPVHTSPPE	600
Qy	601	TLKEXALVEVAASGPPITLSINIPPGYSSMHKLETTQSTGACOSSKISSPCIKADSG	660
Db	601	MLKDKALVEVAPSPPPTLTENIPPGPSSMHKLETTQSTGACHSSKISSPCSKADSG	660
Qy	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRQRSIGPDA	720
Db	661	ACGPDSCPYCARTGAGEPESADHEMPDSDSEAVYEFTQDAQHSDLRDPHSRQRSIGPDA	720
Qy	721	EPSSVLAFWLLICDTFRKIVDSKYFGRGIMIALVNTLSMGIEYHEQBPELTNVAISNI	780
Db	721	EPSSVLAFWLLICDTFRKIVDSKYFGRGIMIALVNTLSMGIEYHEQBPELTNVAISNI	780
Qy	781	VFTSLFALEMLKLLVYGFYKPNYINFDGVIVVISWEIVGQGGGLSVLRTFLMR	840
Db	781	VFTSLFALEMLKLLVYGFYKPNYINFDGVIVVISWEIVGQGGGLSVLRTFLMR	840
Qy	841	VILKVRFLPALQRLVLMKTDNVATFCMLMLFIFISILGMHLPGCKFASERDGTIL	900
Db	841	VILKVRFLPALQRLVLMKTDNVATFCMLMLFIFISILGMHLPGCKFASERDGTIL	900
Qy	901	PDRKNFDSLILWATVTFQILTQEDWNKVLNGWASTSSWAALFYIALMTPGNVFLNLLV	960
Db	901	PDRKNFDSLILWATVTFQILTQEDWNKVLNGWASTSSWAALFYIALMTPGNVFLNLLV	960
Qy	961	AILVEGFQAEIEISKREDASQSLCIQLPVDSQGGDANKSESEDPFSPSLDGDGRKKCL	1020
Db	961	AILVEGFQAEIEISKREDASQSLCIQLPVDSQGGDANKSESEDPFSPSLDGDGRKKCL	1020
Qy	1021	ALVSLGEHPERKSLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRITSSSGSAPGAA	1080
Db	1021	ALVSLGEHPERKSLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRITSSSGSAPGAA	1080
Qy	1081	-HMKKPPPSARSPSPWSAASWTGRRSRNSILGRAPSLKRRSPSGRRSLSSGEGES	1139
Db	1081	-HMKKPPPSARSPSPWSAASWTGRRSRNSILGRAPSLKRRSPSGRRSLSSGEGES	1140
Qy	1140	QDEESSEERFASGSDHRRHRSLEAKSSFDLPTLQVPLGHLRTASRGASAEHQC	1199
Db	1141	QDEESSEERFASGSDHRRHRSLEAKSSFDLPTLQVPLGHLRTASRGASAEHQC	1200

QY 1200 NKSASGLARALRDPDPDGLDGDADDEGNLSKGERVRAWIRARLPACYLERSWSAYIF 1259
Db 1201 NKSASGLARALTRADDPLDGDGDDEGNLSKGERLARWVARLPACCREDRSWSAYIF 1260
QY 1260 PQSFRLLCHRILTHKMFHVVILVIFLNCITIAMERPKIDPHSAERIFLTLNSYIFTA 1319
Db 1261 PQSFRLLCHRILTHKMFHVVILVIFLNCITIAMERPKIDPHSAERIFLTLNSYIFTA 1320
QY 1320 VFLAEMTVKVALGWCFCGEQAYLRSSWNVLGDLVLIISVIDILVSMVSDSGTKILGMLRV 1379
Db 1321 VFLAEMTVKVALGWCFCGEQAYLRSSWNVLGDLVLIISVIDILVSMVSDSGTKILGMLRV 1380
QY 1380 LRLRLTLPLRVISRAQGLKLVETIMGSLKPIGNIVVICCAFFIIFGILGVQLFKGFF 1439
Db 1381 LRLRLTLPLRVISRAQGLKLVETIMGSLKPIGNIVVICCAFFIIFGILGVQLFKGFF 1440
QY 1440 VCOGEDTNI TNKSDCAEASRWVHKYFNFMNLGQALMSFLVLSKDGWVIMYDGLDAV 1499
Db 1441 VCOGEDTNI TNKSDCAEASRWVHKYFNFMNLGQALMSFLVLSKDGWVIMYDGLDAV 1500
QY 1500 GVDQOPI MNHNPMLLYFISFLIIVAFVFLNMVGVVVENHFKRQHOOEESRARRREKR 1559
Db 1501 GVDQOPI MNHNPMLLYFISFLIIVAFVFLNMVGVVVENHFKRQHOOEESRARRREKR 1560
QY 1560 LRLLEKKRR-----KAQCKPYYSYDSRFRLLVHHLCTSHY 1594
Db 1561 LRLLEKKRRSEKQWADMLMDVIASSGSSAASEAQCKPYYSRFRLLVHHLCTSHY 1620
QY 1595 LDLFITGVIGLVNVTMAMEHYQQOILDEALKICNYIPTVIFVLESVFKLVAFGFRFPFQ 1654
Db 1621 LDLFITGVIGLVNVTMAMEHYQQOILDEALKICNYIPTVIFVLESVFKLVAFGFRFPFQ 1680
QY 1655 DRWNQDLAI VLLSIMGITLIEEIVNASLPNPTIIRIMRVLRARVILKLMKAVGMRAL 1714
Db 1681 DRWNQDLAI VLLSIMGITLIEEIVNASLPNPTIIRIMRVLRARVILKLMKAVGMRAL 1740
QY 1715 LDTVMQALPQVNGILMLFFIFAALGVLEFGDCEDETHPCGELGRHATFNFQWAP 1774
Db 1741 LDTVMQALPQVNGILMLFFIFAALGVLEFGDCEDETHPCGELGRHATFNFQWAP 1800
QY 1775 LTLFRVSTGDNWNGIMKDTLRDCQESTCYNTVISPITYFVSFVLTAQFVLVNVVIAVLK 1834
Db 1801 LTLFRVSTGDNWNGIMKDTLRDCQESTCYNTVISPITYFVSFVLTAQFVLVNVVIAVLK 1860
QY 1835 HLEESNKEAEAEAELEAELEEMKTLSPQHPSPGLSPFLWPGVGPSPSPKPGALHPA 1894
Db 1861 HLEESNKEAEAEAELEAELEEMKTLSPQHPSPGLSPFLWPGVGPSPSPKPGADHTT 1920
QY 1895 AHARSASH-PSLEHPTMQPHTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSSTAE 1950
Db 1921 AHGAASSGSFSLHPTMVPHTERGVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRHGSSTAE 1980
QY 1951 GPLGHRGWGLPKAQSGLSVLSVHSOPADTSYILQPKDAPHLLOPHSAPTWTGTPKLP 2010
Db 1981 RSLCHRGWGLPKAQSGLSVLSVHSOPADTSYILQPKDAPHLLOPHSAPTWTGTPKLP 2040
QY 2011 RSPLAQRPLRQAAIRTDSDLVQGLSREDLLAEVSGPSPELARAYSPWQSSTQAQHS 2070
Db 2041 RSPLAQRPLRQAAIRTDSDLVQGLSREDLLAEVSGPSPELARAYSPWQSSTQAQHS 2100
QY 2071 RSHKLSKUMTPAPCGPBPNNKGPPEPTRSSLELDTLSWISGDLPLPGGQEEPPSPR 2130
Db 2101 GSQSKVSKHRLPAPCPGLEPSPWAKDPQETRRSLELDTLSWISGDLPLPGGQEEPPSPR 2159
QY 2131 DLKCKYSVBAQSCORRPTSWLDRHRHSIAVSCLDGSGPHLGTDSNLGGQPLGGPGR 2190
Db 2160 DLKCKYSVBAQSCORRPTSWLDRHRHSIAVSCLDGSGPHLGTDSNLGGQPLGGPGR 2219
QY 2191 PKKLSPPSITIDPPESQGPRTPPSPGICLRRAPSSDKDPLASGPPSPMAASPPPKD 2250
Db 2220 PKKLSPPSITIDPPESQGPRTPPSPGICLRRAPSSDKDPLASGPPSPMAASPPPKD 2279
QY 2251 VLSLSGLSDPADLDP 2266

Db 2280 ALSLSGLSDPTDLDP 2295

RESULT 3

Q9WUB8
ID Q9WUB8 PRELIMINARY; PRT; 2288 AA.
AC Q9WUB8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE T-type calcium channel isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=20081696; PubMed=10615950;
RA Zhuang H., Bhattacharjee A., Hu F., Zhang M., Goswami T., Wang L.,
Wu S., Berggren P.O., Li M.;
RT "Cloning of a T-type Ca2+ channel isoform in insulin-secreting
cells";
RL Diabetes 49:59-64(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
family.
EMBL; AF125161; AAD26858.1; -;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.
GO; GO:0005261; F:voltage-gated calcium channel activity; IEA.
GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.
GO; GO:0006816; P:calcium ion transport; IEA.
GO; GO:0006812; P:calcium transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR002077; Cat_channel_alpha.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR00167; CCHANNEL.
DR PRINTS; PR01629; TVDCCALPHA1.
KW Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW Transmembrane; Transport; Voltage-gated channel.
SQ SEQUENCE 2288 AA; 253476 MW; B89DBB5A1D81757F CRC64;

Query Match 93.3%; Score 11111; DB 2; Length 2288;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;

QY 1 MDEEDGAGAEESQPRSFMRNLDSLGSAGRPGPSAEKDPGSADSEAEGLPYPALAPV 60
Db 1 MDEEDGAGAEESQPRSFMRNLDSLGSAGRPGPSAEKDPGSADSEAEGLPYPALAPV 60

QY 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILNCVTLGMFRPCEDIACDSQRILQAF 120
Db 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILNCVTLGMFRPCEDIACDSQRILQAF 120

QY 121 DDFIFAFFAVEMVVMVALGIFGKKCYLGDWTNRDLDTFFVIAGMLEYSLDLQNVFSAVR 180
Db 121 DDFIFAFFAVEMVVMVALGIFGKKCYLGDWTNRDLDTFFVIAGMLEYSLDLQNVFSAVR 180

QY 181 TVRVLRLPRLAIRNVRPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
Db 181 TVRVLRLPRLAIRNVRPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

QY 241 CFLPENFSLPLSVDLERYYYQTENEDESFFICSQPRENGMRSCRSVFTLRGCGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYYYQTENEDESFFICSQPRENGMRSCRSVFTLRGCGGGPPCGL 300

QY 301 DYEAVNSSNTTCVNNQYVYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360

Db	301	DIETINSSNTTCVNNQYTNCSAGBNPKGAINFDNIGYAMIAFQVILLEGWDIM	360
Qy	361	YFVMDAISFYNYFIYILLIIVGSPFMNLCIWIATOFSETKQRESQIMREQRVPLSNA	420
Db	361	YFVMDAISFYNYFIYILLIIVGSPFMNLCIWIATOFSETKQRESQIMREQRVPLSNA	420
Qy	421	STLASFSEPGSCYBELKYLVIILKAAARLAQVSRAGVRVGLLSSPAPLGGETQSS	480
Db	421	STLASFSEPGSCYBELKYLVIILKAAARLAQVSRAGVRVGLLSSPAPLGGETQSS	480
Qy	481	SCSRSHRLRLSVHLVHHHHHHVHLNGTLRAPRASPEIQDRDANGSRRLMLPPSTP	540
Db	481	SCSRSHRLRLSVHLVHHHHHHVHLNGTLRAPRASPEIQDRDANGSRRLMLPPSTP	540
Qy	541	ALSGAPPGCABSVHSFYHADCHLEPVRQOAPPPSPSEASGRITVSGKVIPTVHTSPPE	600
Db	541	TPSGGPPRGAESVHSFYHADCHLEPVRQOAPPPSPSEASGRITVSGKVIPTVHTSPPE	600
Qy	601	TLKEKALVEVAASSGPPLTSLNIPPGYSSMHKLETOSTGACOSSCKISSPCLKADSG	660
Db	601	ILKOKALVEVAPSPGPPLTSLNIPPGYSSMHKLETOSTGACHSSCKISSPCSKADSG	660
Qy	661	ACGPDSCPCYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRDPHS-RRQRSGLPD	719
Db	661	ACGPDSCPCYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRDPHSRRQRSGLPD	720
Qy	720	AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMTIAILLVNTLSMGIYHEQPEELTNALEISN	779
Db	721	AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMTIAILLVNTLSMGIYHEQPEELTNALEISN	780
Qy	780	IVFTSLFALEMLKLLVYGPFGYIKNPYINFGVIVIVISVWEIVGQGGSLVLTFRLM	839
Db	781	IVFTSLFALEMLKLLVYGPFGYIKNPYINFGVIVIVISVWEIVGQGGSLVLTFRLM	840
Qy	840	RVLKLVRELPAORQOLVLMKMDNVATFCMLLMFIFIFISILGMHLFGCKEASBRDGT	899
Db	841	RVLKLVRELPAORQOLVLMKMDNVATFCMLLMFIFIFISILGMHLFGCKEASBRDGT	900
Qy	900	LPDRKNFDSLILWAIIVTFQILLTQEDWNKVLNMGMASTSSWAALYFIALMTFGNYVLNLL	959
Db	901	LPDRKNFDSLILWAIIVTFQILLTQEDWNKVLNMGMASTSSWAALYFIALMTFGNYVLNLL	960
Qy	960	VAILVEGFOAHEISKREDASQSLCTQLPVDSCGDANKSESPDFPSLDGDGRKKC	1019
Db	961	VAILVEGFOAHEISKREDASQSLCTQLPVDSCGDANKSESPDFPSVDGDGRKKR	1020
Qy	1020	LALVSLGEHPELRKSLPLLIHTAATPMSLPKSTGTGLGEALGPASRRTSSGSAEPGA	1079
Db	1021	LALVSLGEHPELRKSLPLLIHTAATPMSLPKSTGTGLGEALGPASRRTSSGSAEPGA	1080
Qy	1080	A-HEMKSPSARSPPHSPMSAASWTSSRSRNSLGRAPSLKRSPSGERSLLSGEQE	1138
Db	1081	AHEMKSPSARSPPHSPMSAASWTSSRSRNSLGRAPSLKRSPSGERSLLSGEQE	1140
Qy	1139	SQDEEESSEERASPAQSDHHRGSLEREAKSFDLPDITLQVPLHRTASGRGSAEHQD	1198
Db	1141	SQDEEESSEERASPAQSDHHRGSLEREAKSFDLPDITLQVPLHRTASGRGSAEHQD	1200
Qy	1199	CNGKSASGLRALARPDDPLDGDADDENGLSKGERVRAWIRAPACLYERDSWAYI	1258
Db	1201	CNGKSASGLRALARPDDPLDGDADDENGLSKGERIQAQVRSRLPACCRERDSWAYI	1260
Qy	1259	FPQOSRPLICHRITHTKNDHVVVLIIFLNCITIAMERPKIDPHSAERIFLTLNSVIFT	1318
Db	1261	FPQOSRPLICHRITHTKNDHVVVLIIFLNCITIAMERPKIDPHSAERIFLTLNSVIFT	1320
Qy	1319	AVFLAEMTKVVALGWCFCGEAYLRSSNNVLDGLLVLSVIDILVSVMSDSTGKILGMLR	1378
Db	1321	AVFLAEMTKVVALGWCFCGEAYLRSSNNVLDGLLVLSVIDILVSVMSDSTGKILGMLR	1380
Qy	1379	VLRLRLTRPLRVISRAQGLKLVVETLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGK	1438
Db	1381	VLRLRLTRPLRVISRAQGLKLVVETLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGK	1440
Qy	1439	FVCGEDTRNTKNSDCAEASYSRWVRHKYNFDNLQALMSLFLVASKDGMWDIMYDGLDA	1498
Db	1441	FVCGEDTRNTKNSDCAEASYSRWVRHKYNFDNLQALMSLFLVASKDGMWDIMYDGLDA	1500
Qy	1499	VGVDQQPIMNHNPMWLLYFISFLIIVAFVFLNMVGVVVENFHKRQHOEBEERREK	1558
Db	1501	VGVDQQPIMNHNPMWLLYFISFLIIVAFVFLNMVGVVVENFHKRQHOEBEERREK	1560
Qy	1559	RRLRELEKRR-----KAOCKEYSDYSRFRLLVHHLCTSHYLDLFIIT	1600
Db	1561	RRLRELEKRRMLMDVVIAGSSASAASEACKPYSDYSRFRLLVHHLCTSHYLDLFIIT	1620
Qy	1601	GVIGLVVTMAHEHYQOQIILDEALKICNYIIFTVIFVLESVFKLVAFGFRFFQDRMNQL	1660
Db	1621	GVIGLVVTMAHEHYQOQIILDEALKICNYIIFTVIFVLESVFKLVAFGFRFFQDRMNQL	1680
Qy	1661	DLAIVLLSIMGITILEEBIEVNASLPINPTIIRIMVLRITARVLKLLKMAVGRALLDTVMQ	1720
Db	1681	DLAIVLLSIMGITILEEBIEVNASLPINPTIIRIMVLRITARVLKLLKMAVGRALLDTVMQ	1740
Qy	1721	ALPQVGNLGLLPMLLFFIFAALGVLELFGDLECDETHPCGELGRHATFRNFGMAFLTFRV	1780
Db	1741	ALPQVGNLGLLPMLLFFIFAALGVLELFGDLECDETHPCGELGRHATFRNFGMAFLTFRV	1800
Qy	1781	STGDNWNGIMKDTLRDCCQESTCYNTVISPFIYFVSFVLTAQFVLNVVIVIAVMKHEESN	1840
Db	1801	STGDNWNGIMKDTLRDCCQESTCYNTVISPFIYFVSFVLTAQFVLNVVIVIAVMKHEESN	1860
Qy	1841	KEAKEEAELEAELEEMKTLSPQHSPLGSPPLMFGVEGPDSPSKPCALHAAHARSA	1900
Db	1861	KEAKEEAELEAELEEMKTLSPQHSPLGSPPLMFGVEGPDSPSKPCALHAAHARSA	1920
Qy	1901	SHFSLEHPTMOPHTPELP---GPDLLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLGHRG	1957
Db	1921	SGFSLEHPTMOPHTPELP---GPDLLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLGHRG	1980
Qy	1958	WGLPKAQSGLSVLSVHSPADTSTYIQLPKDAPHLOPHSAPTWTGTPKLPFGPSPLAQR	2017
Db	1981	WGLPKAQSGLSVLSVHSPADTSTYIQLPKDAPHLOPHSAPTWTGTPKLPFGPSPLAQR	2040
Qy	2018	PLRRQAARTDSDLVQGLGSRDILLAEVSGPPLARAVSFWGOSSTOACQHSRSHKIS	2077
Db	2041	PLRRQAARTDSDLVQGLGSRDILLAEVSGPPLARAVSFWGOSSTOACQHSRSHKIS	2100
Qy	2078	KHMTPPAPCPGPEPNWKGPPETRSLELDTLSWISGDLPLPPGQEPPEPPSPRDLKKYS	2137
Db	2101	KHMTPPAPCPGPEPNWKGPPETRSLELDTLSWISGDLPLPPGQEPPEPPSPRDLKKYS	2159
Qy	2138	VEAQSQRPRPTSMWLDQRRHSIAVCLDSGSPHLGTDPNLSGQPLGGQPLGGPSRPPKLLSP	2197
Db	2160	VEAQSQRPRPTSMWLDQRRHSIAVCLDSGSPHLGTDPNLSGQPLGGQPLGGPSRPPKLLSP	2219
Qy	2198	PSITIDPPSQGPRTPPSFGICLRRAPSDSKDPLASGPPDSMAASPSPKDVLISGL	2257
Db	2220	PSITIDPPSQGPRTPPSFGICLRRAPSDSKDPLASGPPDSMAASPSPKDVLISGL	2279
Qy	2258	SSDPADLDP 2266	
Db	2280	SSDPTDMDP 2288	
RESULT 4			
CCAG RAT			
ID	CCAG RAT	STANDARD;	PRT; 2254 AA.
AC	OS4898;		
DT	15-JUL-1999	(Rel. 38, Created)	
DT	15-JUL-1999	(Rel. 38, Last sequence update)	
DT	05-JUL-2004	(Rel. 44, Last annotation update)	
DE	Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-		
DE	gated calcium channel alpha subunit Cav3.1).		
GN	Name=Cacnalg;		

OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN: Sprague-Dawley; TISSUE: Brain;
 RX MEDLINE=98154730; PubMed=9495342;
 RA Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J.,
 RA Williamson M.P., Fox M., Rees M., Lee J.-H.;
 RT "Molecular characterization of a neuronal low-voltage-activated T-type
 RL calcium channel.";
 CC Nature 391:896-900(1998).
 CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
 CC entry of calcium ions into excitable cells and are also involved
 CC in a variety of calcium-dependent processes, including muscle
 CC contraction, hormone or neurotransmitter release, gene expression,
 CC cell motility, cell division and cell death. The isoform alpha-1G
 CC gives rise to T-type calcium currents. T-type calcium channels
 CC belong to the "low-voltage activated (LVA)" group and are strongly
 CC blocked by nickel and mibefradil. A particularity of this type of
 CC channels is an opening at quite negative potentials and a voltage-
 CC dependent inactivation. T-type channels serve pacemaking functions
 CC in both central neurons and cardiac nodal cells and support
 CC calcium signaling in secretory cells and vascular smooth muscle.
 CC They may also be involved in the modulation of firing patterns of
 CC neurons which is important for information processing as well as
 CC in cell growth processes.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Moderate expression
 CC in heart; low expression in placenta, kidney and lung.
 CC -!- DOMAIN: Each of the four internal repeats contains five
 CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
 CC positively charged transmembrane segment (S4). S4 segments
 CC probably represent the voltage-sensor and are characterized by a
 CC series of positively charged amino acids at every third position.
 CC -!- PTM: In response to raising of intracellular calcium, the T-type
 CC channels are activated by CaM-kinase II.
 CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
 CC family.
 CC -----
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 CC -----
 DR EMBL; AF027984; AAC67372.1; -.
 DR FIR; T09053; T09053.
 DR RGD; 68942; Cacna1g.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M-channel_nlg.
 DR Pfam; PF00520; TVDCCAlphal.
 DR PRINTS; PR01629; TVDCCALPHAL.
 KW Calcium channel; Calcium-binding; Glycoprotein; Ion transport;
 KW Ionic channel; Multigene family; Phosphorylation; Repeat;
 KW Transmembrane; Voltage-gated channel.
 FT REPEAT 68 398 I.
 FT REPEAT 730 968 II.
 FT REPEAT 1242 1519 III.
 FT REPEAT 1564 1822 IV.
 FT DOMAIN 1 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 101 S1 of repeat I.
 FT DOMAIN 102 119 Extracellular (Potential).
 FT TRANSMEM 120 141 S2 of repeat I (Potential).
 FT DOMAIN 142 150 Cytoplasmic (Potential).
 FT TRANSMEM 151 170 S3 of repeat I.
 FT DOMAIN 171 175 Extracellular (Potential).

FT	TRANSMEM	176	193	S4 of repeat I.
FT	DOMAIN	194	213	Cytoplasmic (Potential).
FT	TRANSMEM	214	234	S5 of repeat I (Potential).
FT	DOMAIN	235	270	Extracellular (Potential).
FT	TRANSMEM	271	295	S6 of repeat I.
FT	DOMAIN	296	344	Cytoplasmic (Potential).
FT	TRANSMEM	345	375	S1 of repeat II (Potential).
FT	DOMAIN	376	406	Extracellular (Potential).
FT	TRANSMEM	407	437	S2 of repeat II (Potential).
FT	DOMAIN	438	468	Cytoplasmic (Potential).
FT	TRANSMEM	469	500	S3 of repeat II (Potential).
FT	DOMAIN	501	531	Extracellular (Potential).
FT	TRANSMEM	532	562	S4 of repeat II (Potential).
FT	DOMAIN	563	593	Cytoplasmic (Potential).
FT	TRANSMEM	594	624	S5 of repeat II (Potential).
FT	DOMAIN	625	655	Extracellular (Potential).
FT	TRANSMEM	656	686	S6 of repeat II (Potential).
FT	DOMAIN	687	717	Cytoplasmic (Potential).
FT	TRANSMEM	718	748	S1 of repeat III (Potential).
FT	DOMAIN	749	779	Extracellular (Potential).
FT	TRANSMEM	780	810	S2 of repeat III (Potential).
FT	DOMAIN	811	841	Cytoplasmic (Potential).
FT	TRANSMEM	842	872	S3 of repeat III (Potential).
FT	DOMAIN	873	903	Extracellular (Potential).
FT	TRANSMEM	904	934	S4 of repeat III (Potential).
FT	DOMAIN	935	965	Cytoplasmic (Potential).
FT	TRANSMEM	966	996	S5 of repeat III (Potential).
FT	DOMAIN	997	1027	Extracellular (Potential).
FT	TRANSMEM	1028	1058	S6 of repeat III (Potential).
FT	DOMAIN	1059	1089	Cytoplasmic (Potential).
FT	TRANSMEM	1090	1120	S1 of repeat IV (Potential).
FT	DOMAIN	1121	1151	Extracellular (Potential).
FT	TRANSMEM	1152	1182	S2 of repeat IV (Potential).
FT	DOMAIN	1183	1213	Cytoplasmic (Potential).
FT	TRANSMEM	1214	1244	S3 of repeat IV (Potential).
FT	DOMAIN	1245	1275	Extracellular (Potential).
FT	TRANSMEM	1276	1306	S4 of repeat IV (Potential).
FT	DOMAIN	1307	1337	Cytoplasmic (Potential).
FT	TRANSMEM	1338	1368	S5 of repeat IV (Potential).
FT	DOMAIN	1369	1399	Extracellular (Potential).
FT	TRANSMEM	1400	1430	S6 of repeat IV (Potential).
FT	DOMAIN	1431	1461	Cytoplasmic (Potential).
FT	TRANSMEM	1462	1492	S1 of repeat V (Potential).
FT	DOMAIN	1493	1523	Extracellular (Potential).
FT	TRANSMEM	1524	1554	S2 of repeat V (Potential).
FT	DOMAIN	1555	1585	Cytoplasmic (Potential).
FT	TRANSMEM	1586	1616	S3 of repeat V (Potential).
FT	DOMAIN	1617	1647	Extracellular (Potential).
FT	TRANSMEM	1648	1678	S4 of repeat V (Potential).
FT	DOMAIN	1679	1709	Cytoplasmic (Potential).
FT	TRANSMEM	1710	1740	S5 of repeat V (Potential).
FT	DOMAIN	1741	1771	Extracellular (Potential).
FT	TRANSMEM	1772	1802	S6 of repeat V (Potential).
FT	DOMAIN	1803	1833	Cytoplasmic (Potential).
FT	TRANSMEM	1834	1864	S1 of repeat VI (Potential).
FT	DOMAIN	1865	1895	Extracellular (Potential).
FT	TRANSMEM	1896	1926	S2 of repeat VI (Potential).
FT	DOMAIN	1927	1957	Cytoplasmic (Potential).
FT	TRANSMEM	1958	1988	S3 of repeat VI (Potential).
FT	DOMAIN	1989	2019	Extracellular (Potential).
FT	TRANSMEM	2020	2050	S4 of repeat VI (Potential).
FT	DOMAIN	2051	2081	Cytoplasmic (Potential).
FT	TRANSMEM	2082	2112	S5 of repeat VI (Potential).
FT	DOMAIN	2113	2143	Extracellular (Potential).
FT	TRANSMEM	2144	2174	S6 of repeat VI (Potential).
FT	DOMAIN	2175	2205	Cytoplasmic (Potential).
FT	TRANSMEM	2206	2236	S1 of repeat VII (Potential).
FT	DOMAIN	2237	2267	Extracellular (Potential).
FT	TRANSMEM	2268	2298	S2 of repeat VII (Potential).
FT	DOMAIN	2299	2329	Cytoplasmic (Potential).
FT	TRANSMEM	2330	2360	S3 of repeat VII (Potential).
FT	DOMAIN	2361	2391	Extracellular (Potential).
FT	TRANSMEM	2392	2422	S4 of repeat VII (Potential).
FT	DOMAIN	2423	2453	Cytoplasmic (Potential).
FT	TRANSMEM	2454	2484	S5 of repeat VII (Potential).
FT	DOMAIN	2485	2515	Extracellular (Potential).
FT	TRANSMEM	2516	2546	S6 of repeat VII (Potential).
FT	DOMAIN	2547	2577	Cytoplasmic (Potential).
FT	TRANSMEM	2578	2608	S1 of repeat VIII (Potential).
FT	DOMAIN	2609	2639	Extracellular (Potential).
FT	TRANSMEM	2640	2670	S2 of repeat VIII (Potential).
FT	DOMAIN	2671	2701	Cytoplasmic (Potential).
FT	TRANSMEM	2702	2732	S3 of repeat VIII (Potential).
FT	DOMAIN	2733	2763	Extracellular (Potential).
FT	TRANSMEM	2764	2794	S4 of repeat VIII (Potential).
FT	DOMAIN	2795	2825	Cytoplasmic (Potential).
FT	TRANSMEM	2826	2856	S5 of repeat VIII (Potential).
FT	DOMAIN	2857	2887	Extracellular (Potential).
FT	TRANSMEM	2888	2918	S6 of repeat VIII (Potential).
FT	DOMAIN	2919	2949	Cytoplasmic (Potential).
FT	TRANSMEM	2950	2980	S1 of repeat IX (Potential).
FT	DOMAIN	2981	3011	Extracellular (Potential).
FT	TRANSMEM	3012	3042	S2 of repeat IX (Potential).
FT	DOMAIN	3043	3073	Cytoplasmic (Potential).
FT	TRANSMEM	3074	3104	S3 of repeat IX (Potential).
FT	DOMAIN	3105	3135	Extracellular (Potential).
FT	TRANSMEM	3136	3166	S4 of repeat IX (Potential).
FT	DOMAIN	3167	3197	Cytoplasmic (Potential).
FT	TRANSMEM	3198	3228	S5 of repeat IX (Potential).
FT	DOMAIN	3229	3259	Extracellular (Potential).
FT	TRANSMEM	3260	3290	S6 of repeat IX (Potential).
FT	DOMAIN	3291	3321	Cytoplasmic (Potential).
FT	TRANSMEM	3322	3352	S1 of repeat X (Potential).
FT	DOMAIN	3353	3383	Extracellular (Potential).
FT	TRANSMEM	3384	3414	S2 of repeat X (Potential).
FT	DOMAIN	3415	3445	Cytoplasmic (Potential).
FT	TRANSMEM	3446	3476	S3 of repeat X (Potential).
FT	DOMAIN	3477	3507	Extracellular (Potential).
FT	TRANSMEM	3508	3538	S4 of repeat X (Potential).
FT	DOMAIN	3539	3569	Cytoplasmic (Potential).
FT	TRANSMEM	3570	3600	S5 of repeat X (Potential).
FT	DOMAIN	3601	3631	Extracellular (Potential).
FT	TRANSMEM	3632	3662	S6 of repeat X (Potential).
FT	DOMAIN	3663	3693	Cytoplasmic (Potential).
FT	TRANSMEM	3694	3724	S1 of repeat XI (Potential).
FT	DOMAIN	3725	3755	Extracellular (Potential).
FT	TRANSMEM	3756	3786	S2 of repeat XI (Potential).
FT	DOMAIN	3787	3817	Cytoplasmic (Potential).
FT	TRANSMEM	3818	3848	S3 of repeat XI (Potential).
FT	DOMAIN	3849	3879	Extracellular (Potential).
FT	TRANSMEM	3880	3910	S4 of repeat XI (Potential).
FT	DOMAIN	3911	3941	Cytoplasmic (Potential).
FT	TRANSMEM	3942	3972	S5 of repeat XI (Potential).
FT	DOMAIN	3973	4003	Extracellular (Potential).
FT	TRANSMEM	4004	4034	S6 of repeat XI (Potential).
FT	DOMAIN	4035	4065	Cytoplasmic (Potential).
FT	TRANSMEM	4066	4096	S1 of repeat XII (Potential).
FT	DOMAIN	4097	4127	Extracellular (Potential).
FT	TRANSMEM	4128	4158	S2 of repeat XII (Potential).
FT	DOMAIN	4159	4189	Cytoplasmic (Potential).
FT	TRANSMEM	4190	4220	S3 of repeat XII (Potential).
FT	DOMAIN	4221	4251	Extracellular (Potential).
FT	TRANSMEM	4252	4282	S4 of repeat XII (Potential).
FT	DOMAIN	4283	4313	Cytoplasmic (Potential).
FT	TRANSMEM	4314	4344	S5 of repeat XII (Potential).
FT	DOMAIN	4345	4375	Extracellular (Potential).
FT	TRANSMEM	4376	4406	S6 of repeat XII (Potential).
FT	DOMAIN	4407	4437	Cytoplasmic (Potential).
FT	TRANSMEM	4438	4468	S1 of repeat XIII (Potential).
FT	DOMAIN	4469	4499	Extracellular (Potential).
FT	TRANSMEM	4500	4530	S2 of repeat XIII (Potential).
FT	DOMAIN	4531	4561	Cytoplasmic (Potential).
FT	TRANSMEM	4562	4592	S3 of repeat XIII (Potential).
FT	DOMAIN	4593	4623	Extracellular (Potential).
FT	TRANSMEM	4624	4654	S4 of repeat XIII (Potential).
FT	DOMAIN	4655	4685	Cytoplasmic (Potential).
FT	TRANSMEM	4686	4716	S5 of repeat XIII (Potential).
FT	DOMAIN	4717	4747	Extracellular (Potential).
FT	TRANSMEM	4748	4778	S6 of repeat XIII (Potential).
FT	DOMAIN	4779	4809	Cytoplasmic (Potential).
FT	TRANSMEM	4810	4840	S1 of repeat XIV (Potential).
FT	DOMAIN	4841	4871	Extracellular (Potential).
FT	TRANSMEM	4872	4902	S2 of repeat XIV (Potential).
FT	DOMAIN	4903	4933	Cytoplasmic (Potential).
FT	TRANSMEM	4934	4964	S3 of repeat XIV (Potential).
FT	DOMAIN	4965	4995	Extracellular (Potential).
FT	TRANSMEM	4996	5026	S4 of repeat XIV (Potential).
FT	DOMAIN	5027	5057	Cytoplasmic (Potential).
FT	TRANSMEM	5058	5088	S5 of repeat XIV (Potential).
FT	DOMAIN	5089	5119	Extracellular (Potential).
FT	TRANSMEM	5120	5150	S6 of repeat XIV (Potential).
FT	DOMAIN	5151	5181	Cytoplasmic (Potential).
FT	TRANSMEM	5182	5212	S1 of repeat XV (Potential).
FT	DOMAIN	5213	5243	Extracellular (Potential).
FT	TRANSMEM	5244	5274	S2 of repeat XV (Potential).
FT	DOMAIN	5275	5305	Cytoplasmic (Potential).
FT	TRANSMEM	5306	5336	S3 of repeat XV (Potential).
FT	DOMAIN	5337	5367	Extracellular (Potential).
FT	TRANSMEM	5368	5398	S4 of repeat XV (Potential).
FT	DOMAIN	5399	5429	Cytoplasmic (Potential).
FT	TRANSMEM	5430	5460	S5 of repeat XV (Potential).
FT	DOMAIN	5461	5491	Extracellular (Potential).
FT	TRANSMEM	5492	5522	S6 of repeat XV (Potential).
FT	DOMAIN	5523	5553	Cytoplasmic (Potential).
FT	TRANSMEM	5554	5584	S1 of repeat XVI (Potential).
FT	DOMAIN	5585	5615	Extracellular (Potential).
FT	TRANSMEM	5616	5646	S2 of repeat XVI (Potential).
FT	DOMAIN	5647	5677	Cytoplasmic (Potential).
FT	TRANSMEM	5678	5708	S3 of repeat XVI (Potential).
FT	DOMAIN	5709	5739	Extracellular (Potential).
FT	TRANSMEM	5740	5770	S4 of repeat XVI (Potential).
FT	DOMAIN	5771	5801	Cytoplasmic (Potential).
FT	TRANSMEM	5802	5832	S5 of repeat XVI (Potential).
FT	DOMAIN	5833	5863	Extracellular (Potential).
FT	TRANSMEM	5864	5894	S6 of repeat XVI (Potential).
FT	DOMAIN	5895	5925	Cytoplasmic (Potential).
FT	TRANSMEM	5926	5956	S1 of repeat XVII (Potential).
FT	DOMAIN	5957	5987	Extracellular (Potential).
FT	TRANSMEM	5988	6018	S2 of repeat XVII (Potential).
FT	DOMAIN	6019	6049	Cytoplasmic (Potential).
FT	TRANSMEM	6050	6080	S3 of repeat XVII (Potential).
FT	DOMAIN	6081	6111	Extracellular (Potential).
FT	TRANSMEM	6112	6142	S4 of repeat XVII (Potential).
FT	DOMAIN	6143	6173	Cytoplasmic (Potential).
FT	TRANSMEM	6174	6204	S5 of repeat XVII (Potential).
FT	DOMAIN	6205	6235	Extracellular (Potential).
FT	TRANSMEM	6236	6266	S6 of repeat XVII (Potential).
FT	DOMAIN	6267	6297	Cytoplasmic (Potential).
FT	TRANSMEM	6298	6328	S1 of repeat XVIII (Potential).
FT	DOMAIN	6329	6359	Extracellular (Potential).
FT	TRANSMEM	6360	6390	S2 of repeat XVIII (Potential).
FT	DOMAIN	6391	6421	Cytoplasmic (Potential).
FT	TRANSMEM	6422	6452	S3 of repeat XVIII (Potential).
FT	DOMAIN	6453	6483	Extracellular (Potential).
FT	TRANSMEM	6484	6514	S4 of repeat XVIII (Potential).
FT	DOMAIN	6515	6545	Cytoplasmic (Potential).
FT	TRANSMEM	6546	6576	S5 of repeat XVIII (Potential).
FT	DOMAIN	6577	6607	Extracellular (Potential).
FT	TRANSMEM	6608	6638	S6 of repeat XVIII (Potential).
FT	DOMAIN	6639	6669	Cytoplasmic (Potential).
FT	TRANSMEM	6670	6700	S1 of repeat XIX (Potential).
FT	DOMAIN	6701	6731	Extracellular (Potential).
FT	TRANSMEM	6732	6762	S2 of repeat XIX (Potential).
FT	DOMAIN	6763	6793	Cytoplasmic (Potential).
FT	TRANSMEM	6794	6824	S3 of repeat XIX (Potential).
FT	DOMAIN	6825	6855	Extracellular (Potential).
FT	TRANSMEM	6856	6886	S4 of repeat XIX (Potential).
FT	DOMAIN	6887	6917	Cytoplasmic (Potential).
FT	TRANSMEM	6918	6948	S5 of repeat XIX (Potential).
FT	DOMAIN	6949	6979	Extracellular (Potential).
FT	TRANSMEM	6980	7010	S6 of repeat XIX (Potential).
FT	DOMAIN	7011	7041	Cytoplasmic (Potential).
FT	TRANSMEM	7042	7072	S1 of repeat XX (Potential).
FT	DOMAIN	7073	7103	Extracellular (Potential).
FT	TRANSMEM	7104	7134	S2 of repeat XX (Potential).
FT	DOMAIN	7135	7165	Cytoplasmic (Potential).
FT	TRANSMEM	7166	7196	S3 of repeat XX (Potential).

Db 61 FFYLSQDSRPSWCLRTVCPWPFRVSMVLVILLNCVTLGMRPCEDACDSQRCRILQAF 120
Qy 121 DDFIFAFFAVMMVMMVALGIFGKKCYLGDTPWNRDLPFIVTAGMLEYSLDLQNVFSFAVR 180
Db 121 DDFIFAFFAVMMVMMVALGIFGKKCYLGDTPWNRDLPFIVTAGMLEYSLDLQNVFSFAVR 180
Qy 181 TVRVLRPLRALNRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQVMAGLLNR 240
Db 181 TVRVLRPLRALNRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQVMAGLLNR 240
Qy 241 CFLPENFSLPLSVDLERYQOTENEDESPFIQSPRENQWRSRCSVPTLRGGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYQOTENEDESPFIQSPRENQWRSRCSVPTLRGGGGPPCGL 300
Qy 301 DYEAYNSSNTTCVNMNQYNTCSAGEHNPFGAIFNIGNIYAWTAIFQVITLEGWVDM 360
Db 301 DYEAYNSSNTTCVNMNQYNTCSAGEHNPFGAIFNIGNIYAWTAIFQVITLEGWVDM 360
Qy 361 YFVMDAHGFYFIYFILLIIVGFFMINCLVVIATQFSETKORESOLMREORVFLSNA 420
Db 361 YFVMDAHGFYFIYFILLIIVGFFMINCLVVIATQFSETKORESOLMREORVFLSNA 420
Qy 421 STLASFSPGSCYEELLKVLVILKAAARLAQVSRAGVRVGLLSSPAPLGQGTQPS 480
Db 421 STLASFSPGSCYEELLKVLVILKAAARLAQVSRAGVRVGLLSSPAPLGQGTQPS 480
Qy 481 SCRSRHRKLSVHLVHHHHHHHHVHLGNGTLPAPASPEIQORDANGSRRLMLPPSTP 540
Db 481 SCRSRHRKLSVHLVHHHHHHHHVHLGNGTLPAPASPEIQORDANGSRRLMLPPSTP 540
Qy 541 ALSGAPPGAEVSFHYADCHLEPVRCOAPPRSPSEASGRVTGSGKYPTVHTSPPE 600
Db 541 TSGGPPRGAESVHSFYADCHLEPVRCOAPPRSPSEASGRVTGSGKYPTVHTSPPE 600
Qy 601 TLKEKALVEAASSGPPTLSLNIIPGYSMEKLELTOSTGACOSSCKISSPCUKADSG 660
Db 601 ILKDKALVEAVSPGPPTLSFNIIPGYSMEKLELTOSTGACHSSCKISSPCSKADSG 660
Qy 661 ACPGSCPCYCARAGAGEVELAREMPDSDSEAVYETQDAQSDLDPHS-RRQSLGPD 719
Db 661 ACPGSCPCYCARAGAGEVELAREMPDSDSEAVYETQDAQSDLDPHSRRQSLGPD 720
Qy 720 AEPSSVLAFLRLCDTFRKIVDSYFGRGIMIALVNTLSMGLEYHQEPEELTNALEISN 779
Db 721 AEPSSVLAFLRLCDTFRKIVDSYFGRGIMIALVNTLSMGLEYHQEPEELTNALEISN 780
Qy 780 IVFTSLFALEMLLKLVYGFPGYIKNPYINFDGVIIVISWEIVGQGGGLSVLRTFLM 839
Db 781 IVFTSLFALEMLLKLVYGFPGYIKNPYINFDGVIIVISWEIVGQGGGLSVLRTFLM 840
Qy 840 RVLKLVRFPLALORQLVLMKTDNATFCMLMLFIFISILGMHLFGCKFASERDGT 899
Db 841 RVLKLVRFPLALORQLVLMKTDNATFCMLMLFIFISILGMHLFGCKFASERDGT 900
Qy 900 LPDRKNFDSLALVTVFQLLTQEDMKNVLYNGMASTSSWAALYFIALMTFGNYVLFNL 959
Db 901 LPDRKNFDSLALVTVFQLLTQEDMKNVLYNGMASTSSWAALYFIALMTFGNYVLFNL 960
Qy 960 VAILVEGFQAEIISKREDASQSLSCIQLPVDSQGGDANKSESEDPFSPSLDGDGRKKC 1019
Db 961 VAILVEGFQAEIISKREDASQSLSCIQLPVDSQGGDANKSESEDPFSPSLDGDGRKKR 997
Qy 1020 LALVSLGEHPELRKSLPLPILIHATAATPMSLPKSTSTGLGEALGPASRRTSSSGSAPGA 1079
Db 998 LALVSLGEHPELRKSLPLPILIHATAATPMSHPKSSSTGVGEALGSGRRRTSSSGSAPGA 1057
Qy 1080 A-HEMKPPSARSPHSPGSAASSWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEGOE 1138
Db 1058 AHHEMKPPSARSPHSPGSAASSWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEGOE 1117
Qy 1139 SQDEESESBERASPAGSDHHRGSLREAKSSFDLPTTQVPLGHLHTASGRGSASHOD 1198
Db 1118 SQDEESESBERASPAGSDHHRGSLREAKSSFDLPTTQVPLGHLHTASGRGSASHOD 1177

Qy 1199 CNGKSASGRALARLPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258
Db 1178 CNGKSASGRALARLTDDPQLDGDADDDEGNLSKGERIQAWVRSLPACCRERDSWSAYI 1237
Qy 1259 FPPQSRFRLCHRIITHKMFEDHVVLVIFLNCITIAMERPKIDPHSAERIEFLTISNYIFT 1318
Db 1238 FPPQSRFRLCHRIITHKMFEDHVVLVIFLNCITIAMERPKIDPHSAERIEFLTISNYIFT 1297
Qy 1319 AVFLAEMTVKVALGWCFGEQAYLRSSNMVLDGLLVILISVIDILVSMVSDSGTKILGMLR 1378
Db 1298 AVFLAEMTVKVALGWCFGEQAYLRSSNMVLDGLLVILISVIDILVSMVSDSGTKILGMLR 1357
Qy 1379 VLRLRLTLRPLRVISRAQGLKLVVETLMSLSKPIGNIVVICAPPIIFGILGVQLFKGKF 1438
Db 1358 VLRLRLTLRPLRVISRAQGLKLVVETLMSLSKPIGNIVVICAPPIIFGILGVQLFKGKF 1417
Qy 1439 FVCOGEDTRNTKNSDCAEASYRVRHKYNFNDLGOALMSLFLVLASKDQWVDIMYDGLDA 1498
Db 1418 FVCOGEDTRNTKNSDCAEASYRVRHKYNFNDLGOALMSLFLVLASKDQWVDIMYDGLDA 1477
Qy 1499 VGVDQOPIMNHPWMLLYFISFLITVAFVFLNMFGVVVNFPHKCRHQHEEERREBK 1558
Db 1478 VGVDQOPIMNHPWMLLYFISFLITVAFVFLNMFGVVVNFPHKCRHQHEEERREBK 1537
Qy 1559 RLRLLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVLGNVVTMA 1611
Db 1538 RLRLLEKKRRSKEQMAEAOCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVLGNVVTMA 1597
Qy 1612 MEHYQOQPOLDEALKICNYIFTVIVLESVKLVAFGRPRFPQDRWNOLDLAILVLSIMG 1671
Db 1598 MEHYQOQPOLDEALKICNYIFTVIVLESVKLVAFGRPRFPQDRWNOLDLAILVLSIMG 1657
Qy 1672 ITLEIEVNASUPINPTIIRIMRVLIARVLKLLXMAVGMRALDITVMQALPQVGNLGLL 1731
Db 1658 ITLEIEVNLSPINPTIIRIMRVLIARVLKLLXMAVGMRALDITVMQALPQVGNLGLL 1717
Qy 1732 FMLLFFIFAALGVLEFGDCEDETHPCBGLGHATFRNPGMAFLTLFRVSTGDNWNGIMK 1791
Db 1718 FMLLFFIFAALGVLEFGDCEDETHPCBGLGHATFRNPGMAFLTLFRVSTGDNWNGIMK 1777
Qy 1792 DTLRCDQBSTCYNTVISEIYFVSFVLTAQFVLVNVVIAVLMKHLEESKEAKEAELEA 1851
Db 1778 DTLRCDQBSTCYNTVISEIYFVSFVLTAQFVLVNVVIAVLMKHLEESKEAKEAELEA 1837
Qy 1852 ELELEMKTLSPHSPGLSPFLWPVGEGPSPDPSKPGALHPAAHARSASHFSLEHTWQ 1911
Db 1838 ELELEMKTLSPHSPGLSPFLWPVGEGVNTDPSKPGAPHTTAHIGAASGFSLEHTWV 1897
Qy 1912 PHPTLP---GPDLLTVRKSGVSRTHSLPNDSYMCHRGSTAEGLCHRGWGLPKAQSGSV 1968
Db 1898 PHPEEVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLCHRGWGLPKAQSGSI 1957
Qy 1969 LSVHSPADTSYTLQPKDAPHLOPHSAPTWTCTIKLPPPGPSPLAQPRRQAIRTD 2028
Db 1958 LSVHSPADTSYTLQPKDAPHLOPHSAPTWTCTIKLPPPGPSPLAQPRRQAIRTD 2017
Qy 2029 SLIDVQGLSGREDLLAEVSGPSPPLARAYSFWGOSSTQAOQHSRSHSKLSKXMTPTPAPCPG 2088
Db 2018 SLIDVQGLSGREDLLAEVSGPSPCLTRSSFWGSSSIQVQORSGIQKSVKHLRLPAPCPG 2077
Qy 2089 PEPNWKGPPTASSILELTELWISGDLLPPGQEPPEPSPRDLKKCYVEACORRPT 2148
Db 2078 LEPSWAKDPPETRSLSLELTELWISGDLL-PSQEPPLFRDLKKCYVETQSCRRPG 2136
Qy 2149 SWLDEORRHIAVCLDSGSGOPHLGTDPSNLGQPLGGPSRPKKLSLSPSITIDPPESQ 2208
Db 2137 FWLDEORRHIAVCLDSGSGOPRLCPSPSLGGQPLGGPSRPKKLSLSPSISIDPPESQ 2196
Qy 2209 GPRTPSPSGTCLRRRASPSSDKPLASGPPDMAASPSPKXVLSLGLSSDPAADLP 2266
Db 2197 GSRPPCPGVCLRRRASPSSDKPVSPLDSTAASPSPKKDTLSLGLSSDPTMDP 2254

RP	RC	RA	RL	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	
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DR	EMBL; BC057399; AAH57399.1; -;	Seq	SEQUENCE	2248 AA; 248888 MW; 332CSA8D9115A64F CRC64;
	Query Match		91.7%; Score 10913; DB 2; Length 2248;	
	Best Local Similarity		92.0%; Pred. No. 0;	
	Matches 2106; Conservative		30; Mismatches 69; Indels 64; Gaps 7;	
QY	1	MDEEDGAGAEESGQPRSFWRINDLSGAGRGPGSAEKDPCGSADSEAGLVPALAPV	60	
DB	1	MDEEDGAGAEESGQPRSFQTLNDLSGAGRGPGSTKDPGSADEAGLVPALAPV	60	
QY	61	FFYLSQDSRPRSCLRTVCMNPFERISMLVILLNCVTILGMFRPCEDIAQSQRILQAF	120	
DB	61	FFYLSQDSRPRSCLRTVCMNPFERSMLVILLNCVTILGMFRPCEDIAQSQRILQAF	120	
QY	121	DDTFAFAFVEMVVKMVALGIPKKCYLGGDTWRLDFFIVIAQMLYSLDLQWSPSAYR	180	
DB	121	DDTFAFAFVEMVVKMVALGIFGKKCYLGGDTWRLDFFIVIAQMLYSLDLQWSPSAYR	180	
QY	181	TVRVLRPLRAINRVPSRIILVTLLDPLMLGNVLLCPFVFIIFGIVGVQLWAGLLRNR	240	
DB	181	TVRVLRPLRAINRVPSRIILVTLLDPLMLGNVLLCPFVFIIFGIVGVQLWAGLLRNR	240	
QY	241	CFLPENFSLPLSVDLERYITENEDESPFIQSPRENGMRSCTSVPTLRDGGGGPPCGL	300	
DB	241	CFLPENFSLPLSVDLERYITENEDESPFIQSPRENGMRSCTSVPTLRDGGGGPPCGL	300	
QY	301	DYEAYNSSNTTCVNNQYVYTCNSAGHNPKGAINFDNIGYAWIAFOVITILEGWMDIM	360	
DB	301	DYEAYNSSNTTCVNNQYVYTCNSAGHNPKGAINFDNIGYAWIAFOVITILEGWMDIM	360	
QY	361	YFVMDAHSFYNYFIYFILLIIVGSPFMINCLVLIATQFSETKQRESQLMREQVRFLSNA	420	
DB	361	YFVMDAHSFYNYFIYFILLIIVGSPFMINCLVLIATQFSETKQRESQLMREQVRFLSNA	403	
QY	421	STLASFSPPGSCYBELLYLVIILRKARLIAQVSRAGVRVGLLSSPAPLGQETQPS	480	
DB	404	STLASFSPPGSCYBELLYLVIILRKARLIAQVSRAGVRVGLLSSPAPLGQETQPS	463	
QY	481	SCSRSHRLSVVHLLVHHHHHHHHVHLNGTLAPRASPEIQORDANGSRRLMLPPSTP	540	
DB	464	SCSRSHRLSVVHLLVHHHHHHHHVHLNGTLAPRASPEIQORDANGSRRLMLPPSTP	523	
QY	541	ALSGAPPAGBSVHSFYHADCHLBPVRQAPPPSPSEAGRTVGSQKVTPTVHTSPPE	600	
DB	524	TPSGGPPRAGBSVHSFYHADCHLBPVRQAPPPSPSEAGRTVGSQKVTPTVHTSPPE	583	
QY	601	TLKEALYVEVAASGPPTLTSLNTPPGYPSSMHMLKETQSTGACQSCCKTSSPCLKADSG	660	
DB	584	MLKDALYVEVAPSPGPTLTGPNTPPGFSSMHMLKETQSTGACHSSCKTSSPSCKADSG	643	
QY	661	ACGPDSCPYCARAGAGEVELADREMPDSDSAVYFTQDAQHSDLRDPHRRQRSLGPD	720	
DB	644	ACGPDSCPYCARTGAGEPESADHEMPDSDSAVYFTQDAQHSDLRDPHRRRPSLGP	703	
QY	721	EPSSVLAFWRLICDTERKIVDSKYPRGIMAILVNTLSMGIEVHEQPEELTNALET	780	
DB	704	EPSSVLAFWRLICDTERKIVDSKYPRGIMAILVNTLSMGIEVHEQPEELTNALET	763	
QY	781	VFTSLFALEMLKLLVYGPFGYIKNPYINFDGVIWISVWEIVQQGGGLSVLTFRLMR	840	
DB	764	VFTSLFALEMLKLLVYGPFGYIKNPYINFDGVIWISVWEIVQQGGGLSVLTFRLMR	823	
QY	841	VLLKVRFLPALORQLVLMKTMNDNVATFCMLIMLFIPTFSLGHMLFGCKFASRDEG	900	
DB	824	VLLKVRFLPALORQLVLMKTMNDNVATFCMLIMLFIPTFSLGHMLFGCKFASRDEG	883	
QY	901	PRKPNFDSLILWALVTVOILTQEDNKNVLYNGMASTSSWAALYFIALMTFGNYLVN	960	
DB	884	PRKPNFDSLILWALVTVOILTQEDNKNVLYNGMASTSSWAALYFIALMTFGNYLVN	943	
QY	961	ALLIVEQFAEEISKREDASQGLSCITQLPVDSCGGDANKSESEPFFSPSLDGDGRK	1020	

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QY 2078 KMTTPAPCPGPEPNWKGPPETRSSLELDTELSTWISGDLPLPGQEQEPPPPDRDLKKYS 2137
D 2061 KHIRLPAPCPGLEPWAQDPQETRSLELDTELSTWISGDLPLPGQEQEPPPPDRDLKKYS 2119
QY 2138 VEASQQRPTSWLDQRRHSIAVCLDSGQPHLGTDPNMGQPLGGPGSRPKKLSLSP 2197
D 2120 VEASQRRPGSWLDQRRHSIAVCLDSGQPHLGTDPNMGQPLGGPGSRPKKLSLSP 2179
QY 2198 PSITIDPESQPRTPPGICLRRAPSSDSKOPLASGPPDSMAASPPKKDVLISLGL 2257
D 2180 PSISIDPESQPRTPPGICLRRAPSSDSKOPLASGPPDSMAASPPKKDVLISLGL 2239
QY 2258 SSDPADLDP 2266
D 2240 SSDPTDLDP 2248

RESULT 8
Q62PX4
ID Q62PX4 PRELIMINARY; PRT; 1389 AA.
AC Q62PX4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIAA1123 protein (Fragment).
GN Name=MKIAA1123;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Brain;
PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Soga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT iii. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
EMBL: AK129294; BAC98104.1; -.
DR GO: GO:0005886; C:plasma membrane; IDA.
DR GO: GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR InterPro: IPR001692; Ca/Na_pore.
DR InterPro: IPR002111; Cat_channel_TripL.
DR InterPro: IPR002077; Ca_channel_alpha.
DR InterPro: IPR005821; Ion_trans_.
DR InterPro: IPR005820; M-channel_nlg.
DR Pfam: PF00520; Ion_trans; 2.
DR PRINTS: PR00167; CACHANNEL.
KW Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW Transmembrane; Transport; Voltage-gated channel.
FT NON TER 1
SQ SEQUENCE 1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;

Query Match 55.2%; Score 6573; DB 2; Length 1389;
Best Local Similarity 92.0%; Pred. No. 1.2e-294;
Matches 1279; Conservative 25; Mismatches 62; Indels 24; Gaps 5;

QY 900 LPDRKNFDSLWIAIVTVFQILTOEDWNKVLNGMASTSSWAALYFIALMTFGNYVFNLL 959
D 1 LPDRKNFDSLWIAIVTVFQILTOEDWNKVLNGMASTSSWAALYFIALMTFGNYVFNLL 60
QY 960 VAILVEGFOAEISKREDASQSLCQLPVDOSGGDANKSESPDFPSLDGDKRKC 1019
D 61 VAILVEGFOAEILCKREDTSQSLCQLPVDOSGGDATKSESPDFPSVDGDKRKR 120
QY 1020 LALVSLGHEPFLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA 1079
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Db 121 LALVALGSHSELKSLPLLIHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGT 180
QY 1080 A-HEMKSPSPARSPHSPWSAASWTSSRSRNSIGRAPSLKRRSPSGERSLSLGEQGE 1138
D 181 AHHEMKSPSPARSPHSPWSAASWTSSRSRNSIGRAPSLKRRSPSGERSLSLGEQGE 240
QY 1139 SODEESESSEERASAPAGSDHHRGSLEREAKSSFDLPDTLQVPGHLRTASGRGSAERHOD 1198
D 241 SODEESESSEERASAPAGSDHHRGSLEREAKSSFDLPDTLQVPGHLRTASGRGSAERHOD 300
QY 1199 CNGKSASGLARALRPDDPPLDGDADDDEGNLSXGERVAMIRARLPACYLERSWSAYI 1258
D 301 CNGKSASGLARALRPDDPPLDGDADDDEGNLSXGERVAMIRARLPACYLERSWSAYI 360
QY 1259 PPQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
D 361 PPQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 420
QY 1319 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLISVIDILVSMVSDSGTKILGMLR 1378
D 421 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLISVIDILVSMVSDSGTKILGMLR 480
QY 1379 VLRLRLTLRLPLRVISRAQGLKVVTETLMSSILKPIGNIVVICCAFFIIFGILGVLFKGF 1438
D 481 VLRLRLTLRLPLRVISRAQGLKVVTETLMSSILKPIGNIVVICCAFFIIFGILGVLFKGF 540
QY 1439 FVCGEDTRNITNKSDCAEASRWVRHKYFNDNLGQALMSIFVLASKDGWVIDMYDGLDA 1498
D 541 FVCGEDTRNITNKSDCAEASRWVRHKYFNDNLGQALMSIFVLASKDGWVIDMYDGLDA 600
QY 1499 VGVDOQPIMHNPWMLLYFISFLIIIVAFVNMFGVVVNFHFKCRHQHSEERAREEK 1558
D 601 VGVDOQPIMHNPWMLLYFISFLIIIVAFVNMFGVVVNFHFKCRHQHSEERAREEK 660
QY 1559 RLRRLEKKR-----KAQCPYYSDYSRFLLVHHLCTSHVLDLFI 1600
D 661 RLRRLEKKRNLDDVIASSGSSASAASEAQCPYYSDYSRFLLVHHLCTSHVLDLFI 720
QY 1601 GVTGLNVVTWAMEHYQQPQILDEALKICNYIFTVIFLESVFKLVAFGFRFFQDRWNQL 1660
D 721 GVTGLNVVTWAMEHYQQPQILDEALKICNYIFTVIFLESVFKLVAFGFRFFQDRWNQL 780
QY 1661 DLAIIVLLSINGITLIEIEVNASLPINPTIIRMRVLRARVLRKLLKMAVGRALLOTVMQ 1720
D 781 DLAIIVLLSINGITLIEIEVNASLPINPTIIRMRVLRARVLRKLLKMAVGRALLOTVMQ 840
QY 1721 ALPQVGNLGLLFFLFFIIFALGVLELFDLECDETHPCGELGRHATFRNFGMAFLTLFRV 1780
D 841 ALPQVGNLGLLFFLFFIIFALGVLELFDLECDETHPCGELGRHATFRNFGMAFLTLFRV 900
QY 1781 STGDNWNGIMKOTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVLAVLMKHLEESN 1840
D 901 STGDNWNGIMKOTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVLAVLMKHLEESN 960
QY 1841 KEAKEAEAELELEEMKTLSPHPSPLGSPFLWPQVEGPDSPDPSKPKGALHPAAHARS 1900
D 961 KEAKEAEAELELEEMKTLSPHPSPLGSPFLWPQVEGPDSPDPSKPKGALHPAAHARS 1020
QY 1901 SH-FSLEHTPMOPHTPELP---GPDLLTVRKSGVSRTHSIPNDSYMCRHGSTAEGLGHR 1956
D 1021 SSGFSLEHTPMOPHTPELP---GPDLLTVRKSGVSRTHSIPNDSYMCRHGSTAEGLGHR 1080
QY 1957 GMGLPKAQSGLSVSHSQPADTSYIQLPKDAPHILQPHSAPTWTGTIPKLPPLPPGSRPLAQ 2016
D 1081 GMGLPKAQSGLSVSHSQPADTSYIQLPKDAPHILQPHSAPTWTGTIPKLPPLPPGSRPLAQ 1140
QY 2017 RPLRQAAIIRTSLDVQGLGSRDELLAIVSGSPPLARAYSFWQSGSTQAQQRSHSKI 2076
D 1141 RPLRQAAIIRTSLDVQGLGSRDELLAIVSGSPPLARAYSFWQSGSTQAQQRSHSKI 1200
QY 2077 SKHMTPPAPCPGPEPNWKGPPETRSSLELDTELSTWISGDLPLPGQEQEPPPPDRDLKKY 2136
```

Db	1201	SKHRLPAPCGLEPSWAKDQETRSSELDTELSWISGDLI-PSSQEEPLSPDLKKCY	1259
Qy	2137	SVEAQSCORRFTSWLDEQRHSIAVSCLDGSGQPHLGTDPNMLGQPIGCGSRPKKLS	2196
Db	1260	SVEAQSCRRPGSWLDEQRHSIAVSCLDGSGQPHLGTDPNMLGQPIGCGSRPKKLS	1319
Qy	2197	PPSITIDPPESQGPRTSPGICLRRAPSSDKDFLAGPPDMAASPKKDVLSLG	2256
Db	1320	PPSISIDPPESQGPRTSPGICLRRAPSSDKDFLAGPPDMAASPKKDVLSLG	1379
Qy	2257	LSSDPADLDP 2266	
Db	1380	LSSDPTDLDP 1389	
RESULT 9			
ID	BAC98104	PRELIMINARY; PRT; 1389 AA.	
AC	BAC98104;		
DT	02-MAR-2004 (Tremblrel. 27, Created)		
DT	02-MAR-2004 (Tremblrel. 27, Last sequence update)		
DT	02-MAR-2004 (Tremblrel. 27, Last annotation update)		
DE	MKIAA1123 protein (Fragment).		
GN	MKIAA1123		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,		
RA	Saga Y., Nagase T., Ohara O., Koga H.;		
RT	"Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:		
RT	III. The Complete Nucleotide Sequences of 500 Mouse KIAA-homologous		
RT	cdNAs Identified by Screening of Terminal Sequences of cDNA Clones		
RT	Randomly Sampled from Size-fractionated Libraries."		
RL	DNA Res. 10:167-180(2003).		
DR	EMBL; AK129294; BAC98104.1; --		
FT	NON TER 1		
SQ	SEQUENCE 1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;		
Query Match			
Best Local Similarity 55.2%; Score 6573; DB 2; Length 1389;			
Matches 1279; Conservative 25; Mismatches 62; Indels 24; Gaps 5;			
Qy	900	LPDRKNFDSLLWAIVTFQILTOEDWNKVLNGMASTSSWAALYFIATMTFGNYVFNLL	959
Db	1	LPDRKNFDSLLWAIVTFQILTOEDWNKVLNGMASTSSWAALYFIATMTFGNYVFNLL	60
Qy	960	VALLVEGFOAEISKREDASGQSCICLPVDSQGGDANKSESPDFPSLDGGRKKC	1019
Db	61	VALLVEGFOAEISKREDASGQSCICLPVDSQGGDANKSESPDFPSLDGGRKKR	120
Qy	1020	LALVSGEHEPELRKSLPLLIHTAATPMSLTKSTGTGCEALGPASRRTSSSGSAEPGA	1079
Db	121	LALVSGEHEPELRKSLPLLIHTAATPMSLTKSTGTGCEALGPASRRTSSSGSAEPGT	180
Qy	1080	A-HEMKSPGARSPHSPWASASWTSRRSRNSLGRAPSKRSPSGERRSLLSGEGQE	1138
Db	181	AHEMKSPGARSPHSPWASASWTSRRSRNSLGRAPSKRSPSGERRSLLSGEGQE	240
Qy	1139	SQDEESSSEERASPGSDHRRGSLEREAKSSFDLPDTLOVPLHRTASGRSASEHQD	1198
Db	241	SQDEESSSEERASPGSDHRRGSLEREAKSSFDLPDTLOVPLHRTASGRSASEHQD	300
Qy	1199	CNGKSASGRLARLPDDPLDGDADDEGNLSKGERVRAWIRARLPACYLERSWSAYI	1258
Db	301	CNGKSASGRLARLPDDPLDGDADDEGNLSKGERVRAWIRARLPACYLERSWSAYI	360
Qy	1259	FPQOSRFLLCRITTHKMFHVVLVIIIFNCITIAMERPKIDPHSAERIFLTLSNYIFT	1318
Db	361	FPQOSRFLLCRITTHKMFHVVLVIIIFNCITIAMERPKIDPHSAERIFLTLSNYIFT	420

Qy	1319	AVELAEMTKVVALGWCFCGEQAYLRSSWNVLDDLIVISVIDILVSMVSDSTKILGMLR	1378
Db	421	AVELAEMTKVVALGWCFCGEQAYLRSSWNVLDDLIVISVIDILVSMVSDSTKILGMLR	480
Qy	1379	VRLRLRTLRLVLSRAQGLKLVVETLMSLKPIGNIVVICAFPIIFGILGVQPKGKF	1438
Db	481	VRLRLRTLRLVLSRAQGLKLVVETLMSLKPIGNIVVICAFPIIFGILGVQPKGKF	540
Qy	1439	FVCGEDTRNTNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKOGWDMYDGLDA	1498
Db	541	FVCGEDTRNTNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKOGWDMYDGLDA	600
Qy	1499	GVDOOPIMNENPMWLLYFISFLIVAFVLMFVGVVVENFHKCRQHQEEEAARRREK	1558
Db	601	GVDOOPIMNENPMWLLYFISFLIVAFVLMFVGVVVENFHKCRQHQEEEAARRREK	660
Qy	1559	RLRLLEKKRR-----KAQCKPYYSYSRPRLVHHLCTSHYLDLFT	1600
Db	661	RLRLLEKKRRLLMDDDVIASGSSASASEAQCKPYYSYSRPRLVHHLCTSHYLDLFT	720
Qy	1601	GVIGLNVVTMAHEHYQQQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNOL	1660
Db	721	GVIGLNVVTMAHEHYQQQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNOL	780
Qy	1661	DLAIVLLSIMGITLBEIEVNASLPIINPTIIRIMRVLIARVLKILKMAVGMALLDTVMQ	1720
Db	781	DLAIVLLSIMGITLBEIEVNASLPIINPTIIRIMRVLIARVLKILKMAVGMALLDTVMQ	840
Qy	1721	ALPQVGNLGLLPMLLFFIFAALGVELFGDCEDETHPCBGLRHATFRNFGMAFLTPRV	1780
Db	841	ALPQVGNLGLLPMLLFFIFAALGVELFGDCEDETHPCBGLRHATFRNFGMAFLTPRV	900
Qy	1781	STGDMNGIMKDTLRDCQESTCYNTVSPYFVSFLVTAQVNVNVTAVLMKHEEN	1840
Db	901	STGDMNGIMKDTLRDCQESTCYNTVSPYFVSFLVTAQVNVNVTAVLMKHEEN	960
Qy	1841	KEAKEAEAELEAELEEMKTLSPQHSPLGSPPLWFGVEGDPSPDKPKALHPAAHARSA	1900
Db	961	KEAKEAEAELEAELEEMKTLSPQHSPLGSPPLWFGVEGDPSPDKPKALHPAAHARSA	1020
Qy	1901	SH-FSLEHPTMQPHTELP---GPDLLTVRKGVSRTHSLPNDSYMCRHGSTAEGPLGHR	1956
Db	1021	SGFSLHPTMQPHTELP---GPDLLTVRKGVSRTHSLPNDSYMCRHGSTAEGPLGHR	1080
Qy	1957	GWGLPKAOSGVLVSHSQPADTSYIQLPKDAPHLLOPHSAPTWGTIPKLPPEGRSPLAQ	2016
Db	1081	GWGLPKAOSGVLVSHSQPADTSYIQLPKDAPHLLOPHSAPTWGTIPKLPPEGRSPLAQ	1140
Qy	2017	RPLRQAARTDSDLVQGLSREDLLAEVSGFSPPLARAYSFWGQSSSTQAQHSRSHKI	2076
Db	1141	RPLRQAARTDSDLVQGLSREDLLAEVSGFSPPLARAYSFWGQSSSTQAQHSRSHKI	1200
Qy	2077	SKHMTPPACDPEPNWKGKPPETRSLELDELTELWSIGDILLPPGQEEPPSPRDLKKCY	2136
Db	1201	SKHMTPPACDPEPNWKGKPPETRSLELDELTELWSIGDILLPPGQEEPPSPRDLKKCY	1259
Qy	2137	SVEAQSCRRPGSWLDEQRHSIAVSCLDGSGQPHLGTDPNMLGQPIGCGSRPKKLS	2196
Db	1260	SVEAQSCRRPGSWLDEQRHSIAVSCLDGSGQPHLGTDPNMLGQPIGCGSRPKKLS	1319
Qy	2197	PPSITIDPPESQGPRTSPGICLRRAPSSDKDFLAGPPDMAASPKKDVLSLG	2256
Db	1320	PPSISIDPPESQGPRTSPGICLRRAPSSDKDFLAGPPDMAASPKKDVLSLG	1379
Qy	2257	LSSDPADLDP 2266	
Db	1380	LSSDPTDLDP 1389	
RESULT 10			
CCAH_RAT STANDARD; PRT; 2359 AA.			
ID	CCAH_RAT		

Q9R060;
28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2).
GN Name=Cacnalh;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC PUBMED=Brain;
RX PubMed=11073957; DOI=10.1074/jbc.M008215200;
RA McKroy J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G., Baillie D.L., Stea A., Snutch T.P.;
RT "Molecular and functional characterization of a family of rat brain T-type calcium channels.";
RL J. Biol. Chem. 276:3999-4011(2001).
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1H gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in brain.
CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.
CC -!- PM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

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DR EMBL; AF290213; AACG35187.1; -.
DR RGD; 68943; Cacnalh.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR005445; TVDCCAlphaI.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR01629; TVDCCALPHA1.
DR Calcium channel; Glycoprotein; Ion transport; Ionic channel;
KW Multigene family; Phosphorylation; Repeat; Transmembrane;
FT Voltage-gated channel.
FT REPEAT 87 422
FT FT REPEAT 776 1015
FT FT REPEAT 1292 1569
FT FT REPEAT 1607 1868
FT FT REPEAT 1 100
FT DOMAIN 101 119
FT CYtoplasmic (Potential).
FT SI of repeat I (potential).

Ion transport; Ionic channel; Multigene family; Phosphorylation; Repeat; Transmembrane; Voltage-gated channel.

AW	repeat; transmembrane	87	422	I.
FT	REPEAT	779	1018	II.
FT	REPEAT	1281	1558	III.
FT	REPEAT	1602	1863	IV.
FT	DOMAIN	1	100	Cytoplasmic (Potential).
FT	TRANSMEM	101	119	S1 of repeat I (Potential).
FT	DOMAIN	120	139	Extracellular (Potential).
FT	TRANSMEM	140	160	S2 of repeat I (Potential).
FT	DOMAIN	161	169	Cytoplasmic (Potential).
FT	TRANSMEM	170	184	S3 of repeat I (Potential).
FT	DOMAIN	185	193	Extracellular (Potential).
FT	TRANSMEM	194	212	S4 of repeat I (Potential).
FT	DOMAIN	213	232	Cytoplasmic (Potential).
FT	TRANSMEM	233	253	S5 of repeat I (Potential).
FT	DOMAIN	254	394	Extracellular (Potential).
FT	TRANSMEM	395	419	S6 of repeat I (Potential).
FT	DOMAIN	420	793	Cytoplasmic (Potential).
FT	TRANSMEM	794	814	S1 of repeat II (Potential).
FT	DOMAIN	815	837	Extracellular (Potential).
FT	TRANSMEM	838	849	S2 of repeat II (Potential).
FT	DOMAIN	850	855	Cytoplasmic (Potential).
FT	TRANSMEM	856	874	S3 of repeat II (Potential).
FT	DOMAIN	883	906	Extracellular (Potential).
FT	TRANSMEM	907	917	S4 of repeat II (Potential).
FT	DOMAIN	918	938	Cytoplasmic (Potential).
FT	TRANSMEM	939	990	Extracellular (Potential).
FT	DOMAIN	991	1015	S6 of repeat II (Potential).
FT	TRANSMEM	1016	1290	Cytoplasmic (Potential).
FT	DOMAIN	1291	1313	S1 of repeat III (Potential).
FT	TRANSMEM	1314	1331	Extracellular (Potential).
FT	DOMAIN	1332	1352	S2 of repeat III (Potential).
FT	TRANSMEM	1353	1362	Cytoplasmic (Potential).
FT	DOMAIN	1363	1382	S3 of repeat III (Potential).
FT	TRANSMEM	1383	1396	Extracellular (Potential).
FT	DOMAIN	1397	1418	S4 of repeat III (Potential).
FT	TRANSMEM	1419	1428	Cytoplasmic (Potential).
FT	DOMAIN	1429	1452	S5 of repeat III (Potential).
FT	TRANSMEM	1453	1529	Extracellular (Potential).
FT	DOMAIN	1530	1555	S6 of repeat III (Potential).
FT	TRANSMEM	1556	1616	Cytoplasmic (Potential).
FT	DOMAIN	1617	1637	S1 of repeat IV (Potential).
FT	TRANSMEM	1638	1651	Extracellular (Potential).
FT	DOMAIN	1652	1673	S2 of repeat IV (Potential).
FT	TRANSMEM	1674	1680	Cytoplasmic (Potential).
FT	DOMAIN	1681	1699	S3 of repeat IV (Potential).
FT	TRANSMEM	1700	1713	Extracellular (Potential).
FT	DOMAIN	1714	1737	S4 of repeat IV (Potential).
FT	TRANSMEM	1738	1751	Cytoplasmic (Potential).
FT	DOMAIN	1752	1772	S5 of repeat IV (Potential).
FT	TRANSMEM	1773	1835	Extracellular (Potential).
FT	DOMAIN	1836	1863	S6 of repeat IV (Potential).
FT	TRANSMEM	1864	2353	Cytoplasmic (Potential).
FT	DOMAIN	520	530	Poly-His.
FT	TRANSMEM	1107	1110	Poly-Ser.
FT	DOMAIN	1583	1586	Poly-Arg.
FT	SITE	378	378	Calcium ion selectivity and permeability (By similarity).
FT	SITE	974	974	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1504	1504	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1808	1808	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	192	192	N-linked (GlcNAc...)
FT	CARBOHYD	271	271	N-linked (GlcNAc...)

Query Match

Query Match 52.2%; Score 6210; DB 1; Length 2353;

Query Match	52.2%;	Score	59;
Best Local Similarity	56.6%;	Pred. NO. 1	ie-277;
Matches 1364;	Conservative 216;	Mismatches	526;
Indels	302;	Gaps	59;

Qy	7	GAGAEESQOP--RSFWRNLNDSGAGRGPGSGAEKPGSADSEABGLPPALAPVVPVFFYLS	65
Db	27	GASPESPGAPGREABRGSEL--GVSPSP--AAEAGAEAGADEEORVPYPALAAATVFCIG	84
Qy	66	QDSRPSRCLRTVCNPNPFRISMLVILNCVTLGMPFCEDACDSORCILQAFDDFIIF	125
Db	85	QOTRPSRCLRLVCNPNPFEHVSMVLVIMLNCVTLGMPFCEDVEGSCRCNILEAFDAFIF	144
Qy	126	APFAVEMVVMVALGIFGKKCYLGDWTNRNLDFFIIVAGMLFYSJLDLQNVSESFAVRTVRVL	185
Db	145	APFAVEMVIMKVALGIFGKKCYLGDWTNRNLDFFIIVAGMMEYSJLDGHNVLSUSAKTRVRVL	204
Qy	186	RELRAINRVPMSRILVTLTDLTPMLGNVLLCCFPVFIFIGIVGQVLWAGLNRKRCFLPE	245
Db	205	RELRAINRVPMSRILVTLTDLTPMLGNVLLCCFPVFIFIGIVGQVLWAGLNRKRCFLDS	264
Qy	246	NFSLPLSVD--LBRYYOTENEDESPFIQSPRENGMRSCRSVP---TIRGDCGGGPPPCGLD	301
Db	265	AFVRNNNLTRPYYYQTEBEGENPFICSSRRDNGMKCKSHIPGRREL-------MPCTLG	318
Qy	302	YEAYN-----SSSNTTCVANNQYTYNCBSAGEHNPPKGAJNFDNIGYAWIAIQVITLE	354
Db	319	WEAYTOQAQBGVGAARNACINWNOYINVCRRGDSNPHNGAJNFDNIGYAWIAIQVITLE	378
Qy	355	GWVDIMYFYMDAHSFNYFIYFILLIIVGSEFFMINCLVVIATQPSFETKQRSQMLREORV	414
Db	379	GWVDIMYVYMDAHSFYNYFIYFILLIIVGSEFFMINCLVVIATQPSFETKQRSQMLREORA	438
Qy	415	RFLSNASTLASSEFGSCYEELKLYVLILAKAARELAQVSRAGVRVGLLSSPAPLGGQ	474
Db	439	RHLNSDSTLASSEFGSCYEELKLYVGHIFRKRKRSRLRLVARMQSRWRKVDVSAVOGQ	498
Qy	475	ETQPSSSCSGRSHRR--LSVHHLV--HHHHHHHHHYHLNGTTLRAPRASPIQDRDANGSRRL	532
Db	499	--GPHRQRRAGRHATASVHHLVYHHHHHHHHHYHFSHGSPREPGPEPGACD-----TRLV	551
Qy	533	MUPPPPTPALSAGPPGABSVHSFYHADCHLE--PVRQAPPSPSPSPASGR--TVGSGKV	589
Db	552	RAGAPSPSPGPGPPDAESVHSIYHADCHIEGQOERARVAHAATAAASURLATGLGTM	611
Qy	590	-YPTV-----HTSP-----PPETLKEKALVEVAASSGPPPTLTSLNPPGPPY	629
Db	612	NYPTILPSGVGSGKSTSPCKGWAGGPPGT-----GGHGPLSLNS---PDY 657	
Qy	630	SSMHKLETTQSTGACQS-----SKTSSPCLKADSGACGPDSPCYCARA--GAGEVELA	681
Db	658	EKIPHVVGHEGLQAQPHLSGLSVPCPLPSP--PAGTLTCELKSCPYCTRALEDPEGELS	715
Qy	682	DREMPDSSEAVYEFQDQAQSDLRDP-----HRRRQHSIGDEAPSSV	725
Db	716	GSESGSDRGVYEFQDVRHGRWDPTPPRATDTPGPGPGSPQRAQRAAPGPGWM	775
Qy	726	LAEWRLICDTRFXIVDSKYFGRGIMAILVNTLSMGIYHEQPEELTNALEISNIVFTSL	785
Db	776	GRLVVTFSGKLRLIVDSKYFSRGIMAILVNTLSMGVEYHEQPEELTNALEISNIVFTSM	835
Qy	786	FALEMLLKLIVGPGFYKPNYINPGVIVWISWEIVGQGGGLSVLTFPLRMVLKVLV	845
Db	836	FALEMLLKLIIACPLGVIIRPNYINFDGIIWISWEIVGQGGGLSVLTFPLRLRVKLVLV	895
Qy	846	RFPALORQVLVLMKTMNDVNATFCMLLMFIFFISILGMHLFGCKFPASERD--GDTLPDRK	904
Db	896	RFIPALRRQVLVLMKTMNDVNATFCTLLMFIFFISILGMHLFGCKESLKTGDIVDPDK	955
Qy	905	NFDSLLWAIYVTFQILTQEDWNKVLYNGMASTSSWAALFYFIAMTFGNVFLNLLVAILV	964
Db	956	NFDSLLWAIYVTFQILTQEDWNVLYNGMASTSSWAALFYFVALMTFGNVFLNLLVAILV	1015
Qy	965	EGFCAEELSKREDASGQLSCIQLPVDSQGDGANKSESPDFTSPSLDGD-----GD	1015
Db	1016	EGFOAE-----GDANRSDTDEKTSVHVEEDFHKLRELQTTIE	1052
Qy	1016	RKKCLIALVSGHEPELFXSLLPELLIHTAATPMSLPKSTSTGLGEALGPASRRTSSGGA	1075

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 CC or send an email to license@isb-sib.ch)

DR EMBL; AF226868; AAK21607.2; --
 DR EMBL; AY026385; AAK21607.2; JOINED.
 DR EMBL; AF051947; AAC67240.1; --
 DR MGD; MGI:1928842; Cactnath.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M-channel_nlg.
 DR InterPro; IPR005445; TVDCCALPhal.
 DR Pfam; PF00520; Ion_trans; 4.
 DR PRINTS; PR01629; TVDCCALPhal.
 KW Calcium channel; Glycoprotein; Ion transport; Ionic channel;
 KW Multigene family; Phosphorylation; Repeat; Transmembrane;
 KW Voltage-gated channel.
 FT REPEAT 87 422 I.
 FT REPEAT 776 1015 II.
 FT REPEAT 1292 1569 III.
 FT REPEAT 1613 1874 IV.
 FT DOMAIN 1 100 Cytoplasmic (Potential).
 FT TRANSMEM 101 119 S1 of repeat I (Potential).
 FT DOMAIN 120 139 Extracellular (Potential).
 FT TRANSMEM 140 160 S2 of repeat I (Potential).
 FT DOMAIN 161 169 Cytoplasmic (Potential).
 FT TRANSMEM 170 184 S3 of repeat I (Potential).
 FT DOMAIN 185 193 Extracellular (Potential).
 FT TRANSMEM 194 212 S4 of repeat I (Potential).
 FT DOMAIN 213 232 Cytoplasmic (Potential).
 FT TRANSMEM 233 253 S5 of repeat I (Potential).
 FT DOMAIN 254 394 Extracellular (Potential).
 FT TRANSMEM 395 419 S6 of repeat I (Potential).
 FT DOMAIN 420 790 Cytoplasmic (Potential).
 FT TRANSMEM 791 811 S1 of repeat II (Potential).
 FT DOMAIN 812 824 Extracellular (Potential).
 FT TRANSMEM 825 846 S2 of repeat II (Potential).
 FT DOMAIN 847 852 Cytoplasmic (Potential).
 FT TRANSMEM 853 871 S3 of repeat II (Potential).
 FT DOMAIN 872 879 Extracellular (Potential).
 FT TRANSMEM 880 903 S4 of repeat II (Potential).
 FT DOMAIN 904 914 Cytoplasmic (Potential).
 FT TRANSMEM 915 935 S5 of repeat II (Potential).
 FT DOMAIN 936 987 Extracellular (Potential).
 FT TRANSMEM 988 1012 S6 of repeat II (Potential).
 FT DOMAIN 1013 1301 Cytoplasmic (Potential).
 FT TRANSMEM 1302 1324 S1 of repeat III (Potential).
 FT DOMAIN 1325 1342 Extracellular (Potential).
 FT TRANSMEM 1343 1363 S2 of repeat III (Potential).
 FT DOMAIN 1364 1373 Cytoplasmic (Potential).
 FT TRANSMEM 1374 1393 S3 of repeat III (Potential).
 FT DOMAIN 1394 1407 Extracellular (Potential).
 FT TRANSMEM 1408 1429 S4 of repeat III (Potential).
 FT DOMAIN 1430 1439 Cytoplasmic (Potential).
 FT TRANSMEM 1440 1463 S5 of repeat III (Potential).
 FT DOMAIN 1464 1540 Extracellular (Potential).
 FT TRANSMEM 1541 1566 S6 of repeat III (Potential).
 FT DOMAIN 1567 1627 Cytoplasmic (Potential).
 FT TRANSMEM 1628 1648 S1 of repeat IV (Potential).
 FT DOMAIN 1649 1662 Extracellular (Potential).
 FT TRANSMEM 1663 1684 S2 of repeat IV (Potential).
 FT DOMAIN 1685 1691 Cytoplasmic (Potential).
 FT TRANSMEM 1692 1710 S3 of repeat IV (Potential).
 FT DOMAIN 1711 1724 Extracellular (Potential).
 FT TRANSMEM 1725 1748 S4 of repeat IV (Potential).
 FT DOMAIN 1749 1762 Cytoplasmic (Potential).
 FT TRANSMEM 1763 1783 S5 of repeat IV (Potential).
 FT DOMAIN 1784 1846 S6 of repeat IV (Potential).
 FT TRANSMEM 1847 1874 Cytoplasmic (Potential).
 FT DOMAIN 1875 2365 Poly-His.
 FT DOMAIN 521 531

FT DOMAIN 1594 1597 Poly-Arg.
 FT SITE 378 Calcium ion selectivity and permeability
 FT SITE 971 (By similarity).
 FT SITE 971 Calcium ion selectivity and permeability
 FT SITE 1515 (By similarity).
 FT SITE 1515 Calcium ion selectivity and permeability
 FT SITE 1819 (By similarity).
 FT SITE 1819 Calcium ion selectivity and permeability
 FT CARBOHYD 192 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 271 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1477 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 1823 GIM -> ARG (in Ref. 2).
 FT CONFLICT 1914 D -> E (in Ref. 2).
 FT CONFLICT 1945 APA -> LIQ (in Ref. 2).
 FT CONFLICT 1952 S -> A (in Ref. 2).
 FT CONFLICT 1953 Missing (in Ref. 2).
 FT CONFLICT 2351 Missing (in Ref. 2).
 FT SEQUENCE 2365 AA; 261944 MW; 9A8A17570C210596 CRC64;
 SQ
 Query Match 51.9%; Score 6176.5; DB 1; Length 2365;
 Best Local Similarity 56.6%; Pred. No. 4e-276;
 Matches 1365; Conservative 235; Mismatches 528; Indels 285; Gaps 61;
 QY 2 DEEDGAGABESGQPRSMRLNDLS-GAGGRP---GPQS---AEXDPGS---AD---SEA 48
 DB 9 DEVRVPLGASPSA-PAAPVRASPGVPGVEEQRSGSSVLAPESPGTECGADLGADEE 67
 QY 49 EGLPYPALAPVYFFVYLSQDSRPSKLCRTVCNPFERISMLVILLNCVTGLMFRPCEDIA 108
 DB 68 QVPYFALAAVFFCLGQTTRPSWCLRLVCNPFHEHSMVLINLCVTGLMFRPCEDVE 127
 QY 109 CDSQRCRILOAFDDFTFAFFAVEMVVKWVALGFGKCYLGDTWRLDFFIVAGMLEYS 168
 DB 128 CSERCSILEAFDDFTFAFFAVEMVVKWVALGFGKCYLGDTWRLDFFIVAGMWEYS 187
 QY 169 LDQNVFSAVTVRVRLPRAINRVPSMRLIIVTLTDLPLMGNVLLLCFFVFFFGIV 228
 DB 188 LDGHNVLSAIRTVRVRLPRAINRVPSMRLIIVTLTDLPLMGNVLLLCFFVFFFGIV 247
 QY 229 GYQLWAGLLRNRCFLPNESLPLVD-LERYVQTEDESPFICSPQENGMRSCRSVPT 287
 DB 248 GYQLWAGLLRNRCFLDFAVRNNLTFLPYVQTEGEENPFICSSRDNGMKCSHIP 307
 QY 288 ---LRGDGGGGPPCGLDYEAY-----NSSNNTTCVNNQYVTCAGSEHPNFKGAINF 337
 DB 308 RRELRL-----VQCTLGWEAYGQPAEDGGAGRNACINNNQYVNCRSGEFNPNGAINF 361
 QY 338 DNIQYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYILLIIVGSPFMINLCVVIATQ 397
 DB 362 DNIQYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYILLIIVGSPFMINLCVVIATQ 421
 QY 398 FSETKQRESQLMREQRVRLSNASTLASFPSCSYEELIKYLVYTLRKAARLAQVRA 457
 DB 422 FSETKQRENQLMREQARYLSDSTLASFPSCSYEELIKYVGHIFRKVRRSLRYAR 481
 QY 458 AGVRVGLLSSP-APLGQGTQTPSSSCSRSHRR-LSVHHVIV-HHHHHHHHHYHLNGTLRA 514
 DB 482 WQSRWKVKVDPSSSTLHGQ--GPRRRPRRAGRRTASVHHLVYHHHHHHHHYHPSHGPRR 539
 QY 515 PRASPEIQDRDANGSRILM--LPPPTPALSGAPGGAESVHSFYHADCHLEPVRCOAPP 572
 DB 540 P--SPE-----PGAGDTRLVRACVPPSPSPSGHGPP--DSSESVHSIYIADCHVEGPEARV 592
 QY 573 PRSPSEASGRTVGSG---KVYPTV-----HTSPPTETIKEXALVEVAASSGPPTL 619
 DB 593 AHTIATAASLKASGLGTWNYPIPLPSGAVNSKGSTSRPKGLR-----SAGTPGA 643
 QY 620 TS---LNI-PPGPYSMMHKLELTQSTGACQS-----SKYISPCIKADSGAGCPDSCP 668
 DB 644 TAAHPSLSLGSFSPYEKIQHVVGQGLGRASSHLSGLSVPCPLPSP--QAGTLTCEUKSCP 701
 QY 669 YCARA-GAGRVELADREMPDSDSEAVYFTQDAQHSDLRDP-----HSRRQR 714
 DB 669 YCARA-GAGRVELADREMPDSDSEAVYFTQDAQHSDLRDP-----HSRRQR 714

Db 702 YCALEDEPEFEFGSGSDAHGYEFTQDVRHGDRCDPVQOPHEGGTGPCHGNRWRP 761
QY 715 SLGPDAPESVLAFLWRLICDTPRKIVDSKYFCRGIMIALIVNTLSMGLYEHQPELNTA 774
Db 762 PLRTASQPGCLGRLLWASPSKLRRIVDSKYFNRGIMAAVLNLSMGVEYHEQPELNTA 821
QY 775 LEISNIVFTSLPALEMLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQGGGLSVLR 834
Db 822 LEISNIVFTSMFALEMLKLLACGPLGYIRNPYNIFDGVIVVISWEIVGQADGGLSVLR 881
QY 835 TFLMRVLKLVRFPLALOROLVLMKMTDNVATFCMLLMFLFIFISILGMHLFGCKPASE 894
Db 882 TFLMRVLKLVRFPLALOROLVLMKMTDNVATFCMLLMFLFIFISILGMHLFGCKPASE 941
QY 895 RD-GDRTLDRKNFDSLLWAVTFVFOILLTOEDWNKVLYNGMASTSSWAAALYFIALMTFCNY 953
Db 942 TDSGDTVPDRKNFDSLLWAVTFVFOILLTOEDWNKVLYNGMASTSSWAAALYFIALMTFCNY 1001
QY 954 VLFNLLVAILVEGFOAEFISKREDAAGQLSCIQLPVDSSQGGDANKSESEPFPPSLDGD 1013
Db 1002 VLFNLLVAILVEGFOAEFISKREDAAGQLSCIQLPVDSSQGGDANKSESEPFPPSLDGD 1038
QY 1014 GDRK-----CLALVSLGHEPRLKSLPLLIHTAATPMNSLPKSTSTGLGEALG 1063
Db 1039 FDKLDRVATRMKMYSLAVTPNG-HLEGRGLSPPLIHTAATPMPTPKS-SPHLDMAHT 1096
QY 1064 PASRRTSSGSAEPGAHEMSPSPARSPPSPASPSAASWTSSRRSSNLGRAPSLKRS 1123
Db 1097 LLDSSRSSGSDVQLG-DQKSLASLRSSPCAPGPNAGSRRSSNLSGRAPSLKRS 1155
QY 1124 PSGRRSLSGEGESODEE-ESSEBERASPAGSDHRRGLSLEA-----KSSFOL--- 1174
Db 1156 QCGERSLSGEGKSGTDEAEDSRNSGTHPGASGPRATPLRAESLGHRSIWDLCPP 1215
QY 1175 -PDTLQVPLHRTASGRSASEHODCKNSAGSLARALRDPDPPLDGDADDGNNLSKG 1233
Db 1216 RPATL-LP-----TKFRDCNGQWALPSEFFLRIDSHKEDAAEPDDDIEDSCC 1262
QY 1234 ERVAMTARLPACYLERSDSVAIFPPQSRFRLLCHRIITHKMFHDHVLVILFNCITI 1293
Db 1263 FLHKVLEPAPQWCSSRESWALVLPQNRVRSCKVIAHRKMFHDHVLVILFNCITI 1322
QY 1294 AMERPKIDPSAERIFITLSNYIFTAVFLABMTVKVVALGWCFOEQAYLRSSMNVLDGLL 1353
Db 1323 ALERPDIDPGSTERAFLSVSNYIFTAIFVVMVVKVVALGLLWGEHAYLQSSMNVLDGLL 1382
QY 1354 VLSVIDILSMYSDSTKILGMLRVLRLTLRPLRVISRAQGLKLVETLMSLXPIG 1413
Db 1383 VLSVLDIIVAVASAGAKILGVLRVLRLLTLRPLRVISRAQGLKLVETLMSLXPIG 1442
QY 1414 NIIVICCAFFIIFGILGVOLFQKGFYVCGEDTRNITKNKSDCABASVVRWRHKNYDNLG 1473
Db 1443 NIVLICCAFFIIFGILGVOLFQKGFYVCGEDTRNITKAACHAHRWRKRYNFNLG 1502
QY 1474 QALMSLFLVASKGDVIMYDGLDVGVDQOPQIMNHPMMLXIFISFLIVAFVLMNV 1533
Db 1503 QALMSLFLVSKDGNIMYDGLDVGVDQOPQIMNHPMMLXIFISFLIVAFVLMNV 1562
QY 1534 GVVENFHKCRQOEAEAREERREKRLRLKRR-----KAQCKPYSDYGRFLLVH 1587
Db 1563 GVVENFHKCRQOEAEAREERREKRLRLRLRRRRSTFPNPEAQRRPYADYSHTRSIH 1622
QY 1588 HLCTSHYLDLFIITGVIGINVTVMAMEHYQOQILDEALKICNIFTVIFVLESVKLVAF 1647
Db 1623 SLCTSHYLDLFIITCLNVTMSMEHYNQPSLDEALKICNIFTVIFVFEALKLVAF 1682
QY 1648 GFRFFODRNQDLATVLLSIMGITLLEEIVNASLFPINPTIIRIMVLRVLRVLLKLM 1707
Db 1683 GFRFFODRNQDLATVLLSIMGIALEEIEMNAALPINPTIIRIMVLRVLRVLLKLM 1742
QY 1708 AVCMBALLDTVMQALPOVGNLGLLFFMILFFIFALGVLELPGDLECDETHPCGGLRHATF 1767
Db 1743 ATGMBALLDTVMQALPOVGNLGLLFFMILFFIYAALGVLELPGDLECDENPCGGLRHATF 1802

QY 1768 RNFGMAFLTLFRVSTGDNWNGIMKDTLRDC---DOESTCYNTVISPVIYVSVFLVAQFVL 1824
Db 1803 TNFGMAFLTLFRVSTGDNWNGIMKDTLRCTRECTREKHLCLSYLPALSPVYFVTFVLVAQFVL 1862
QY 1825 VNVVAVLKMKLEESKEAEAELEAELEM-KTSLPQSPHPLGSPFLWFGVGPDPSP 1883
Db 1863 VNVVAVLKMKLEESKEAREDAEMDAIELEIAOGSTAQPPSTAQES-----QGTDP-P 1915
QY 1884 DSPKGAHLPAHAARSASHFSLEHPTMQPHPTLTKVRKSGVSRTHSLPNDSYMC 1943
Db 1916 DT-----PNLLVVRKVSVMRLSLPNDSYME 1941
QY 1944 RHGTAEGFLHGRGNGLP-----KAQSGSVLSVHSQPADTSYILQLPKDAPHLLOPHSA 1997
Db 1942 RPVAPAAAPHSH-----PLQEVEMETYTGPVTSAHSPSLEPRTSQVPSAASPARA-SD 1995
QY 1998 PTWGTIPKLPKPPGRSPLAQRPLRQAAIRLQSLDVQGLSGREDLLAEVSGSPPLARAYS 2057
Db 1996 PLCALSPRDTLP--RSLSLRILYQEAHAESELGQIDGAGEDGIDPDTYEPAEINISQA 2053
QY 2058 FWG-----QSSTQAQQHRSRSHSKISKHMTTPAPCPGPEPNWKGKPPETRSSLELD 2107
Db 2054 PLGLTRSPPCSPRPAASVTRKHTFGQHCISRR--PPT-----LGGDDAAADPAD 2101
QY 2108 TELSWISGDLPL-----PGQOEPP-----SPDLKKCYSVBAQSCORRPTSWLD 2152
Db 2102 EEVSHITSSAHPWPATEPHSPASPTASPAKTVGSGRDPHRFCGVDAQAQSLDKP-GRPD 2160
QY 2153 EQRHSTAVSCLDSGSPHLGTDPNLGGQPL-GPGSRPKKLLSPSITIDPP-ESQGP 2210
Db 2161 AQRWSSVE--LDNG-DCHLESGEVRASELEPALGARKKKMSPPCISIDPTEDEGS 2216
QY 2211 RTPSP--GICLRRAPSSDSK-----DPLASGPPDSMAASPSPKDV 2251
Db 2217 SRPPAEGGNTLRRTPSCAALHRDCPESTEGTGGTGVAKGERWQA---SCRAEH 2273
QY 2252 LSLSLSSDPAFL 2264
Db 2274 LTVENFAFEPLDM 2286
RESULT 13
CCAI HUMAN
ID _CAAI_HUMAN STANDARD; PRT; 2223 AA.
AC Q9P0X4; Q95504; Q726S9; Q8NFX6; Q9NZC8; Q9UH15; Q9UH30; Q9ULJ9;
AC Q9UNE6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1I subunit (Voltage-gated calcium channel alpha subunit Cav3.3) (Ca(v)3.3).
GN Name=CACNA1I; Synonym=KIAA1120;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=99381950; PubMed=10454147;
RA Mittman S., Guo J., Emerick M.C., Agnew W.S.;
RT "Structure and alternative splicing of the gene encoding alpha1, a human brain T calcium channel alphasubunit";
RL Neurosci. Lett. 269:121-124(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Brain;
RX MEDLINE=20287513; PubMed=10749850; DOI=10.1074/jbc.C000090200;
RA Monteil A., Chemin J., Leuranger V., Altier C., Mennessier G., Bourinet E., Lory P., Nargeot J.;
RT "Specific properties of T-type calcium channels generated by the human alpha1 subunit.";

RL	J. Biol. Chem. 275:16530-16535 (2000).	CC	voltage-dependent inactivation. T-type channels serve pacemaking
RN	[3]	CC	functions in both central neurons and cardiac nodal cells and
RP	SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT VAL-1040.	CC	support calcium signaling in secretory cells and vascular smooth
RC	TISSUE=Brain;	CC	muscle. They may also be involved in the modulation of firing
RE	MEDLINE=22074770; PubMed=12080115;	CC	patterns of neurons which is important for information processing
RA	Gomora J.C., Murbarian J., Arias J.M., Lee J.-H., Perez-Reyes E.;	CC	as well as in cell growth processes. Gates in voltage ranges
RT	"Cloning and expression of the human T-type channel Ca(v)3.3: insights	CC	similar to, but higher than alpha 1G or alpha 1H (By similarity).
RT	into prepulse facilitation."	CC	- - SUBCELLULAR LOCATION: Integral membrane protein.
RL	Biophys. J. 83:229-241 (2002).	CC	- - ALTERNATIVE PRODUCTS:
RP	[4]	CC	Event=Alternative splicing; Named isoforms=4;
RE	SEQUENCE FROM N.A.	CC	Name=1; Synonyms=Delta36b;
RX	MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;	CC	Isoid=Q9P0X4-1; Sequence=Displayed;
RA	Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,	CC	Name=2;
RA	Clark M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,	CC	Isoid=Q9P0X4-2; Sequence=VSP_000951;
RA	Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,	CC	Name=3; Synonyms=Alpha11-a;
RA	Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,	CC	Isoid=Q9P0X4-3; Sequence=VSP_000950, VSP_000951;
RA	Burrill M.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,	CC	Name=4;
RA	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,	CC	Isoid=Q9P0X4-4; Sequence=VSP_000950;
RA	Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,	CC	- - TISSUE SPECIFICITY: Brain specific.
RA	Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,	CC	- - DOMAIN: Each of the four internal repeats contains five
RA	Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,	CC	hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
RA	Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,	CC	positively charged transmembrane segment (S4). S4 segments
RA	Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,	CC	probably represent the voltage-sensor and are characterized by a
RA	Hunt S.E., Jones M.C., Kereshaw J., Kimberley A.M., King A.,	CC	series of positively charged amino acids at every third position.
RA	Laird G.K., Langford C.F., Levarsha M.A., Lloyd D.M.,	CC	- - PTM: In response to raising of intracellular calcium, the T-type
RA	Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,	CC	channels are activated by CaM-kinase II (By similarity).
RA	McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T.,	CC	- - SIMILARITY: Belongs to the calcium channel alpha-1 subunits
RA	O'Dell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,	CC	family.
RA	Phillips S.E., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,	CC	- - CAUTION: Ref.4 (CAB62996) sequence differs from that shown due to
RA	Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,	CC	erroneous gene model prediction.
RA	Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,	CC	-----
RA	Vaudin M., Walli M., Wallis J.M., Whiteley M.N., Willey D.L.,	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
RA	Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RA	Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,	CC	the European Bioinformatics Institute. There are no restrictions on its
RA	Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,	CC	use by non-profit institutions as long as its content is in no way
RA	Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuoyama S.,	CC	modified and this statement is not removed. Usage by and for commercial
RA	Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
RA	Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,	CC	or send an email to licenses@isb-sib.ch).
RA	Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,	CC	-----
RA	Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,	DR	EMBL; AF129133; RAD45251.1; -
RA	Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,	DR	EMBL; AF142567; AAF27222.1; -
RA	Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,	DR	EMBL; AF211189; AAF44626.1; -
RA	Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,	DR	EMBL; AF393329; AAM67414.1; -
RA	Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,	DR	EMBL; AL008716; CAAL5494.1; -
RA	Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,	DR	EMBL; AL022312; CAB62988.1; -
RA	Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,	DR	EMBL; AL022319; CAB62996.1; ALT_SEQ.
RA	Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,	DR	EMBL; AL022319; CAD92536.1; -
RA	Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,	DR	EMBL; AB032946; BAA86434.1; -
RA	Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,	DR	GeneW; HGNC:1396; CACNAL1.
RA	Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,	DR	MIM; 608230; -
RA	Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,	DR	GO; GO:0005891; C-voltage-gated calcium channel complex; NAS.
RA	O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,	DR	GO; GO:0008332; F-low voltage-gated calcium channel activity; NAS.
RA	Khan A.S., Lane L., Tillahun Y., Wright H.;	DR	GO; GO:0006816; P-calcium ion transport; NAS.
RT	"the DNA sequence of human chromosome 22.;"	DR	InterPro; IPR001682; Ca/Na_Pore.
RL	Nature 402:489-495 (1999).	DR	InterPro; IPR002111; Cat_channel_TripL.
RN	[5]	DR	InterPro; IPR002077; Ca_channel_alpha.
RP	SEQUENCE OF 1200-2223 FROM N.A. (ISOFORM 1).	DR	InterPro; IPR005821; Ion trans.
RC	TISSUE=Brain;	DR	InterPro; IPR005820; M+channel_nlg.
RX	MEDLINE=20039618; PubMed=10574461;	DR	InterPro; IPR005445; TVDCCAlphal.
RA	Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,	DR	Pfam; PF00520; Ion trans; 4.
RA	Ohara O.;	DR	PRINTS; PR00167; CACHANNEL.
RT	"Characterization of cDNA clones selected by the GeneMark analysis	DR	PRINTS; PR01629; TVDCCALPHA1.
RT	from size-fractionated cDNA libraries from human brain.;"	DR	Alternative splicing; Calcium channel; Multigene family; Phosphorylation;
RL	DNA Res. 6:329-336 (1999).	KW	Ion transport; Ionic channel; Transmembrane; Voltage-gated channel.
CC	- - FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the	KW	Polymorphism; Repeat: 401
CC	entry of calcium ions into excitable cells and are also involved	FT	REPEAT 626 865
CC	in a variety of calcium-dependent processes, including muscle	FT	REPEAT 1157 1434
CC	contraction, hormone or neurotransmitter release, gene expression,	FT	REPEAT 1472 1733
CC	cell motility, cell division and cell death. Isoform alpha-11	FT	DOMAIN 1 78
CC	gives rise to T-type calcium currents. T-type calcium channels	FT	TRANSMEM 79 99
CC	belong to the "low-voltage activated (LVA)" group and are strongly	FT	DOMAIN 100 120
CC	blocked by nickel and mibefradil. A particularity of this type of	FT	TRANSMEM 121 141
CC	channels is an opening at quite negative potentials, and a		

FT	DOMAIN	142	148	Cytoplasmic (Potential).
FT	TRANSMEM	149	168	S3 of repeat I (Potential).
FT	DOMAIN	169	173	Extracellular (Potential).
FT	TRANSMEM	174	191	S4 of repeat I (Potential).
FT	DOMAIN	192	211	Cytoplasmic (Potential).
FT	TRANSMEM	212	232	S5 of repeat I (Potential).
FT	DOMAIN	233	377	Extracellular (Potential).
FT	TRANSMEM	378	398	S6 of repeat I (Potential).
FT	DOMAIN	399	640	Cytoplasmic (Potential).
FT	TRANSMEM	641	661	S1 of repeat II (Potential).
FT	DOMAIN	662	676	Extracellular (Potential).
FT	TRANSMEM	677	697	S2 of repeat II (Potential).
FT	DOMAIN	698	702	Cytoplasmic (Potential).
FT	TRANSMEM	703	721	S3 of repeat II (Potential).
FT	DOMAIN	722	729	Extracellular (Potential).
FT	TRANSMEM	730	753	S4 of repeat II (Potential).
FT	DOMAIN	754	764	Cytoplasmic (Potential).
FT	TRANSMEM	765	785	S5 of repeat II (Potential).
FT	DOMAIN	786	841	Extracellular (Potential).
FT	TRANSMEM	842	862	S6 of repeat II (Potential).
FT	DOMAIN	863	1166	Cytoplasmic (Potential).
FT	TRANSMEM	1167	1187	S1 of repeat III (Potential).
FT	DOMAIN	1188	1209	Extracellular (Potential).
FT	TRANSMEM	1210	1230	S2 of repeat III (Potential).
FT	DOMAIN	1231	1244	Cytoplasmic (Potential).
Query Match 46.2%; Score 5496.5; DB 1; Length 2223;				
Best Local Similarity 51.3%; Pred. No. 8.2e-245; Mismatches 217; Indels 435; Gaps 60;				
Matches 1241; Conservative 217; Mismatches 527; Indels 435; Gaps 60;				
QY	31	RPGSGAEKPGSADSEAG----	LPYPALAPVVFVYLSQDSRPRSWCLRTVCNPFERI	86
DB	25	QPGPRSPSPGLEEPDGDHPHDPDLAPIAFFCLQRTSPRNCKIKVNCNPFECV	84	
QY	87	SMVLILLNCVTLGNFRPCEDTACDSQRILQAFDDTIFAFVEMVMVMVALGFGKC	146	
DB	85	SMVLILLNCVTLGNMQPCDDMCLSDCKILQVDFDTIFPFAMEMVLKVMVALGFGKC	144	
QY	147	YLGDTWNRLOFFIVIAAGMLEYSLDLQNVSRGAVTVRLRLAINRVPMSRIILVLLD	206	
DB	145	YLGDTWNRLOFFIVAGWVEYSLDLQNLINLSAIRTVRRLKAINRVPMSRIILVLLD	204	
QY	207	TLPLMGNVLLCPFFVFFIFGIVGVLWAGLRNRCFLPNFSLPLSLDLERYOTENEDE	266	
DB	205	TLPLMGNVLLCPFFVFFIFGIVGVLWAGLRNRCFLPNFSLPLSLDLERYOTENEDE	264	
QY	267	SPFICSQPRENGMRSRVSPTLRDGGGGPPCGL-----DYEAYNSSNTT--CVNMNQ	318	
DB	265	MPFICSLSGDNGIMGCHEIPLKEQ--GRECCLSKDDVDYFGAGRQDLNAGLVCVNNR	321	
QY	319	YYTNCAGEHNPFGKAINFDNIGVAMTAFQVITLEGWDMIMVMDAHSFYNIYFILL	378	
DB	322	YNNVCRGTSANPKGAINFDNIGVAMTAFQVITLEGWDMIMVMDAHSFYNIYFILL	381	
QY	379	IIVGSPFMILCLVVIATQFSETKQRESQLMREQRVFLSNASTLASFPGSCYBELLK	438	
DB	382	IIVGSPFMILCLVVIATQFSETKQREHRLMLEQRQYLS--SSIVASYAEPGDCYEIFQ	440	
QY	439	YLVIYLKAAARLAQVSRAGVRVLLSSAPLQGGTQPTSSSCSRSHRLSVHHLVHHH	498	
DB	441	YVCHILRKAKR-----RALGLYQALQSRQALGPEAPAKP-----GPH	480	
QY	499	HHHHHHYH--LNGTTLRAPRASPEIQRDAN--GSRRLM-LPPSTPALSAPPGAESV	553	
DB	481	AKPRPHVHGTKGOG-----DEGRHLGSRHCQTLDGPASP--GNDHSGRE--	523	
QY	554	HSFYHADCHLEPVRCQAPPSPSEASGRVTGSGKVYPTVHTGPPPTLKEKALVEVAAS	613	
DB	524	-----LC---POHSPLDATPHTL-----VQPIPAFL-----	546	
QY	614	SGPPTLTSLNIPGPPYSSMHKLLTOSTGTACQSSCKISSLPCLKADSGACGDCPCYCAR-	672	
DB	547	-----ASDPASCPCQOHE-----	559	

QY	673	-----AGAGEVELADRENPDSDSEAVYFTQDAQOASHDLRDPHRRQRSLGPDAPSSVL-	726
DB	560	DGRRPSSGLGSTD-SQEGSGSGSSAGGE--DEADGDGARSGSDGASSBLKEEHEEQAD	616
QY	727	-----AFWRLICDTERKIVDSKYFGGIMATLAVNTLSMGIEVHEQPEELTNALEISN	779
DB	617	GAVWLGVWRETRAKLRGIVDSKYFNRGIMAILVNTVSMGIEHHEQPEELTNTLEICN	676
QY	780	IVTSLFALEMLKLVLVYGPFGYIKNPYNIIDGVIIVISVWEIVGQCGGLSVLRTFLRM	839
DB	677	VVFTSMFALEMLKLAAFGLDYLRNPYNIIDFIIIVISWEIVGQAGGLSVLRTFLRL	736
QY	840	RVLKLRFLPALQROLVVMKTMONVATFCMLMLFIFISILGMLHFGCKPASERD-GD	898
DB	737	RVLKLRFLPALRRQLVVMKTMONVATFCMLMLFIFISILGMLHFGCKPASERD-GD	796
QY	899	TLPRKKNFDSLMLVAIVTFQLLTQEDMNKVLNGMASTSSWAALYFIAMTFGNVLENL	958
DB	797	TVPRKKNFDSLMLVAIVTFQLLTQEDMNKVLNGMASTSSWAALYFIAMTFGNVLENL	856
QY	959	LVAILVGEFQAEIISKREDASQGLSCIQLPVDSCQDGANKSESEPPDFSPS-----	1009
DB	857	LVAILVGEFQAEIISKREDASQGLSCIQLPVDSCQDGANKSESEPPDFSPS-----	893
QY	1010	-LDGDDGRKKCLALVSLGHEPRLKSLPLLIHHTAATPMSLPKSTSTGLGEALGPASRR	1068
DB	894	GLDSSGDPKLCIPITPNHG-----LDP-----SLPLGHLGPAGAAGPADRL	936
QY	1069	T-----SSSGSAEPGAHMKMSPSARSSPHSPSWSAASSWTSSRSRSLGR	1115
DB	937	SLQPDPMVLVALGRKSSVMGLRMSYQDRSLSSRSSTYGGWGSAAWASRRSWN----	992
QY	1116	APSLKRRSPSGERRSLSGE--GQESQDEESES--BRASPAGSDH-----	1158
DB	993	--SLKHKPPSAEHSLSAERGGGARVEAADSGPPRAAPLHTPHAHIHGHPLAHRH	1050
QY	1159	-RHGSLERAKSFDLPDLQVPLHRTASGR--GSAEHDQDNGKSGASRLARALRPD	1215
DB	1051	RHRRRTLSLNRSDVLAELVPAVGAHPRAAWAAGPAGPAGHEDCNGRMPSTAKDVFTKWG	1110
QY	1216	DPPLDGDADDGKSLKGRVRAWIRARLPACYLERSWSAYTFPPQSRRLCHRIITH	1275
DB	1111	DRGDRGED-BEEDYTLCTFRKMDIVYKPDWCVEWEDWSVYLFSPENRFRVLQCTIAH	1169
QY	1276	KMFHDVVLVIFILNCITIAMERPKIDPHSAERFPLTSLNIFYTAVFLAEMTKVVALGWC	1335
DB	1170	KLFDYVVLAFIFLNCITIALERQIEAGSTERIFLTVSNIFYTAVFGEMTLKVSLGLY	1229
QY	1336	FGQAYLRSSWNVDGLLLVLSVIDILVSMVSDSGTKILGMLRVLLRLTLRLPLRVSRA	1395
DB	1230	FGQAYLRSSWNVDGLFLVFSIIDIVSLASAGAKILGLVRLVRLRLTLRLPLRVSRA	1289
QY	1396	QGLKLVVETLMSLKPITGNIVLCCAFFIIFGLVQLFKGKFFVCGEDTRITNKSDC	1455
DB	1290	PGKLVVETLMSLKPITGNIVLCCAFFIIFGLVQLFKGKFFVCGEDTRITNKSDC	1349
QY	1456	AEASYRWVRHKYNFDNLGQALMSLFVLASKDGMVDIMYDGLDVGVDVQOPIMHNPMLL	1515
DB	1350	MAANYRWVRHKYNFDNLGQALMSLFVLASKDGMVIMYDGLDVGVDVQOPIMHNPMLL	1409
QY	1516	YFISFLIIVAFVFLNMFVGVVFNHFKCRQHOEERREKRLRLEKRRKAQCKPY	1575
DB	1410	YFISFLIIVSFFFLNMFVGVVFNHFKCRQHOEERREKRLRLEKRRKAQCKPY	1469
QY	1576	YSDYSRFRLLVHLCVTSYLDLFIITGVIGNVVTMAHEVYQOPIIDLEALKINYPITVI	1635
DB	1470	YATYCTRLLHSMCTSHYLDLFIITGVIGNVVTMAHEVYQOPIIDLEALKINYPITVI	1529
QY	1636	FVLESFVLVAFGRFRFFQDRWNQDLAIVLLSIMGITILEEIVNASLPTNPITIRMRV	1695
DB	1530	FVLEAVLKLVAFLGRFRFFQDRWNQDLAIVLLSIMGITILEEIVNASLPTNPITIRMRV	1589

TRANSMEM	172	189	S4 of repeat I (Potential).	FT	CONFLICT	1094	1094	D -> CC (in Ref. 3).
DOMAIN	190	209	Cytoplasmic (Potential).	FT	CONFLICT	1197	1198	SS -> TD (in Ref. 3).
TRANSMEM	210	230	S5 of repeat I (Potential).	FT	CONFLICT	1229	1231	Missing (in Ref. 3).
DOMAIN	231	371	Extracellular (Potential).	FT	CONFLICT	1422	1422	K -> Y (in Ref. 3).
TRANSMEM	372	396	S6 of repeat I (Potential).	FT	CONFLICT	1623	1625	FGM -> SAR (in Ref. 3).
DOMAIN	397	598	Cytoplasmic (Potential).	FT	CONFLICT	1656	1656	S -> T (in Ref. 3).
TRANSMEM	599	619	S1 of repeat II (Potential).	FT	CONFLICT	1737	1737	P -> A (in Ref. 3).
DOMAIN	620	632	Extracellular (Potential).	SQ	SEQUENCE	1835	AA; 205348 MW; E6025E0F1BE80CCA CRC64;	
TRANSMEM	633	654	S2 of repeat II (Potential).					
DOMAIN	655	660	Cytoplasmic (Potential).					
TRANSMEM	661	679	S3 of repeat II (Potential).					
DOMAIN	680	687	Extracellular (Potential).					
TRANSMEM	688	711	S4 of repeat II (Potential).					
DOMAIN	712	722	Cytoplasmic (Potential).					
TRANSMEM	723	743	S5 of repeat II (Potential).					
DOMAIN	744	795	Extracellular (Potential).					
TRANSMEM	796	820	S6 of repeat II (Potential).					
DOMAIN	821	1125	Cytoplasmic (Potential).					
TRANSMEM	1126	1148	S1 of repeat III (Potential).					
DOMAIN	1149	1166	Extracellular (Potential).					
TRANSMEM	1167	1187	S2 of repeat III (Potential).					
DOMAIN	1188	1197	Cytoplasmic (Potential).					
TRANSMEM	1198	1217	S3 of repeat III (Potential).					
DOMAIN	1218	1231	Extracellular (Potential).					
TRANSMEM	1232	1253	S4 of repeat III (Potential).					
DOMAIN	1254	1263	Cytoplasmic (Potential).					
TRANSMEM	1264	1287	S5 of repeat III (Potential).					
DOMAIN	1288	1364	Extracellular (Potential).					
TRANSMEM	1365	1390	S6 of repeat III (Potential).					
DOMAIN	1391	1445	Cytoplasmic (Potential).					
TRANSMEM	1446	1466	S1 of repeat IV (Potential).					
DOMAIN	1467	1480	Extracellular (Potential).					
TRANSMEM	1481	1502	S2 of repeat IV (Potential).					
DOMAIN	1503	1509	Cytoplasmic (Potential).					
TRANSMEM	1510	1528	S3 of repeat IV (Potential).					
DOMAIN	1529	1542	Extracellular (Potential).					
TRANSMEM	1543	1566	S4 of repeat IV (Potential).					
DOMAIN	1567	1580	Cytoplasmic (Potential).					
TRANSMEM	1581	1601	S5 of repeat IV (Potential).					
DOMAIN	1602	1664	Extracellular (Potential).					
TRANSMEM	1665	1692	S6 of repeat IV (Potential).					
DOMAIN	1693	1835	Cytoplasmic (Potential).					
SITE	355	355	Calcium ion selectivity and permeability (By similarity).					
SITE	779	779	Calcium ion selectivity and permeability (By similarity).					
SITE	1339	1339	Calcium ion selectivity and permeability (By similarity).					
SITE	1637	1637	Calcium ion selectivity and permeability (By similarity).					
CARBOHYD	171	171	N-linked (GlcNAc. . .) (Potential).					
CARBOHYD	242	242	N-linked (GlcNAc. . .) (Potential).					
CARBOHYD	309	309	N-linked (GlcNAc. . .) (Potential).					
CARBOHYD	1301	1301	N-linked (GlcNAc. . .) (Potential).					
CARBOHYD	1304	1304	N-linked (GlcNAc. . .) (Potential).					
CONFLICT	193	193	M -> L (in Ref. 3).					
CONFLICT	291	291	C -> V (in Ref. 3).					
CONFLICT	394	394	V -> L (in Ref. 3).					
CONFLICT	406	406	E -> N (in Ref. 3).					
CONFLICT	485	485	D -> Y (in Ref. 3).					
CONFLICT	512	512	C -> S (in Ref. 3).					
CONFLICT	558	558	S -> R (in Ref. 3).					
CONFLICT	683	683	G -> S (in Ref. 3).					
CONFLICT	691	691	F -> S (in Ref. 3).					
CONFLICT	739	740	MH -> ID (in Ref. 3).					
CONFLICT	833	833	C -> Y (in Ref. 3).					
CONFLICT	846	846	F -> L (in Ref. 3).					
CONFLICT	856	856	S -> R (in Ref. 3).					
CONFLICT	905	905	L -> R (in Ref. 3).					
CONFLICT	913	913	M -> YW (in Ref. 3).					
CONFLICT	936	936	W -> G (in Ref. 3).					
CONFLICT	996	996	I -> R (in Ref. 3).					
CONFLICT	1060	1060	I -> M (in Ref. 3).					

FT	CONFLICT	1094	1094	D -> CC (in Ref. 3).
FT	CONFLICT	1197	1198	SS -> TD (in Ref. 3).
FT	CONFLICT	1229	1231	Missing (in Ref. 3).
FT	CONFLICT	1422	1422	K -> Y (in Ref. 3).
FT	CONFLICT	1623	1625	FGM -> SAR (in Ref. 3).
FT	CONFLICT	1656	1656	S -> T (in Ref. 3).
FT	CONFLICT	1737	1737	P -> A (in Ref. 3).
SQ	SEQUENCE	1835	AA; 205348 MW; E6025E0F1BE80CCA CRC64;	

Query Match

Best Local Similarity 45.2%; Score 5383; DB 1; Length 1835;

Best Local Similarity 56.9%; Pred. No. 1.1e-239;

Matches 1139; Conservative 184; Mismatches 344; Indels 336; Gaps 38

QY	27	GAGRGPGSAEKDPGSADSEAG----	LPYPALAPVVFYLLSQDSRPSRWCURTVCN	QY	27	GAGRGPGSAEKDPGSADSEAG----	LPYPALAPVVFYLLSQDSRPSRWCURTVCN
DB	19	GITEQGPGRPPPPPGLEBEPLEGTNPDVPHPLPAVAFCLQRTTSRNCWKIMVCN	DB	19	GITEQGPGRPPPPPGLEBEPLEGTNPDVPHPLPAVAFCLQRTTSRNCWKIMVCN		
QY	83	PERISMLVILLNCVTILQMPRPCEDIACDSORCILQAFDDFI	QY	83	PERISMLVILLNCVTILQMPRPCEDIACDSORCILQAFDDFI		
DB	79	PECVSMVLILLNCVTILQMPRPCEDIACDSORCILQAFDDFI	DB	79	PECVSMVLILLNCVTILQMPRPCEDIACDSORCILQAFDDFI		
QY	143	GKCYLGDTWNRLLDFFITVIAGMLEYSLDLQNVSFSAVTRVRLRLRAINRVESM	QY	143	GKCYLGDTWNRLLDFFITVIAGMLEYSLDLQNVSFSAVTRVRLRLRAINRVESM		
DB	139	GKCYLGDTWNRLLDFFITVIAGMLEYSLDLQNVSFSAVTRVRLRLRAINRVESM	DB	139	GKCYLGDTWNRLLDFFITVIAGMLEYSLDLQNVSFSAVTRVRLRLRAINRVESM		
QY	203	LLDITLPMGLNVLLCFVFFIFIGIVGVQLWAGLLNRCLP	QY	203	LLDITLPMGLNVLLCFVFFIFIGIVGVQLWAGLLNRCLP		
DB	199	LLDITLPMGLNVLLCFVFFIFIGIVGVQLWAGLLNRCLP	DB	199	LLDITLPMGLNVLLCFVFFIFIGIVGVQLWAGLLNRCLP		
QY	263	NEDESPFICSPQRENGMRSCRSVPTLRDGGGGPPCGL-----	QY	263	NEDESPFICSPQRENGMRSCRSVPTLRDGGGGPPCGL-----		
DB	259	EDDEMPFICSLTGDNGIMGHEIPPLKEQ---GRECLSKDDVYFGAGRQDLN	DB	259	EDDEMPFICSLTGDNGIMGHEIPPLKEQ---GRECLSKDDVYFGAGRQDLN		
QY	315	NWQYTYNCAGBNHPFKGAINFDNIGYAWIAIFQVITLEGWVDIMFYVMDAHSF	QY	315	NWQYTYNCAGBNHPFKGAINFDNIGYAWIAIFQVITLEGWVDIMFYVMDAHSF		
DB	316	NWRYNVCRGTGNANPHKGAINFDNIGYAWIAIFQVITLEGWVDIMFYVMDAHSF	DB	316	NWRYNVCRGTGNANPHKGAINFDNIGYAWIAIFQVITLEGWVDIMFYVMDAHSF		
QY	375	FILLIIVGSFFMINCLVVIATQFSTKQREHLMLEQRYLS--SSTVASVAEP	QY	375	FILLIIVGSFFMINCLVVIATQFSTKQREHLMLEQRYLS--SSTVASVAEP		
DB	376	FILLIIVGSFFMINCLVVIATQFSTKQREHLMLEQRYLS--SSTVASVAEP	DB	376	FILLIIVGSFFMINCLVVIATQFSTKQREHLMLEQRYLS--SSTVASVAEP		
QY	435	ELLKYLVIYLRKAARLAQVSAAGVRVGLLSAPLPGQETQPSSSCSRSHRRLSV	QY	435	ELLKYLVIYLRKAARLAQVSAAGVRVGLLSAPLPGQETQPSSSCSRSHRRLSV		
DB	435	EIFQYVCHILRKAKRRALGYALQNR-----	DB	435	EIFQYVCHILRKAKRRALGYALQNR-----		
QY	495	VHEHHHHHHYHLNGTLPRAASPEIQDRDANGSRRLMLPPPTPALSGAPPG	QY	495	VHEHHHHHHYHLNGTLPRAASPEIQDRDANGSRRLMLPPPTPALSGAPPG		
DB	462	-----RQMG-----PGTPA--PAKGP-----	DB	462	-----RQMG-----PGTPA--PAKGP-----		
QY	555	SFVHADCHLEPVRCQAPPPRSPSEASGRVTGSGKVYPTVHTSPPETIK	QY	555	SFVHADCHLEPVRCQAPPPRSPSEASGRVTGSGKVYPTVHTSPPETIK		
DB	478	---HAX---EPSHCKLCPRHPLD-----PTPHTLVQ-----	DB	478	---HAX---EPSHCKLCPRHPLD-----PTPHTLVQ-----		
QY	615	GPPTLTSLNIPGCVSSMHKLEQTOSTGACQSSCKISPCLKADSGACGPD	QY	615	GPPTLTSLNIPGCVSSMHKLEQTOSTGACQSSCKISPCLKADSGACGPD		
DB	505	-----ISAILASD-----PSSCPHQEA	DB	505	-----ISAILASD-----PSSCPHQEA		
QY	673	-----AGAGEVELADREMPDSSEAVVEFTQDAHSDLRDPHSRRQSL	QY	673	-----AGAGEVELADREMPDSSEAVVEFTQDAHSDLRDPHSRRQSL		
DB	524	GRPSGLGSTD--SGQEGSGSGSAEANGDG----LQSSDEGVSSDLGKEE	DB	524	GRPSGLGSTD--SGQEGSGSGSAEANGDG----LQSSDEGVSSDLGKEE		
QY	728	-----FWRLICDTRFKIVDSKYPGRGIMIAILVNTLSMGIEYHEQPELT	QY	728	-----FWRLICDTRFKIVDSKYPGRGIMIAILVNTLSMGIEYHEQPELT		
DB	579	LCGDVWRETRKKLRGIVDSKYFNRMGIMAILVNTVSMGIEHHEQPELT	DB	579	LCGDVWRETRKKLRGIVDSKYFNRMGIMAILVNTVSMGIEHHEQPELT		
QY	784	SLPALEMLLKLAVYGPFGVKNPNYINFDGVIVWISVWEIVCQGGGLSV	QY	784	SLPALEMLLKLAVYGPFGVKNPNYINFDGVIVWISVWEIVCQGGGLSV		
DB	639	SMFALEMLLKAAFGFLDYLRPNPNYINFDGVIVWISVWEIVCQGGGLSV	DB	639	SMFALEMLLKAAFGFLDYLRPNPNYINFDGVIVWISVWEIVCQGGGLSV		
QY	844	LVRFPLAQORQLVLMKTMNDVATFCMLLMFIFFISILGMHLFGCKFASERD	QY	844	LVRFPLAQORQLVLMKTMNDVATFCMLLMFIFFISILGMHLFGCKFASERD		
DB	699	LVRFWPALEQLVLMKTMNDVATFCMLLMFIFFISILGMHLFGCKFASERD	DB	699	LVRFWPALEQLVLMKTMNDVATFCMLLMFIFFISILGMHLFGCKFASERD		

Query Match 45.2%; Score 5383; DB 1; Length 1835;
 Best Local Similarity 56.9%; Pred. No. 1.1e-239;
 Matches 1139; Conservative 184; Mismatches 344; Indels 336; Gaps 38;

QY	27	GAGRRPGSGSAKDPGADSEAG-----LPPALAPVVFYLSQDSRRSCLRTVCMWP	82
DB	19	GITEQPGRPSPPPSPGLEPTEGTFDPVPHDLAPVAFFCLRTQTSPPNNCIKMWCPW	78
QY	83	PERISMLVILNCVTLMGPRCEDIACDSORCRILQAFDFIFAFEAIVEMVKVALGIF	142
DB	79	PECVSMVLVILNCVTLMGYPQDDMECLSRCKLQVDFDFIFFAWEMVKVALGIF	138
QY	143	GKCYLGDWNRLDFFIVIAAGMEYSLDLQVSPSAVTRVRLRLRAINRVPMSRLIVT	202
DB	139	GKCYLGDWNRLDFFIVIAAGMEYSLDLQVSPSAVTRVRLRLRAINRVPMSRLIVN	198
QY	203	LLLDLTLMLGNVLLCFVFFIGVIGVQLWAGLLNRCLPENFSLPLSVDLERYQTE	262
DB	199	LLLDLTLMLGNVLLCFVFFIGVIGVQLWAGLLNRCLPENFSLPLSVDLERYQTE	258
QY	263	NEDESPFICSPRENGMRSRCSVPTLRDGGGGPPCGL-----DYAYNSSNTT--CV	314
DB	259	EDDEMPFICSLTGNGIMGHEIPPLKQ---GRECCSKDDVDYDFGAGQDLNASGLCV	315
QY	315	NWQYTNCSAGBNHPKGAINFNDNIGYAMIAIQVITLEGWVDIMYFVMDAISFYNYIY	374
DB	316	NWRYNVNCRGTGNANPHKGAINFNDNIGYAMIVIFQVITLEGWVEIMYVMDAISFYNYIY	375
QY	375	FILLIIVGSFFMINCLVIVATOPSETKQBSQMRQRVRLSNASTLASFEPSGCYE	434
DB	376	FILLIIVGSFFMINCLVIVATOPSETKQBSQMRQRVRLSNASTLASFEPSGCYE	434
QY	435	ELLKYLVIILKKAARLAQVSRAGVRLGSLSPALPGQETQPSSCSRSHRLSVHHL	494
DB	435	EIFQYVCHILRKAKRRALGLYQALQNR-----RQMG-----PGTA--PAKEGP	461
QY	495	VHEHHHHHHYHLNGTGLRAPRASPIQDRDANGSRRLMLPPSTPALSGAPPGEASVH	554
DB	462	-----RQMG-----PGTA--PAKEGP-----	477
QY	555	SFYHADCHLEPVRCQAPPPSPSEASGRVVGSKVYPTVHTSPPTLKEKALVEVAAS	614
DB	478	---HAX---EPSCKLCPRHPLD-----PTPHTLVQP-----	504
QY	615	GPPTLTSLNIPPGPYSSMKLLETQSTGACQSSCKTSSPCLKADSGACGPDSCPYCAR--	672
DB	505	-----ISAILASD-----PSSCPHCQHEA	523
QY	673	---AGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRRQRSLGSDAPSSVLA-	727
DB	524	GRRPSGLGSTD--SGQBSGSGSGSAEANGDG---LQSEDCVSSDLGKEEEDGAAR	578
QY	728	----FWLLICDTFKIVDSKYFGRGIMAILNVTLSMGIEYHEQPELNALEISNIVFT	783
DB	579	LCGDVNRTRKKLRGIVDSKYFNRGIMAILNVTLSMGIEYHEQPELNALEISNIVFT	638
QY	784	SLFALEMLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRFLMRVLK	843
DB	639	SNFALEMLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRFLMRVLK	698
QY	844	LVRFLPALQRIQVLMKTMNDNVATFCMLIMLFIPIFSLGMELFGCKPASERD--GDTLPD	902
DB	699	LVRFPALRRQLVLMKTMNDNVATFCMLIMLFIPIFSLGMELFGCKPASERD--GDTLPD	758

QY 903 RKNFDSLLWAVTVFQILTOEDWNVLYNGMASTSSAAALYFIALMTGNYVLENLVAI 962
Db 759 RKNFDSLLWAVTVFQILTOEDWNVLYNGMASTTPWASLYFVALTFGNVLFNLLVAI 818
QY 963 LVEGQAEIKREDASQLSQILQVPVDSQGDANKSRSEDPFFSPS-----LDG 1012
Db 819 LVEGQAE-----GDNRSCSDEDDQSSNLEEDPKLPEGLDN 855
QY 1013 DGRKKCLALVSLGEPHPELKSLLPPLIHTAATPMSLPKSTSTGLGALGPA-SRRTS 1071
Db 856 SRDLKCLPMPNGH-----LDP-----LGAHLGPAAGTMGAP 892
QY 1072 SGSABPG-----AAHEMKSPPSARSPHSPWGAASWTSRRSRNSL 1113
Db 893 RLSLQDPFVLVALDSRKSVMSLGRMSYDQSLSSRSYYGPWRSRGTWARRSWN-- 950
QY 1114 GRAPLSKRSPGRRSLSGEQSODEE-BSSBEE--RASPGASDH----- 1158
Db 951 ----SLKHPFSAEHESLLSGEGGCVACAGAREEAPRTAPLHAPHAAHAGPHLA 1006
QY 1159 ----RHRSLEBAKSSFDLPOTLQVGLHRTAS--GRGSAHQDCNGKSASGLARAL 1212
Db 1007 HSHRRHRTLSLDRDSVDLGLBFLVVGAAHRAWRGAGQAPGHEDCNGRMPNIAKV 1066
QY 1213 RPDPLDGDADDDEGNLSKGRVRAWTPARLPACVLERDSAYIFPPQSRFRLLCHRI 1272
Db 1067 KMDDRDRGED-EEEDYTLCLFRVRKMDIVYKPCWEVREDMSVLYFSENFRLCQTI 1125
QY 1273 ITHKMFHVLVIIIFLNCITIAMERPKIDPHSAERIFLTSNYIFTAVFAEMTVKVAL 1332
Db 1126 IAKHLDYVVLAFIFLNCITIALERPOIEAGSTERIFLTVSNYIFTAVFVGMETLKVSL 1185
QY 1333 GMCPEQAYLRSSNNVLDGLLIVSIDILVMSVSDSGTKILGNLVLRLTLRLRVI 1392
Db 1186 GLYFGEQAYLRSSNNVLDGLFVSVIIDIWVSASAGAKILGLVRLTLRLRVI 1245
QY 1393 SRAQGLKVVETLMSLKPIGNIVLCCAFFIIFGLVQLFKGFVQCGEDTRNITNK 1452
Db 1246 SRAPGKLVVETLISLKPIGNIVLCCAFFIIFGLVQLFKGPKYHCLGVDTRNITNR 1305
QY 1453 SDCAEASVWRHRYNFDNLGQALMSLFLVLSKDGWVDIMYDGLDVGVDQOPIMHNPW 1512
Db 1306 SDCAVANYWRHRYNFDNLGQALMSLFLVLSKDGWVIMYDGLDVGVDQOPIMHNPW 1365
QY 1513 MLIYFTSFLIIVAFVNLVFGVVENFHKROHQOEERARRRERKLEKRRKAQC 1572
Db 1366 MLIYFTSFLIIVFVNLVFGVVENFHKROHQOEERARRRERKLEKRRKAQR 1425
QY 1573 KPYSDYSRFLVHLCTSHYLDLFTITVIGLVNVTMAEHYQQPQILDEALKICNYIF 1632
Db 1426 LPYATYCTRLLIHSWCTSHYLDLFTITVIGLVNVTMAEHYQQPQILDEALKICNYIF 1485
QY 1633 TVIFVLESFVKLVAFGRFRFQDRWQOLDIAVLLSIMGITLLEEIVNASLPINPTIIRI 1692
Db 1486 TVIFVLEAVLKVAFGLRFRFQDRWQOLDIAVLLSIMGITLLEEIVNASLPINPTIIRI 1545
QY 1693 MRVLRARVLKLMVAGRRALDVTQVALPOVGNLGLLFWLFFFAALGVELFGDEC 1752
Db 1546 MRVLRARVLKLMVAGRRALDVTQVALPOVGNLGLLFWLFFFAALGVELFGKLVC 1605
QY 1753 DETHPCBGLGRHATFRNFGMAFTLPRVSTGDNWNGIMKDTLRDC-DOESTCYNTV--IS 1809
Db 1606 NDENPCBGRHATFRNFGMAFTLPRVSTGDNWNGIMKDTLRDC-DOESTCYNTV--IS 1665
QY 1810 PIYFVSFVLTAQFVLVNVVIAVLMKHLBESNKAKAEABAELELEM-KTILSPQHSPL 1868
Db 1666 PIYFVSFVLTAQFVLVNVVIAVLMKHLBESNKAKAEABAELELEM-KTILSPQHSPL 1721
QY 1869 GSPLFWQVEGDPSPDKPCGALHPAAHARSASHFSLEHPTMQPHTLPGDPLLTIV-- 1925
Db 1722 ----GCPG-----FCPCPCPCFCPLPTSSPG 1747
QY 1926 ---RKSGVSRTHSLFNDSYMCRH 1945

Db 1748 APERGSGGAGAGG-DTSHLGRH 1769
RESULT 15
Q7Z6S8 PRELIMINARY; PRT; 1994 AA.
ID Q7Z6S8
AC Q7Z6S8;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE DJ172B20.1 (Calcium channel, voltage-dependent, alpha 1I subunit)
DE (Fragment).
GN Name=CACNA1I;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Phillips S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022319; CAD92537.1; .
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na.pore.
DR InterPro; IPR002111; Cat channel TrpL.
DR InterPro; IPR000345; Cytochrome_B5.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans; 4.
DR PROSITE; PS00190; Cytochrome_C; UNKNOWN 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1
SQ SEQUENCE 1994 AB; 220004 MW; A5BFAE5FA32DCF76 CRC64;
Query Match 40.6%; Score 4836; DB 2; Length 1994;
Best Local Similarity 49.8%; Pred. No. 2e-214;
Matches 1117; Conservative 188; Mismatches 484; Indels 456; Gaps 55;
QY 197 MRILVTLTLDLTPMLGNVLLCFVFFIIGVQVWAGLLNRRCFLPENFSLPLVDLE 256
Db 1 MRILVTLTLDLTPMLGNVLLCFVFFIIGVQVWAGLLNRRCFLPENFSLPLVDLE 60
QY 257 RYQVTEDESPICSPRENGMRSCSVPTLRGCGGGPPCGL-----DYEAYNSSN 310
Db 61 PYQPEDDEMFICSLSGDNGIMGCHETPLKEQ---GRECCLSKDDVDFGAGRQDLN 117
QY 311 TT--CVNNQYNTCSAGEHNPFGKAINFDNTIGYAMIAIPQVITLGGWIDIMYVMDAHS 368
Db 118 ASGLCVNNRYNVCRTGSANPHKGAINFEDNIGYAMIVIPQVITLGGWIDIMYVMDAHS 177
QY 369 FYNFIYFILLIIVGSFPMINLCVVIATOFSETKORESOLMRQRVRFSLNASTLASFSE 428
Db 178 FYNFIYFILLIIVGSFPMINLCVVIATOFSETKQREHRLMLQEQRYLS-SSTVASYAE 236
QY 429 PGSCYBEELKLVYLKRAARLAQVSRAGVRLSSPAPLGGQFTQPSSSCSRSHRR 488
Db 237 PGSCYBEIYQVCHILRKAKR-----RALGLYQALQSRQALG----- 274
QY 489 LSVHHLVHHHHHHHHHGLNGLTIRAPRASPEIQDRDANGSRRLMLPPPSTPALSAPP 548
Db 275 -----PAAPA--PAKP 284
QY 549 GABSVHSFYHADCHLEPVRQAPPSPSPSEASGRVTGSGKVYVTVHTSPPTILKEKALV 608
Db 285 P-----FAK---EPHQLCFQSPDATHTL-----VQPIPAL----- 317
QY 609 EVAASGPTLITSLNPPPGPYSSMHKILETQSTGACOSSCKISSPCLKADSGAGCPDSCP 668
Db 318 -----ASDPASCP 325

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:41 ; Search time 40.3132 Seconds
(without alignments)
3727.727 Million cell updates/sec

Title: US-09-611-257A-37

Perfect score: 11904

Sequence: 1 MDEEDGAGAEESGQPRSPM.....PKKDVLSLSGLSDPADLDP 2366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCUTS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	11862.5	99.7	2273	3	US-09-426-998-5
2	6315.5	53.1	1207	4	US-09-398-522-52
3	6211	52.2	2353	3	US-08-984-709A-50
4	5492.5	46.1	2175	3	US-09-404-650-2
5	5492.5	46.1	2175	4	US-09-935-541-2
6	5484	46.1	2188	3	US-09-404-650-4
7	5484	46.1	2188	4	US-09-935-541-4
8	5366	45.1	1835	3	US-09-404-650-5
9	5366	45.1	1835	4	US-09-935-541-5
10	1750.5	14.7	2343	3	US-08-268-163-4
11	1749	14.7	2337	3	US-08-713-118-2
12	1749	14.7	2337	1	US-08-452-007-2
13	1748.5	14.7	2339	3	US-08-455-543A-47
14	1748.5	14.7	2339	2	US-08-223-305C-47
15	1746.5	14.7	2339	3	US-08-268-163-6
16	1743	14.6	2237	1	US-08-455-543A-48
17	1743	14.6	2237	3	US-08-223-305C-48
18	1741	14.6	2237	3	US-09-268-163-8
19	1722	14.5	2336	3	US-09-268-163-10
20	1632.5	13.7	1873	1	US-08-435-675B-4
21	1622.5	13.6	1873	1	US-08-336-257A-7
22	1619.5	13.6	1984	3	US-08-836-325-10
23	1619.5	13.6	1984	4	US-09-457-571-10
24	1619.5	13.6	1985	4	US-09-495-714C-6
25	1616	13.6	1872	6	5386025-6
26	1615.5	13.6	1989	3	US-08-836-325-12
27	1615.5	13.6	1989	4	US-09-457-571-12

ALIGNMENTS

RESULT 1

US-09-426-998-5
; Sequence 5, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYAT, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: BRANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
; FILE REFERENCE: CHANNEL (ALPHAIG-C)
; CURRENT APPLICATION NUMBER: US/09/426.998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 5
; LENGTH: 2273
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-426-998-5

Query Match	99.7%	Score 11862.5;	DB 3;	Length 2273;
Best Local Similarity	99.4%	Pred. No. 0;		
Matches 2260;	Conservative	4;	Mismatches	2;
			Indels	7;
			Gaps	1;
QY	1	MDEEDGAGAEESGQPRSPMRLNDLSGAGGPGGSAEKDPGSADSEAGLPYPALAPVV	60	
Db	1	MDEEDGAGAEESGQPRSPMRLNDLSGAGGPGGSAEKDPGSADSEAGLPYPALAPVV	60	
QY	61	FFVLSQDSRPSRCLRTVCNPFERISMLVILNCVLTGMFRPCEDTACDSQRILQAF	120	
Db	61	FFVLSQDSRPSRCLRTVCNPFERISMLVILNCVLTGMFRPCEDTACDSQRILQAF	120	
QY	121	DDFIFAFFAVEMVKVAGLIGFKKCYLGDWNRDFFVIVAGLMLEYSLDLQNVFSAVR	180	
Db	121	DDFIFAFFAVEMVKVAGLIGFKKCYLGDWNRDFFVIVAGLMLEYSLDLQNVFSAVR	180	
QY	181	TVRVLRLPRAINRVSRLVTLVLLDTPMLGNVLLCFVFFIFGIVGVLWAGLLNR	240	
Db	181	TVRVLRLPRAINRVSRLVTLVLLDTPMLGNVLLCFVFFIFGIVGVLWAGLLNR	240	
QY	241	CFLPENFSLPLSVDLERYQTENEDESPICSPQRENGMRSRCSVPTLRGDGGGPPCGL	300	
Db	241	CFLPENFSLPLSVDLERYQTENEDESPICSPQRENGMRSRCSVPTLRGDGGGPPCGL	300	
QY	301	DYEATNSSNTTCVNNQYTNCSAGEHNPFGKAINFNIGNIYAWIAIFQVITLEGWVDM	360	
Db	301	DYEATNSSNTTCVNNQYTNCSAGEHNPFGKAINFNIGNIYAWIAIFQVITLEGWVDM	360	

QY	361	YFVMDAHGFYNFIYFILLIIVGSPFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNA	420
Db	361	YFVMDAHGFYNFIYFILLIIVGSPFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNA	420
QY	421	STLASFSBPGSCYEBLLKYLVTILKKAARLQAQVSRAAQVRVGLLSSPAPLGGQETQPS	480
Db	421	STLASFSBPGSCYEBLLKYLVTILKKAARLQAQVSRAAQVRVGLLSSPAPLGGQETQPS	480
QY	481	SCSRSHRLSVHHLVHHHHHHHHVHLGNGTILRAPRASPEIQORDANGSRRLMLPPSTP	540
Db	481	SCSRSHRLSVHHLVHHHHHHHHVHLGNGTILRAPRASPEIQORDANGSRRLMLPPSTP	540
QY	541	ALSGAPPGCAESVHSFYHADCHLEPVRCAQPPRSPSEASGRITVSGKYPTVHTSPDPE	600
Db	541	ALSGAPPGCAESVHSFYHADCHLEPVRCAQPPRSPSEASGRITVSGKYPTVHTSPDPE	600
QY	601	TLKEKALVEVAASSGPPILTSLNIPPGYSSMHKLELTQSTGACOSSCKISSFCLKADSG	660
Db	601	TLKEKALVEVAASSGPPILTSLNIPPGYSSMHKLELTQSTGACOSSCKISSFCLKADSG	660
QY	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRORSGLGDA	720
Db	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRORSGLGDA	720
QY	721	EPSSVLAPWRILCOTFRKXIVDSKYFGRGIMIAILLVNTLSMGIEYHEQEPEELTNALEISNI	780
Db	721	EPSSVLAPWRILCOTFRKXIVDSKYFGRGIMIAILLVNTLSMGIEYHEQEPEELTNALEISNI	780
QY	781	VFTSLFALEMLKLLVVGPGYIKNPYNIIPGVIVVISWEIVGQGGGLSVLRTFLMR	840
Db	781	VFTSLFALEMLKLLVVGPGYIKNPYNIIPGVIVVISWEIVGQGGGLSVLRTFLMR	840
QY	841	VKLVRFLPALQRLVLMKTMNDVATFCMLMLFIFITSLGWHLFCKEFASEBDGTL	900
Db	841	VKLVRFLPALQRLVLMKTMNDVATFCMLMLFIFITSLGWHLFCKEFASEBDGTL	900
QY	901	PDRKNFSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVFLNLLV	960
Db	901	PDRKNFSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVFLNLLV	960
QY	961	AILVEGFQAEIISKREDASGOLSCIOIPVDSQGDANKSEBEPFSPSLDGDGRKKCL	1020
Db	961	AILVEGFQAEIISKREDASGOLSCIOIPVDSQGDANKSEBEPFSPSLDGDGRKKCL	1020
QY	1021	ALVSLGEHPELRKSLPLLIHTAATPMSLPKSTGTGLGALGPASRRTSSSGSAEPGAA	1080
Db	1021	ALVSLGEHPELRKSLPLLIHTAATPMSLPKSTGTGLGALGPASRRTSSSGSAEPGAA	1080
QY	1081	HEMKSPSPASRSPHSPPWASAASWTSRRSSNLSGRAPSLKRRSPSGERRSLLSGEGESQ	1140
Db	1081	HEMKSPSPASRSPHSPPWASAASWTSRRSSNLSGRAPSLKRRSPSGERRSLLSGEGESQ	1140
QY	1141	DEEESSEERASPAGSDHRRHGSLEPAKSSFDLPDTLQVPGLHRTASRGSAASEHQDCN	1200
Db	1141	DEEESSEERASPAGSDHRRHGSLEPAKSSFDLPDTLQVPGLHRTASRGSAASEHQDCN	1200
QY	1201	GKSASGRALARLPDDPPLTDGDDADDEGNLSKGERVRAWIRARLPACYLBERDSWSAYIFP	1260
Db	1201	GKSASGRALARLPDDPPLTDGDDADDEGNLSKGERVRAWIRARLPACYLBERDSWSAYIFP	1260
QY	1261	POSREFLLCHRIITHKOFDHHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1320
Db	1261	POSREFLLCHRIITHKOFDHHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1320
QY	1321	FLAEMTVKVVALGCWCFGEQAYLRSSNNVLDGLLVLISVDILVSMVSDSGTKILGMLRVL	1380
Db	1321	FLAEMTVKVVALGCWCFGEQAYLRSSNNVLDGLLVLISVDILVSMVSDSGTKILGMLRVL	1380
QY	1381	RLRLTLRPLRVISRAQGLKLVVETLMSLLKPIGNVIVICAPPIIFGLIGVOLFKGKFFV	1440
Db	1381	RLRLTLRPLRVISRAQGLKLVVETLMSLLKPIGNVIVICAPPIIFGLIGVOLFKGKFFV	1440

QY	1441	COGEDTRNITNKSCAEEASYEWVSHKYNFNDNLGQALMSLFLVLAASKGWVDIMYDGLDVG	1500
Db	1441	COGEDTRNITNKSCAEEASYEWVSHKYNFNDNLGQALMSLFLVLAASKGWVDIMYDGLDVG	1500
QY	1501	VDQQPIMHNPNWMLLYFTISLLIYVAFVLNFWFVUVVFNPHKCRHQHEEBAARRBEKRL	1560
Db	1501	VDQQPIMHNPNWMLLYFTISLLIYVAFVLNFWFVUVVFNPHKCRHQHEEBAARRBEKRL	1560
QY	1561	RLLEKRR-----KAQCKPYGYDYSRFRLLVHHLCTSHYLDLFTIGVILGNVVTWAME	1613
Db	1561	RLLEKRRSKQWAEQAQCKPYGYDYSRFRLLVHHLCTSHYLDLFTIGVILGNVVTWAME	1620
QY	1614	HYQOQILDEALKICNVIFTVIFVLESVFKLVAFGFRFRFQDRWNOLDLAILLSIMGIT	1673
Db	1621	HYQOQILDEALKICNVIFTVIFVLESVFKLVAFGFRFRFQDRWNOLDLAILLSIMGIP	1680
QY	1674	LEEIEVNASLPINPTIIRIMVLRARIARVLKLLKMAVGMRAALDITVMOALPOVCNGLLPM	1733
Db	1681	LEQIEVNASUPINPTIIRIMVLRARIARVLKLLKMAVGMRAALDITVMOALPOVCNGLLPM	1740
QY	1734	LLFTIFAALGVELPGDLCEDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT	1793
Db	1741	LLFTIFAALGVELPGDLCEDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT	1800
QY	1794	LRDCDQESTCNTVISPITYFVSFLTAQFVLNVNVTAVLMKHLAESNKAKEABELEAL	1853
Db	1801	LRDCDQESTCNTVISPITYFVSFLTAQFVLNVNVTAVLMKHLAESNKAKEABELEAL	1860
QY	1854	ELEMKTLSPQFHSPLGSPFFLWPGVEGDFSPDKPGALHPAAHARSASHFSLEHTMTQPH	1913
Db	1861	ELEMKTLSPQFHSPLGSPFFLWPGVEGDFSPDKPGALHPAAHARSASHFSLEHTMTQPH	1920
QY	1914	PTELPGDILLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLGHRGWLKPAQSGSVLSVHS	1973
Db	1921	PTELPGDILLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLGHRGWLKPAQSGSVLSVHS	1980
QY	1974	QPADTSYILQPKDAPHLLOPHSAPTWGTIPKLPPEGSRSLAQRLRQCAAIRTDSLQVQ	2033
Db	1981	QPADTSYILQPKDAPHLLOPHSAPTWGTIPKLPPEGSRSLAQRLRQCAAIRTDSLQVQ	2040
QY	2034	GLGSRDILLAEVGGSPFPIARAYSFWGQSTQAOQHSRSHSKISKXHTPTTAPFCGPEPNW	2093
Db	2041	GLGSRDILLAEVGGSPFPIARAYSFWGQSTQAOQHSRSHSKISKXHTPTTAPFCGPEPNW	2100
QY	2094	GKGFPETRSLDLDTLSWISGDLPLPGQOEPPSPRDLKKCYSVBAQSCORRTSMUDE	2153
Db	2101	GKGFPETRSLDLDTLSWISGDLPLPGQOEPPSPRDLKKCYSVBAQSCORRTSMUDE	2160
QY	2154	QRHSTIAVCLDSGSOPLHGTDPNSLGGQPLGGPGSRPKKLSPPSITIDPPHSQGRPTP	2213
Db	2161	QRHSTIAVCLDSGSOPLHGTDPNSLGGQPLGGPGSRPKKLSPPSITIDPPHSQGRPTP	2220
QY	2214	PSPGICLRRRAPSSDSKOPLAGSPDSSMAASFPKDVLSLGLSSDFADLDP	2266
Db	2221	PSPGICLRRRAPSSDSKOPLAGSPDSSMAASFPKDVLSLGLSSDFADLDP	2273

RESULT 2

US-09-398-522-52

; Sequence 52, Application US/09398522

; Patent No. 6783933

; GENERAL INFORMATION:
: APPLICANT: ISSU: IS

APPLICANT: Issa, Jean-Pierre
TITLE OF INVENTION: CACNAIC

1. TITLE OF INVENTION: CACNAIG POLYNUCLEOTIDE POLYPEPTIDE AND
2. TITLE OF INVENTION: METHODS OF USE THEREOF

FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JH01590

; CURRENT APPLICATION NUMBER

; CURRENT FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 120

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; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 52
: LENGTH: 1307

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; LENGTH: 1207
; TYPE: ppt

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THA: EAT

